Phyre^2

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Description	P32670
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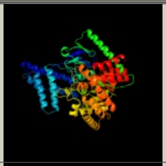
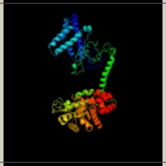
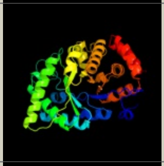
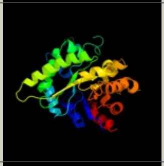
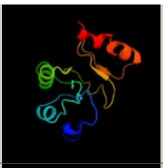
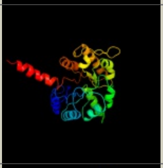
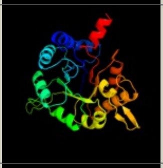
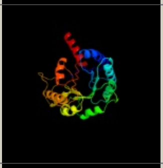
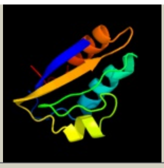
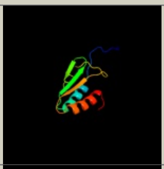
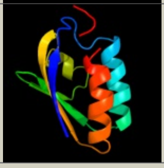
Unique Job ID	80d2f4070b402b64

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hwgA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
2	c2hroA_	Alignment		100.0	36	**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
3	c1h6zA_	Alignment		100.0	26	**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
4	c2bg5C_	Alignment		100.0	42	**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)
5	c1kblA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
6	c1vbhA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
7	c2olsA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
8	d1vbga1	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
9	d1h6za1	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
10	d1kbla1	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
11	c1ezaA_	Alignment		100.0	22	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure

12	d1zyma2	Alignment		99.9	23	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
13	d1zyma1	Alignment		99.9	24	**Fold:**SAM domain-like **Superfamily:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain **Family:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
14	c3qz6A_	Alignment		99.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
15	d1dxea_	Alignment		99.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
16	c2a0jA_	Alignment		99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein; **PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis
17	c3urrB_	Alignment		99.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn; **PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn)
18	d1izca_	Alignment		99.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
19	c1izcA_	Alignment		99.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
20	d2hpra_	Alignment		99.8	22	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
21	d1a6ja_	Alignment		99.8	20	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
22	c3oxpB_	Alignment		99.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
23	c3oxpA_	Alignment		99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
24	c3le1B_	Alignment		99.8	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis

25	d1ka5a_	Alignment		99.8	23	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
26	c2oqtD_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein spy0176; **PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas
27	d1mo1a_	Alignment		99.8	30	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
28	d1pcha_	Alignment		99.8	26	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
29	d1qr5a_	Alignment		99.8	22	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
30	c3ihsB_	Alignment	not modelled	99.8	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
31	c3bjvA_	Alignment		99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpa; **PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
32	c2v5jB_	Alignment	not modelled	99.8	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
33	d1ptfa_	Alignment	not modelled	99.8	27	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
34	d1xiza_	Alignment	not modelled	99.8	22	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
35	c2vwtA_	Alignment	not modelled	99.8	20	**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
36	d1a3aa_	Alignment	not modelled	99.8	22	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
37	d2nzul1	Alignment	not modelled	99.7	22	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
38	d1cm3a_	Alignment	not modelled	99.7	26	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
39	c2oq3A_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase **PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli
40	d1vbga2	Alignment	not modelled	99.7	23	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
41	d1zvvj1	Alignment	not modelled	99.7	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
42	d1kbla2	Alignment	not modelled	99.7	27	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
43	d1h6za2	Alignment	not modelled	99.7	25	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
44	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
45	c3qqwC_	Alignment	not modelled	99.3	13	**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

46	c1sgjB_	Alignment	not modelled	99.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase, beta subunit; **PDBTitle:** crystal structure of citrate lyase beta subunit
47	c2e28A_	Alignment	not modelled	99.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
48	d1sgja_	Alignment	not modelled	99.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
49	d2g50a2	Alignment	not modelled	99.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
50	d1e0ta2	Alignment	not modelled	99.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
51	c3r4iB_	Alignment	not modelled	99.0	17	**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
52	d1a3xa2	Alignment	not modelled	99.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
53	d1pkla2	Alignment	not modelled	98.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
54	d1u5ha_	Alignment	not modelled	98.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
55	c1u5vA_	Alignment	not modelled	98.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
56	d1liua2	Alignment	not modelled	98.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
57	c3cuzA_	Alignment	not modelled	98.7	15	**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	c3cuxA_	Alignment	not modelled	98.2	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
59	c3pugA_	Alignment	not modelled	97.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate
60	d1d8ca_	Alignment	not modelled	97.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
61	c3e0vB_	Alignment	not modelled	96.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
62	c1aqfB_	Alignment	not modelled	96.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
63	c2vgbB_	Alignment	not modelled	96.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
64	c1t5aB_	Alignment	not modelled	96.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
65	c1pklB_	Alignment	not modelled	96.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
66	c3ma8A_	Alignment	not modelled	96.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
67	c3eoeC_	Alignment	not modelled	96.5	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
68	c1e0tD_	Alignment	not modelled	96.2	14	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
69	c1a3wB_	Alignment	not modelled	96.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
70	c3khdC_	Alignment	not modelled	95.3	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
71	c2zbtB_	Alignment	not modelled	94.3	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
						PDB header:biosynthetic protein, transferase

72	c3femB_	Alignment	not modelled	94.0	22	**Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
73	c2nv2U_	Alignment	not modelled	93.8	20	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
74	d1eepa_	Alignment	not modelled	92.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
75	d2hi6a1	Alignment	not modelled	89.8	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
76	d1hl2a_	Alignment	not modelled	87.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
77	d1vrda1	Alignment	not modelled	87.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
78	d1jr1a1	Alignment	not modelled	86.9	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
79	c2v9dB_	Alignment	not modelled	86.5	17	**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
80	d1pvna1	Alignment	not modelled	86.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
81	c3lerA_	Alignment	not modelled	84.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
82	c2vc6A_	Alignment	not modelled	84.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
83	c2a7rD_	Alignment	not modelled	84.2	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
84	d1o5ka_	Alignment	not modelled	83.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
85	c3cprB_	Alignment	not modelled	83.7	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
86	c3qjaA_	Alignment	not modelled	83.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
87	c1vrdA_	Alignment	not modelled	83.2	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
88	c3lciA_	Alignment	not modelled	81.9	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
89	c1jcnA_	Alignment	not modelled	81.8	24	**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
90	c3khjE_	Alignment	not modelled	80.8	25	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
91	c2ehhE_	Alignment	not modelled	79.6	26	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
92	d1tb3a1	Alignment	not modelled	79.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
93	d1zfja1	Alignment	not modelled	79.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
94	c2infB_	Alignment	not modelled	79.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
95	c3pueA_	Alignment	not modelled	77.7	25	**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
96	d1n8ia_	Alignment	not modelled	77.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
97	d1j93a_	Alignment	not modelled	75.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD

98	c3r2gA_	Alignment	not modelled	75.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
99	c3s5oA_	Alignment	not modelled	74.8	10	**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
100	c2r8wB_	Alignment	not modelled	74.6	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
101	c3noeA_	Alignment	not modelled	74.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
102	c3daqB_	Alignment	not modelled	73.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
103	d1xxxa1	Alignment	not modelled	73.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
104	c2c3zA_	Alignment	not modelled	72.6	21	**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
105	d1a53a_	Alignment	not modelled	72.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
106	c1jpkA_	Alignment	not modelled	70.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
107	d1jcna1	Alignment	not modelled	70.2	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
108	c2f7fA_	Alignment	not modelled	69.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
109	c3n2xB_	Alignment	not modelled	68.7	21	**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
110	d2a6na1	Alignment	not modelled	68.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
111	d2cu0a1	Alignment	not modelled	67.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
112	d2i14a1	Alignment	not modelled	66.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
113	c2zrvC_	Alignment	not modelled	66.4	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase; **PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn.
114	c1me9A_	Alignment	not modelled	65.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
115	c3na8A_	Alignment	not modelled	65.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
116	d1f74a_	Alignment	not modelled	64.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
117	c2hmcA_	Alignment	not modelled	64.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
118	c1ypfB_	Alignment	not modelled	63.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
119	c2ejaB_	Alignment	not modelled	63.5	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
120	c3g0sA_	Alignment	not modelled	63.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2