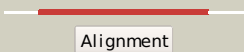
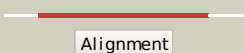
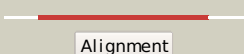
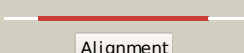
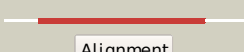
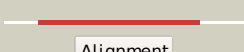
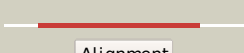
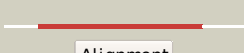
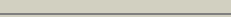
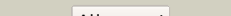
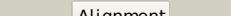
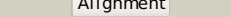
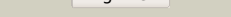
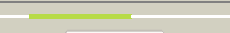
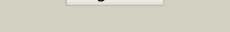
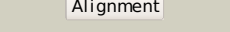
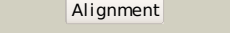
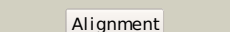
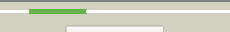
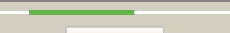
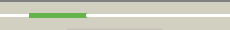
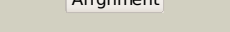
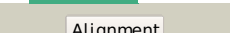
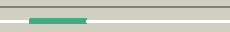
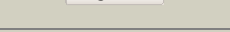
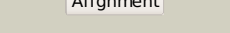
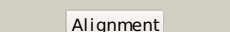


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r4iB_	 Alignment		100.0	19	PDB header: lyase Chain: B; PDB Molecule: citrate lyase; PDBTitle: crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
2	c3pugA_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: malate synthase; PDBTitle: haloferax volcanii malate synthase native at 3mm glyoxylate
3	c3qqwC_	 Alignment		100.0	18	PDB header: lyase Chain: C; PDB Molecule: putative citrate lyase; PDBTitle: crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
4	c3cuzA_	 Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: malate synthase a; PDBTitle: atomic resolution structures of escherichia coli and2 bacillus anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
5	c3qllB_	 Alignment		100.0	33	PDB header: lyase Chain: B; PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis
6	c1sgjB_	 Alignment		100.0	31	PDB header: lyase Chain: B; PDB Molecule: citrate lyase, beta subunit; PDBTitle: crystal structure of citrate lyase beta subunit
7	d1sgja_	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
8	c1u5vA_	 Alignment		100.0	31	PDB header: lyase Chain: A; PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
9	d1u5ha_	 Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
10	c3cuxA_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillus anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
11	d1dxea_	 Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase

12	c2v5jB_	Alignment		100.0	18	PDB header: lyase Chain: B: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
13	c2vwtA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
14	clizcA_	Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
15	dlizca_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpai aldolase
16	c3qz6A_	Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
17	dle0ta2	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
18	dln8ia_	Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
19	dla3xa2	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
20	dld8ca_	Alignment		99.9	21	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
21	d1pkla2	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
22	d1liua2	Alignment	not modelled	99.8	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
23	d2g50a2	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
24	d1h6za1	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
25	c2hwgA_	Alignment	not modelled	99.5	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
26	c2hroA_	Alignment	not modelled	99.5	16	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
27	c2vgbB_	Alignment	not modelled	99.5	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
28	c3khdC_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.

29	c2bg5C_	Alignment	not modelled	99.4	19	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
30	d1vbga1	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
31	d1kbla1	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
32	c1e0tD_	Alignment	not modelled	99.4	23	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
33	c1h6za_	Alignment	not modelled	99.4	15	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
34	c1pk1B_	Alignment	not modelled	99.3	21	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
35	c1a3wB_	Alignment	not modelled	99.3	23	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
36	c3e0vB_	Alignment	not modelled	99.3	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
37	c1t5aB_	Alignment	not modelled	99.3	25	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
38	c1kblA_	Alignment	not modelled	99.3	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
39	c1aqfB_	Alignment	not modelled	99.3	26	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
40	c2e28A_	Alignment	not modelled	99.3	21	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
41	c3t07D_	Alignment	not modelled	99.3	21	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
42	c3ma8A_	Alignment	not modelled	99.3	19	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
43	c1vbhA_	Alignment	not modelled	99.2	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
44	c3eoeC_	Alignment	not modelled	99.2	21	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
45	c2olsA_	Alignment	not modelled	99.1	17	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
46	c3odmE_	Alignment	not modelled	98.5	12	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
47	c3fa4D_	Alignment	not modelled	96.5	22	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
48	c3b8fF_	Alignment	not modelled	96.4	18	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+.
49	d1ujqa_	Alignment	not modelled	96.3	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
50	d1jqna_	Alignment	not modelled	96.2	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
51	c3eool_	Alignment	not modelled	96.0	15	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
52	c1jqoA_	Alignment	not modelled	95.6	15	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
53	d1jqoa_	Alignment	not modelled	95.6	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
54	d1muma_	Alignment	not modelled	94.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like

55	c1zlpA	 Alignment	not modelled	94.8	15	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
56	c2ze3A	 Alignment	not modelled	94.3	21	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
57	d1s2wa	 Alignment	not modelled	94.0	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
58	c2qiwa	 Alignment	not modelled	93.1	17	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
59	c3lyeA	 Alignment	not modelled	92.1	19	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
60	c3thaB	 Alignment	not modelled	91.7	18	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
61	c3ih1A	 Alignment	not modelled	90.7	10	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylm2 from bacillus anthracis
62	c2bdqA	 Alignment	not modelled	90.5	13	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
63	c2hjpA	 Alignment	not modelled	88.1	23	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
64	d1h1ya	 Alignment	not modelled	87.2	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
65	d1lssa	 Alignment	not modelled	86.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
66	d1qopa	 Alignment	not modelled	81.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
67	d1piia2	 Alignment	not modelled	79.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
68	d1zfja1	 Alignment	not modelled	76.6	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
69	c2c3zA	 Alignment	not modelled	76.3	20	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfobolus solfataricus
70	d2hmva1	 Alignment	not modelled	75.5	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
71	d1tqja	 Alignment	not modelled	75.1	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
72	d1rd5a	 Alignment	not modelled	73.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
73	d1o4ua1	 Alignment	not modelled	71.7	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
74	d2flia1	 Alignment	not modelled	70.8	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
75	c3gndC	 Alignment	not modelled	69.1	8	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
76	d1j5ta	 Alignment	not modelled	69.0	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
77	c3llva	 Alignment	not modelled	67.8	18	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
78	dli4na	 Alignment	not modelled	66.3	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
79	d1tqxa	 Alignment	not modelled	66.0	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
80	d1twda	 Alignment	not modelled	65.9	14	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like

81	c3navB	 Alignment	not modelled	63.6	15	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
82	c3ct7E	 Alignment	not modelled	60.8	12	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
83	c1e1cA	 Alignment	not modelled	59.7	15	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
84	c3ez4B	 Alignment	not modelled	58.3	18	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
85	d1vrda1	 Alignment	not modelled	57.8	20	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
86	d1ld1a	 Alignment	not modelled	57.5	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
87	c3s5oA	 Alignment	not modelled	54.5	8	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
88	c3lciA	 Alignment	not modelled	52.1	17	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
89	d1vc4a	 Alignment	not modelled	51.4	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
90	c2rfgB	 Alignment	not modelled	51.3	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
91	c2r8wB	 Alignment	not modelled	47.8	17	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
92	c3pueA	 Alignment	not modelled	47.8	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
93	c2vc6A	 Alignment	not modelled	46.9	10	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
94	d1hl2a	 Alignment	not modelled	46.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	c3o63B	 Alignment	not modelled	46.5	14	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
96	c3cprB	 Alignment	not modelled	46.1	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
97	c3bicA	 Alignment	not modelled	45.9	13	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
98	c1zfjA	 Alignment	not modelled	45.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (imphd; ec 1.1.1.205) from2 streptococcus pyogenes
99	c2ekcA	 Alignment	not modelled	44.2	10	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
100	c3noeA	 Alignment	not modelled	42.5	18	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
101	c2v9dB	 Alignment	not modelled	42.2	13	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
102	c3fwzA	 Alignment	not modelled	41.4	19	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
103	d2a6na1	 Alignment	not modelled	40.7	8	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
104	c2ehhE	 Alignment	not modelled	39.9	12	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
105	c3qc3B	 Alignment	not modelled	39.6	15	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribul

106	c3g0sA_	Alignment	not modelled	39.5	8	Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
107	d1xkya1	Alignment	not modelled	39.4	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
108	d2fy8a1	Alignment	not modelled	38.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
109	c3qfeB_	Alignment	not modelled	37.7	12	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
110	d1xcfa_	Alignment	not modelled	36.7	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
111	c2g1uA_	Alignment	not modelled	35.6	12	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
112	c3l4bG_	Alignment	not modelled	35.4	14	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
113	d1geqa_	Alignment	not modelled	34.2	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
114	c3fkkA_	Alignment	not modelled	33.9	14	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
115	c2w91A_	Alignment	not modelled	33.7	23	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-n-acetylglucosaminidase d; PDBTitle: structure of a streptococcus pneumoniae family 85 glycoside2 hydrolase, endo-d.
116	c3eywA_	Alignment	not modelled	32.8	9	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
117	c3inpA_	Alignment	not modelled	32.3	14	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.
118	c3fhaD_	Alignment	not modelled	31.7	20	PDB header: hydrolase Chain: D: PDB Molecule: endo-beta-n-acetylglucosaminidase; PDBTitle: structure of endo-beta-n-acetylglucosaminidase a
119	c3gdbA_	Alignment	not modelled	31.7	23	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein spr0440; PDBTitle: crystal structure of spr0440 glycoside hydrolase domain,2 endo-d from streptococcus pneumoniae r6
120	c2qjhH_	Alignment	not modelled	31.2	22	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate