Phyre2

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Description	RVBD3075c_(-)_3438047_3438970
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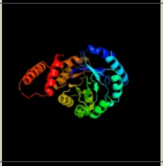
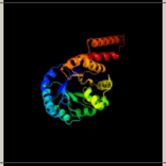
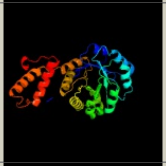
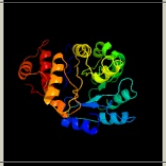
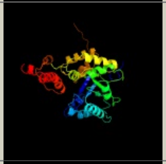
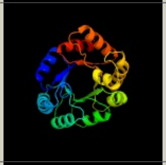
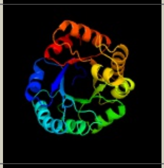
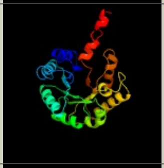
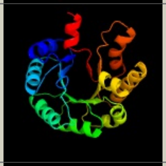
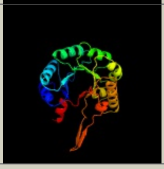
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4l7zC_	Alignment		100.0	25	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** crystal structure of chloroflexus aurantiacus malyl-coa lyase
2	c4roqA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**malyl-coa lyase/beta-methylmalyl-coa lyase; **PDBTitle:** crystal structure of malyl-coa lyase from methylobacterium extorquens
3	c6arbA_	Alignment		100.0	33	**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
4	c5vxsF_	Alignment		100.0	30	**PDB header:**lyase **Chain:** F: **PDB Molecule:**citrate lyase subunit beta-like protein, mitochondrial; **PDBTitle:** crystal structure analysis of human clybl in apo form
5	c4l9zA_	Alignment		100.0	27	**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
6	c3r4iB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of a citrate lyase (bxe_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
7	c3qqwC_	Alignment		100.0	21	**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
8	c3pugA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate
9	c3qllB_	Alignment		100.0	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of ripc from yersinia pestis
10	c1u5vA_	Alignment		100.0	34	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp form2 mycobacterium tuberculosis
11	d1u5ha_	Alignment		100.0	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase

12	c1sgjB_	Alignment		100.0	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase, beta subunit; **PDBTitle:** crystal structure of citrate lyase beta subunit
13	d1sgja_	Alignment		100.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
14	c3cuzA_	Alignment		100.0	16	**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
15	c3cuxA_	Alignment		100.0	17	**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
16	d1dxea_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
17	c4tv6A_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyglucarate aldolase; **PDBTitle:** crystal structure of citrate synthase variant sbng e151q
18	c4mf4F_	Alignment		100.0	22	**PDB header:**lyase **Chain:** F: **PDB Molecule:**hpch/hpai aldolase/citrate lyase family protein; **PDBTitle:** crystal structure of a hpch/hpal aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
19	c4b5sB_	Alignment		100.0	18	**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
20	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
21	c2vwtA_	Alignment	not modelled	100.0	17	**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
22	d1izca_	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
23	c1izcA_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
24	c6r62A_	Alignment	not modelled	100.0	23	**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
25	c3qz6A_	Alignment	not modelled	99.9	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
26	d1e0ta2	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
27	d1a3xa2	Alignment	not modelled	99.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
28	d1pkla2	Alignment	not modelled	99.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
						Fold:TIM beta/alpha-barrel

29	d2g50a2	Alignment	not modelled	99.7	16	**Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
30	d1liua2	Alignment	not modelled	99.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
31	d1n8ia_	Alignment	not modelled	99.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
32	d1d8ca_	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
33	c5vfbB_	Alignment	not modelled	99.6	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malate synthase g; **PDBTitle:** 1.36 angstrom resolution crystal structure of malate synthase g from2 pseudomonas aeruginosa in complex with glycolic acid.
34	c4fxjB_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes m1/m2; **PDBTitle:** structure of m2 pyruvate kinase in complex with phenylalanine
35	c3e0vB_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
36	c4imaD_	Alignment	not modelled	99.2	17	**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
37	c3qtgA_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from pyrobaculum aerophilum
38	c3khdC_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
39	c6du6D_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of the pyruvate kinase (pk1) from the mosquito aedes2 aegypti
40	c1t5aB_	Alignment	not modelled	99.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
41	c1a3wB_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
42	c1pklB_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
43	d1h6za1	Alignment	not modelled	99.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
44	c1e0tD_	Alignment	not modelled	99.1	17	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
45	c2vgbB_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
46	c1aqfB_	Alignment	not modelled	99.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
47	c3t07D_	Alignment	not modelled	99.1	15	**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
48	c5ws9C_	Alignment	not modelled	99.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase (pyk) from mycobacterium tuberculosis in complex with2 oxalate, atp and allosteric activator amp
49	c3khdA_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
50	c3ma8A_	Alignment	not modelled	99.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
51	c3eoeC_	Alignment	not modelled	99.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
52	c2e28A_	Alignment	not modelled	99.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
53	c2hwgA_	Alignment	not modelled	99.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
54	c2bg5C_	Alignment	not modelled	98.9	14	**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)
						PDB header:transferase

55	c1h6zA_	Alignment	not modelled	98.9	20	**Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
56	c2hroA_	Alignment	not modelled	98.9	17	**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
57	d1vbga1	Alignment	not modelled	98.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
58	d1kbla1	Alignment	not modelled	98.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
59	c1kblA_	Alignment	not modelled	98.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
60	c1vbhA_	Alignment	not modelled	98.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
61	c2olsA_	Alignment	not modelled	98.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
62	c3odmE_	Alignment	not modelled	98.2	21	**PDB header:**lyase **Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase
63	c1jqoA_	Alignment	not modelled	96.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
64	d1jqoa_	Alignment	not modelled	96.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
65	d1jqna_	Alignment	not modelled	96.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
66	c3fa4D_	Alignment	not modelled	92.0	18	**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
67	c3eooL_	Alignment	not modelled	85.0	12	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
68	c4mg4G_	Alignment	not modelled	84.0	18	**PDB header:**unknown function **Chain:** G: **PDB Molecule:**phosphonomutase; **PDBTitle:** crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
69	c3lyeA_	Alignment	not modelled	80.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
70	c5nc8B_	Alignment	not modelled	79.9	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**potassium efflux system protein; **PDBTitle:** shewanella denitrificans kef ctd in amp bound form
71	c3ih1A_	Alignment	not modelled	78.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
72	d1ujqa_	Alignment	not modelled	77.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
73	c1zlpA_	Alignment	not modelled	77.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
74	c3b8iF_	Alignment	not modelled	76.7	15	**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+.
75	c2ze3A_	Alignment	not modelled	75.4	20	**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
76	c4g65A_	Alignment	not modelled	73.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**trk system potassium uptake protein trka; **PDBTitle:** potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
77	c2bdqA_	Alignment	not modelled	71.0	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast strucural genomics target sar15.
78	d1lssa_	Alignment	not modelled	70.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
79	d1id1a_	Alignment	not modelled	70.8	4	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
80	d2hmva1	Alignment	not modelled	69.2	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain

81	d1muma_	Alignment	not modelled	67.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
82	d1o4ua1	Alignment	not modelled	55.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
83	c2g1uA_	Alignment	not modelled	55.3	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
84	c3fwzA_	Alignment	not modelled	53.5	12	**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
85	c3s5oA_	Alignment	not modelled	51.2	11	**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
86	d1s2wa_	Alignment	not modelled	50.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
87	c2hjpA_	Alignment	not modelled	49.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
88	c4hpfB_	Alignment	not modelled	49.4	8	**PDB header:**membrane protein, transport protein **Chain:** B: **PDB Molecule:**potassium channel subfamily u member 1; **PDBTitle:** structure of the human slo3 gating ring
89	c3eywA_	Alignment	not modelled	46.8	14	**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
90	c1o4uA_	Alignment	not modelled	44.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
91	c2qiwA_	Alignment	not modelled	44.0	15	**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
92	c1fcbA_	Alignment	not modelled	43.3	18	**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
93	c2rfgB_	Alignment	not modelled	40.4	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
94	d1f74a_	Alignment	not modelled	38.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
95	c2c3zA_	Alignment	not modelled	35.1	17	**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 sulfolobus solfataricus
96	c3d0cB_	Alignment	not modelled	34.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
97	c4gx5D_	Alignment	not modelled	32.1	14	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**trka domain protein; **PDBTitle:** gsuk channel
98	c3lciA_	Alignment	not modelled	31.8	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
99	c4uxdC_	Alignment	not modelled	29.4	15	**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
100	d1tqja_	Alignment	not modelled	27.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
101	d1zfja1	Alignment	not modelled	27.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
102	c5d87A_	Alignment	not modelled	25.9	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable siderophore biosynthesis protein sbna; **PDBTitle:** staphyloferrin b precursor biosynthetic enzyme sbna y152f/s185g2 variant
103	d1a53a_	Alignment	not modelled	23.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
104	c4dppB_	Alignment	not modelled	23.4	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase 2, chloroplastic; **PDBTitle:** the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
						PDB header:transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-

105	c3c85A_	Alignment	not modelled	23.2	9	efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
106	d1j5ta_	Alignment	not modelled	22.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
107	c5odcD_	Alignment	not modelled	22.7	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**methyl-viologen reducing hydrogenase subunit d; **PDBTitle:** heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
108	c4iegD_	Alignment	not modelled	21.9	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rna-dependent rna polymerase p2; **PDBTitle:** structure and interactions of the rna-dependent rna polymerase from2 bacteriophage phi12 (p1 crystal form)
109	d1o5ka_	Alignment	not modelled	21.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
110	c4lsbA_	Alignment	not modelled	20.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lyase/mutase; **PDBTitle:** crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315