

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f61a_	Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
2	c3i4eA_	Alignment		100.0	67	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
3	d1dqua_	Alignment		100.0	40	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
4	c5e9fD_	Alignment		100.0	40	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
5	d1igwa_	Alignment		100.0	61	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
6	c3e5bB_	Alignment		100.0	65	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
7	c3eolB_	Alignment		100.0	56	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.0a crystal structure of isocitrate lyase from brucella melitensis2 (p43212)
8	c6g1oA_	Alignment		100.0	31	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: structure of pseudomonas aeruginosa isocitrate lyase, icl
9	c5uncB_	Alignment		100.0	23	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	31	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
11	d1muma_	Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like

12	c3b8fF_	Alignment		100.0	24	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+.
13	c3ih1A_	Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
14	c3fa4D_	Alignment		100.0	27	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
15	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
16	c3lyeA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
17	c2hjpA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
18	d1ujqa_	Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
19	d1s2wa_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
20	c4lsbA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
21	c2qiwa_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
22	c2ze3A_	Alignment	not modelled	100.0	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
23	c4mg4G_	Alignment	not modelled	100.0	28	PDB header: unknown function Chain: G: PDB Molecule: phosphonmutase; PDBTitle: crystal structure of a putative phosphonmutase from burkholderia2 cenocepacia j2315
24	d1m3ua_	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
25	c3ez4B_	Alignment	not modelled	99.9	19	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	99.9	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
27	d1o66a_	Alignment	not modelled	98.4	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
28	c2p10D_	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a

					resolution
29	c6daqA	Alignment	not modelled	97.1	18 PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
30	c5afdA	Alignment	not modelled	97.1	18 PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: native structure of n-acetylneuraminase lyase (sialic acid aldolase)2 from aliiivibrio salmonicida
31	c3daqB	Alignment	not modelled	97.0	17 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
32	c3si9B	Alignment	not modelled	97.0	15 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
33	d1o5ka	Alignment	not modelled	97.0	17 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
34	d2p10a1	Alignment	not modelled	96.8	20 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MI19387-like
35	c3lerA	Alignment	not modelled	96.8	18 PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
36	d2a6na1	Alignment	not modelled	96.8	21 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
37	c2yxqD	Alignment	not modelled	96.8	22 PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
38	c4n4qD	Alignment	not modelled	96.7	19 PDB header: lyase Chain: D: PDB Molecule: acylneuraminase lyase; PDBTitle: crystal structure of n-acetylneuraminase lyase from mycoplasma2 synoviae, crystal form ii
39	c4i7vD	Alignment	not modelled	96.7	21 PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhdp5 with pyruvate
40	c5c54D	Alignment	not modelled	96.7	24 PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminase lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
41	c2r8wB	Alignment	not modelled	96.7	20 PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
42	c4ur7B	Alignment	not modelled	96.6	19 PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
43	c2rfqB	Alignment	not modelled	96.6	21 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
44	c6mqhA	Alignment	not modelled	96.6	18 PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
45	c3g0sA	Alignment	not modelled	96.6	21 PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
46	c3cprB	Alignment	not modelled	96.6	21 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
47	c3s5oA	Alignment	not modelled	96.6	19 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
48	c3na8A	Alignment	not modelled	96.6	15 PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
49	c3noeA	Alignment	not modelled	96.5	20 PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
50	c3fluD	Alignment	not modelled	96.5	22 PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
51	c4ah7C	Alignment	not modelled	96.5	17 PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
52	c6daoB	Alignment	not modelled	96.4	21 PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
53	c3fkka	Alignment	not modelled	96.4	15 PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
54	c3h5dD	Alignment	not modelled	96.4	18 PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase;

54	c1b0bB	Alignment	not modelled	96.4	18	PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae PDB header: lyase
55	c5ud6B	Alignment	not modelled	96.4	19	Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhcps from cyanidioschyzon merolae with lysine2 bound
56	c4icnB	Alignment	not modelled	96.4	22	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
57	c4n6eA	Alignment	not modelled	96.4	17	PDB header: lyase/biosynthetic protein Chain: A; PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
58	c3b4uB	Alignment	not modelled	96.4	16	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
59	c3d0cB	Alignment	not modelled	96.3	13	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
60	c3pueA	Alignment	not modelled	96.3	23	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
61	c4nq1B	Alignment	not modelled	96.3	21	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
62	c4dppB	Alignment	not modelled	96.3	17	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase 2, chloroplastic; PDBTitle: the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
63	c3e96B	Alignment	not modelled	96.3	13	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
64	c4zqrD	Alignment	not modelled	96.2	24	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
65	c5kt1A	Alignment	not modelled	96.2	21	PDB header: lyase Chain: A; PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
66	c3lciA	Alignment	not modelled	96.1	17	PDB header: lyase Chain: A; PDB Molecule: n-acetylneuraminase lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
67	c3qfeB	Alignment	not modelled	96.1	14	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
68	c3eb2A	Alignment	not modelled	96.1	23	PDB header: lyase Chain: A; PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
69	c5ismF	Alignment	not modelled	96.1	22	PDB header: oxidoreductase Chain: F; PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
70	c3ffsC	Alignment	not modelled	96.1	22	PDB header: oxidoreductase Chain: C; PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
71	d1f74a	Alignment	not modelled	96.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	c2nuxB	Alignment	not modelled	96.0	10	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
73	d1xxxa1	Alignment	not modelled	96.0	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
74	c2v9dB	Alignment	not modelled	96.0	22	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
75	c2vc6A	Alignment	not modelled	95.8	21	PDB header: lyase Chain: A; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. melloti with pyruvate bound
76	d1w3ia	Alignment	not modelled	95.8	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
77	d1xkya1	Alignment	not modelled	95.7	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
78	c4xkyC	Alignment	not modelled	95.7	23	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
						PDB header: lyase

79	c5ui3C_	Alignment	not modelled	95.7	17	Chain: C; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from chlamydomonas reinhardtii
80	c3n2xB_	Alignment	not modelled	95.5	24	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
81	c4af0B_	Alignment	not modelled	95.5	21	PDB header: oxidoreductase Chain: B; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
82	c1jcnA_	Alignment	not modelled	95.5	19	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
83	c6h4eB_	Alignment	not modelled	95.4	16	PDB header: lyase Chain: B; PDB Molecule: putative n-acetylneuraminate lyase; PDBTitle: proteus mirabilis n-acetylneuraminate lyase
84	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
85	d1xm3a_	Alignment	not modelled	95.4	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
86	c3bw2A_	Alignment	not modelled	95.3	23	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
87	c4mjmD_	Alignment	not modelled	95.2	17	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
88	c4fxsA_	Alignment	not modelled	95.2	17	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
89	c1zfa_	Alignment	not modelled	95.1	19	PDB header: oxidoreductase Chain: A; PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
90	c1me9A_	Alignment	not modelled	95.1	23	PDB header: oxidoreductase Chain: A; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
91	d1zfa1	Alignment	not modelled	95.0	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
92	c4uxdC_	Alignment	not modelled	95.0	16	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
93	d1pvna1	Alignment	not modelled	94.8	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
94	c5z9yB_	Alignment	not modelled	94.7	19	PDB header: transferase Chain: B; PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
95	c2rdtA_	Alignment	not modelled	94.7	24	PDB header: oxidoreductase Chain: A; PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
96	c1kbiB_	Alignment	not modelled	94.7	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
97	d1goxa_	Alignment	not modelled	94.6	23	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	d1tb3a1	Alignment	not modelled	94.6	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
99	c5upxA_	Alignment	not modelled	94.5	18	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
100	c4ff0B_	Alignment	not modelled	94.5	18	PDB header: oxidoreductase Chain: B; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
101	d1jr1a1	Alignment	not modelled	94.4	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
102	c6hkaA_	Alignment	not modelled	94.4	14	PDB header: oxidoreductase Chain: A; PDB Molecule: nitronate monooxygenase;

102	c00k8A	Alignment	not modelled	94.4	14	PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus PDB header: lyase
103	c2ehhE	Alignment	not modelled	94.3	18	Chain: E; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
104	d1p4ca	Alignment	not modelled	94.2	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
105	c4xtiA	Alignment	not modelled	94.2	20	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
106	c3khjE	Alignment	not modelled	94.1	18	PDB header: oxidoreductase Chain: E; PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
107	c1vrda	Alignment	not modelled	94.0	26	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
108	c3bi8A	Alignment	not modelled	94.0	18	PDB header: lyase Chain: A; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
109	c4mz1A	Alignment	not modelled	94.0	18	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
110	c6arhA	Alignment	not modelled	93.9	18	PDB header: lyase Chain: A; PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: crystal structure of human nal at a resolution of 1.6 angstrom
111	c3bo9B	Alignment	not modelled	93.8	21	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
112	d1hl2a	Alignment	not modelled	93.8	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
113	d1vr6a1	Alignment	not modelled	93.6	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
114	c2htmB	Alignment	not modelled	93.6	14	PDB header: biosynthetic protein Chain: B; PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
115	d1eepea	Alignment	not modelled	93.6	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
116	d1jcna1	Alignment	not modelled	93.5	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
117	c3tsdA	Alignment	not modelled	93.5	18	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
118	c2r94B	Alignment	not modelled	93.5	18	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
119	c6a0gA	Alignment	not modelled	93.4	23	PDB header: flavoprotein Chain: A; PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
120	c4q33F	Alignment	not modelled	93.4	20	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