

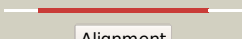













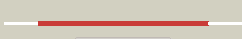







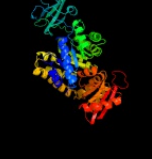








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1617_(pykA)_1816196_1817614
Date	Fri Aug 2 13:30:21 BST 2019
Unique Job ID	fb20b4546ca96fb2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ws9C_	 Alignment		100.0	100	PDB header: transferase Chain: C; PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase (pyk) from mycobacterium tuberculosis in complex with 2 oxalate, atp and allosteric activator amp
2	c2e28A_	 Alignment		100.0	42	PDB header: transferase Chain: A; PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
3	c3t07D_	 Alignment		100.0	39	PDB header: transferase/transferase inhibitor Chain: D; PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
4	c1t5aB_	 Alignment		100.0	37	PDB header: transferase Chain: B; PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
5	c1aqfB_	 Alignment		100.0	37	PDB header: transferase Chain: B; PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
6	c3e0vB_	 Alignment		100.0	36	PDB header: transferase Chain: B; PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
7	c6du6D_	 Alignment		100.0	37	PDB header: transferase Chain: D; PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of the pyruvate kinase (pk1) from the mosquito aedes2 aegypti
8	c3ma8A_	 Alignment		100.0	35	PDB header: transferase Chain: A; PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
9	c1a3wB_	 Alignment		100.0	35	PDB header: transferase Chain: B; PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
10	c1pkIB_	 Alignment		100.0	36	PDB header: transferase Chain: B; PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
11	c3eoeC_	 Alignment		100.0	36	PDB header: transferase Chain: C; PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007

12	c2vgbB	Alignment		100.0	37	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
13	c3khdA	Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
14	c1e0tD	Alignment		100.0	39	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
15	c3qtgA	Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
16	c4imaD	Alignment		100.0	37	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: the structure of c436m-hlpyk in complex with citrate/mn/atp/fru-1,6-bp
17	c4fxjB	Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
18	c3khdC	Alignment		100.0	43	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
19	d1pkla2	Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
20	d2g50a2	Alignment		100.0	50	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
21	d1a3xa2	Alignment	not modelled	100.0	49	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
22	d1liua2	Alignment	not modelled	100.0	45	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
23	d1e0ta2	Alignment	not modelled	100.0	48	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
24	d1liua3	Alignment	not modelled	100.0	22	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
25	d2g50a3	Alignment	not modelled	100.0	20	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
26	d1e0ta3	Alignment	not modelled	100.0	29	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
27	d1pkla3	Alignment	not modelled	100.0	20	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
28	d1a3xa3	Alignment	not modelled	99.9	20	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
29	d2g50a1	Alignment	not modelled	99.9	32	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like

					Family: Pyruvate kinase beta-barrel domain
30	d1e0ta1	Alignment	not modelled	99.9	33 Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
31	d1liua1	Alignment	not modelled	99.8	31 Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
32	d1pkma1	Alignment	not modelled	99.8	32 Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
33	d1pkla1	Alignment	not modelled	99.8	31 Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
34	d1a3xa1	Alignment	not modelled	99.8	24 Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
35	c4tv6A_	Alignment	not modelled	99.3	18 PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
36	c4mf4F_	Alignment	not modelled	99.3	20 PDB header: lyase Chain: F: PDB Molecule: hpch/hpai aldolase/citrate lyase family protein; PDBTitle: crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
37	c2v5jB_	Alignment	not modelled	99.2	20 PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
38	d1dxea_	Alignment	not modelled	99.2	22 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpai aldolase
39	c2vwtA_	Alignment	not modelled	99.2	21 PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii aldolase from escherichia coli k12 - mg-pyruvate product3 complex
40	c6r62A_	Alignment	not modelled	99.2	21 PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate
41	c4b5sB_	Alignment	not modelled	99.1	21 PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
42	c3qz6A_	Alignment	not modelled	99.1	22 PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
43	c1sgjB_	Alignment	not modelled	99.0	19 PDB header: lyase Chain: B: PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
44	d1sgja_	Alignment	not modelled	99.0	19 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpai aldolase
45	c1izcA_	Alignment	not modelled	98.9	19 PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
46	d1izca_	Alignment	not modelled	98.9	19 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpai aldolase
47	c3qllB_	Alignment	not modelled	98.9	21 PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis
48	c4l9zA_	Alignment	not modelled	98.6	17 PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase; PDBTitle: crystal structure of rhodobacter sphaeroides malyl-coa lyase in2 complex with magnesium, oxalate, and coa
49	c6arbA_	Alignment	not modelled	98.5	20 PDB header: lyase Chain: A: PDB Molecule: citrate lyase subunit beta-like protein; PDBTitle: crystal structure of protein cite from mycobacterium tuberculosis in2 complex with magnesium, pyruvate and coenzyme a
50	c3qqwC_	Alignment	not modelled	98.5	12 PDB header: lyase Chain: C: PDB Molecule: putative citrate lyase; PDBTitle: crystal structure of a putative lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
51	c1u5vA_	Alignment	not modelled	98.5	20 PDB header: lyase Chain: A: PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp form2 mycobacterium tuberculosis
52	d1u5ha_	Alignment	not modelled	98.4	20 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpCH/Hpai aldolase
53	c4l7zC_	Alignment	not modelled	98.3	21 PDB header: lyase Chain: C: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus malyl-coa lyase
54	c5vxsF_	Alignment	not modelled	98.3	19 PDB header: lyase Chain: F: PDB Molecule: citrate lyase subunit beta-like protein, mitochondrial; PDBTitle: crystal structure analysis of human clybl in apo form
55	c3r4iB_	Alignment	not modelled	98.2	17 PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of a citrate lyase (bx_e_b2899) from

						burkholderia2 xenovorans lb400 at 2.24 a resolution
56	c4rogA	Alignment	not modelled	98.1	19	PDB header: lyase Chain: A: PDB Molecule: malyl-coa lyase/beta-methylmalyl-coa lyase; PDBTitle: crystal structure of malyl-coa lyase from methylobacterium extorquens
57	c3cuzA	Alignment	not modelled	97.8	14	PDB header: transferase Chain: A: PDB Molecule: malate synthase a; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
58	c3pugA	Alignment	not modelled	97.7	13	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
59	c2bg5C	Alignment	not modelled	97.6	18	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
60	c2hroA	Alignment	not modelled	97.6	13	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
61	c2olsA	Alignment	not modelled	97.5	29	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
62	c2hwgA	Alignment	not modelled	97.5	14	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
63	c1kblA	Alignment	not modelled	97.4	15	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
64	c1h6zA	Alignment	not modelled	97.4	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
65	c3cuxA	Alignment	not modelled	97.4	22	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
66	d1kblA1	Alignment	not modelled	97.3	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
67	d1vbga1	Alignment	not modelled	97.3	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
68	d1h6za1	Alignment	not modelled	97.2	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
69	c1zfiA	Alignment	not modelled	97.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
70	c1vbhA	Alignment	not modelled	97.0	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
71	c4fxsA	Alignment	not modelled	96.8	21	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
72	d1jr1a1	Alignment	not modelled	96.7	22	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
73	c4xtiA	Alignment	not modelled	96.5	17	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
74	c5upxA	Alignment	not modelled	96.4	23	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
75	d1zfiA1	Alignment	not modelled	96.2	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
76	c1jcnA	Alignment	not modelled	96.2	18	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
77	c3odmE	Alignment	not modelled	96.2	14	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
78	c4af0B	Alignment	not modelled	96.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase PDB header: oxidoreductase

79	c3tsdA_	Alignment	not modelled	95.8	20	Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
80	c3gndC_	Alignment	not modelled	95.7	16	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
81	c4q33F_	Alignment	not modelled	95.2	22	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
82	c4z87B_	Alignment	not modelled	95.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
83	c4ff0B_	Alignment	not modelled	95.0	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
84	c4mjmD_	Alignment	not modelled	94.9	19	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
85	c4dqwB_	Alignment	not modelled	94.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
86	d2flia1	Alignment	not modelled	94.4	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
87	c5x8oA_	Alignment	not modelled	94.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
88	c3f4wA_	Alignment	not modelled	93.8	13	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
89	c1vrdA_	Alignment	not modelled	93.4	25	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
90	c4xp7A_	Alignment	not modelled	92.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
91	c3khjE_	Alignment	not modelled	92.3	18	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
92	c5zjnB_	Alignment	not modelled	92.3	15	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
93	c4zqrD_	Alignment	not modelled	92.3	23	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
94	c3b0vD_	Alignment	not modelled	91.8	17	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
95	c4mz1A_	Alignment	not modelled	91.6	20	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
96	d1h1ya_	Alignment	not modelled	91.4	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
97	c4axkB_	Alignment	not modelled	91.2	18	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
98	c3w9zA_	Alignment	not modelled	91.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
99	d1vrda1	Alignment	not modelled	90.6	22	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
100	d1t57a_	Alignment	not modelled	90.5	17	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like PDB header: oxidoreductase

101	c2y0fD_	Alignment	not modelled	90.5	14	Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispq) from thermus thermophilus hb27
102	d1xcfa_	Alignment	not modelled	89.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
103	d1y0ea_	Alignment	not modelled	89.4	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
104	c5ocsB_	Alignment	not modelled	89.1	19	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-dependent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
105	d1vp8a_	Alignment	not modelled	88.8	23	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
106	c3inpA_	Alignment	not modelled	88.7	9	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
107	c4iqiB_	Alignment	not modelled	88.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn
108	c2vp8A_	Alignment	not modelled	88.2	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
109	d1rpxa_	Alignment	not modelled	87.4	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
110	c3r2gA_	Alignment	not modelled	87.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
111	c3ffsC_	Alignment	not modelled	86.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
112	d1eepa_	Alignment	not modelled	85.6	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
113	c2qr6A_	Alignment	not modelled	85.3	18	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
114	c1jqoA_	Alignment	not modelled	85.1	21	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
115	d1jqoa_	Alignment	not modelled	85.1	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
116	c2gjlA_	Alignment	not modelled	85.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
117	c4muzA_	Alignment	not modelled	84.9	14	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 archaeoglobus fulgidus complexed with inhibitor bmp
118	d1tqja_	Alignment	not modelled	83.5	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
119	d2tpsa_	Alignment	not modelled	82.4	21	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
120	c4gx9A_	Alignment	not modelled	82.4	21	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit epsilon,dna polymerase iii PDBTitle: crystal structure of a dna polymerase iii alpha-epsilon chimera