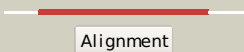

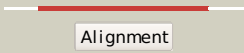



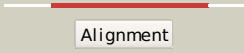





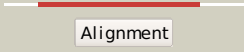

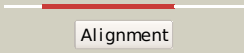





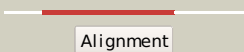












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cuzaA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malate synthase a; <b>PDBTitle:</b> atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
2	<a href="#">c3cuxA_</a>	 Alignment		100.0	55	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malate synthase; <b>PDBTitle:</b> atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
3	<a href="#">d1n8ia_</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Malate synthase G <b>Family:</b> Malate synthase G
4	<a href="#">d1d8ca_</a>	 Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Malate synthase G <b>Family:</b> Malate synthase G
5	<a href="#">c3puga_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malate synthase; <b>PDBTitle:</b> haloferax volcanii malate synthase native at 3mm glyoxylate
6	<a href="#">c3r4iB_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> citrate lyase; <b>PDBTitle:</b> crystal structure of a citrate lyase (bx_e_b2899) from burkholderia2 xenovorans 1b400 at 2.24 a resolution
7	<a href="#">c3qqwC_</a>	 Alignment		100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> putative citrate lyase; <b>PDBTitle:</b> crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
8	<a href="#">c1sgjB_</a>	 Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> citrate lyase, beta subunit; <b>PDBTitle:</b> crystal structure of citrate lyase beta subunit
9	<a href="#">d1sgja_</a>	 Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpcH/Hpal aldolase
10	<a href="#">c1u5vA_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cite; <b>PDBTitle:</b> structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
11	<a href="#">d1u5ha_</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpcH/Hpal aldolase

12	<a href="#">d1dxea</a>	Alignment		99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Hpch/Hpai aldolase
13	<a href="#">c2v5jB</a>	Alignment		99.8	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> apo class ii aldolase hpch
14	<a href="#">clizcA</a>	Alignment		99.8	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophomate synthase intermolecular diels-alderase; <b>PDBTitle:</b> crystal structure analysis of macrophomate synthase
15	<a href="#">d1izca</a>	Alignment		99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Hpch/Hpai aldolase
16	<a href="#">c2vwtA</a>	Alignment		99.8	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase; <b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
17	<a href="#">c3qz6A</a>	Alignment		99.7	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
18	<a href="#">d1e0ta2</a>	Alignment		99.7	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
19	<a href="#">d1a3xa2</a>	Alignment		99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
20	<a href="#">d1pkla2</a>	Alignment		99.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
21	<a href="#">d2g50a2</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
22	<a href="#">d1liua2</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
23	<a href="#">c2hwaA</a>	Alignment	not modelled	98.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
24	<a href="#">c2hroA</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
25	<a href="#">c2bg5C</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoenolpyruvate-protein kinase; <b>PDBTitle:</b> crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
26	<a href="#">d1h6za1</a>	Alignment	not modelled	98.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain
27	<a href="#">d1vbga1</a>	Alignment	not modelled	98.6	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain
28	<a href="#">c1vbha</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate,orthophosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase with bound mq-pep from

					maize
29	<a href="#">c1t5aB_</a>	Alignment	not modelled	98.4	18 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase, m2 isozyme; <b>PDBTitle:</b> human pyruvate kinase m2
30	<a href="#">c2vgbB_</a>	Alignment	not modelled	98.3	14 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase isozymes r/l; <b>PDBTitle:</b> human erythrocyte pyruvate kinase
31	<a href="#">c1aqfB_</a>	Alignment	not modelled	98.3	18 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
32	<a href="#">c3khdC_</a>	Alignment	not modelled	98.3	20 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pff1300w.
33	<a href="#">c1h6zA_</a>	Alignment	not modelled	98.3	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase; <b>PDBTitle:</b> 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
34	<a href="#">d1kbla1</a>	Alignment	not modelled	98.1	12 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate phosphate dikinase, C-terminal domain
35	<a href="#">c1e0tD_</a>	Alignment	not modelled	98.1	19 <b>PDB header:</b> phosphotransferase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> r292d mutant of e. coli pyruvate kinase
36	<a href="#">c1kblA_</a>	Alignment	not modelled	98.1	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase
37	<a href="#">c1a3wB_</a>	Alignment	not modelled	98.0	20 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
38	<a href="#">c3ma8A_</a>	Alignment	not modelled	98.0	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
39	<a href="#">c1pkIB_</a>	Alignment	not modelled	97.9	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyruvate kinase); <b>PDBTitle:</b> the structure of leishmania pyruvate kinase
40	<a href="#">c2olsA_</a>	Alignment	not modelled	97.9	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate synthase; <b>PDBTitle:</b> the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
41	<a href="#">c3e0vB_</a>	Alignment	not modelled	97.8	19 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
42	<a href="#">c2e28A_</a>	Alignment	not modelled	97.7	21 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure analysis of pyruvate kinase from bacillus2 stearotherophilus
43	<a href="#">c3eoeC_</a>	Alignment	not modelled	97.7	18 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
44	<a href="#">c3t07D_</a>	Alignment	not modelled	97.6	20 <b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
45	<a href="#">c3odmE_</a>	Alignment	not modelled	97.6	19 <b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> phosphoenolpyruvate carboxylase; <b>PDBTitle:</b> archaeal-type phosphoenolpyruvate carboxylase
46	<a href="#">d1jqoa_</a>	Alignment	not modelled	76.0	10 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate carboxylase
47	<a href="#">c1jqoA_</a>	Alignment	not modelled	76.0	10 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxylase; <b>PDBTitle:</b> crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
48	<a href="#">d1jqna_</a>	Alignment	not modelled	71.4	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate carboxylase
49	<a href="#">c3r3sD_</a>	Alignment	not modelled	62.3	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> structure of the ygha oxidoreductase from salmonella enterica
50	<a href="#">c3i1jB_</a>	Alignment	not modelled	61.0	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain <b>PDBTitle:</b> structure of a putative short chain dehydrogenase from2 pseudomonas syringae
51	<a href="#">c2x3mA_</a>	Alignment	not modelled	52.0	36 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein orf239; <b>PDBTitle:</b> crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
52	<a href="#">c3g5oC_</a>	Alignment	not modelled	40.9	13 <b>PDB header:</b> toxin/antitoxin <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein rv2866; <b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
53	<a href="#">d1yxma1</a>	Alignment	not modelled	40.9	23 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
54	<a href="#">d1qasa3</a>	Alignment	not modelled	35.5	28 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
					<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

55	<a href="#">d1g0oa_</a>	Alignment	not modelled	30.2	22	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
56	<a href="#">d2zkmx4</a>	Alignment	not modelled	28.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
57	<a href="#">c3iv6C_</a>	Alignment	not modelled	26.6	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative zn-dependent alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative zn-dependent alcohol dehydrogenases from2 rhodobacter sphaeroides.
58	<a href="#">c2qjmA_</a>	Alignment	not modelled	26.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoperoxidase; <b>PDBTitle:</b> crystal structure of buffalo lactoperoxidase at 2.75a resolution
59	<a href="#">c3qkbB_</a>	Alignment	not modelled	25.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
60	<a href="#">d1q45a_</a>	Alignment	not modelled	24.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
61	<a href="#">c3ohmB_</a>	Alignment	not modelled	22.4	18	<b>PDB header:</b> signaling protein / hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase <b>PDBTitle:</b> crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
62	<a href="#">c1djyB_</a>	Alignment	not modelled	22.0	28	<b>PDB header:</b> lipid degradation <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoinositide-specific phospholipase c, <b>PDBTitle:</b> phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
63	<a href="#">c3bbnD_</a>	Alignment	not modelled	22.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
64	<a href="#">d1mn3a_</a>	Alignment	not modelled	20.6	23	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
65	<a href="#">c1bknA_</a>	Alignment	not modelled	20.4	25	<b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> mutl; <b>PDBTitle:</b> crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
66	<a href="#">d1geea_</a>	Alignment	not modelled	19.9	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
67	<a href="#">d1gtea2</a>	Alignment	not modelled	19.8	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
68	<a href="#">c1ddxA_</a>	Alignment	not modelled	19.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (prostaglandin h2 synthase-2); <b>PDBTitle:</b> crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
69	<a href="#">c3pggD_</a>	Alignment	not modelled	19.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cyclooxygenase-2; <b>PDBTitle:</b> cyclooxygenase-2 (prostaglandin synthase-2) complexed with a non-2 selective inhibitor, flurbiprofen
70	<a href="#">c2fjuB_</a>	Alignment	not modelled	18.9	18	<b>PDB header:</b> signaling protein,apoptosis/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate <b>PDBTitle:</b> activated rac1 bound to its effector phospholipase c beta 2
71	<a href="#">c3gdbA_</a>	Alignment	not modelled	18.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein spr0440; <b>PDBTitle:</b> crystal structure of spr0440 glycoside hydrolase domain,2 endo-d from streptococcus pneumoniae r6
72	<a href="#">d1cvua1</a>	Alignment	not modelled	18.3	19	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Myeloperoxidase-like
73	<a href="#">c3ivuB_</a>	Alignment	not modelled	18.3	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homocitrate synthase, mitochondrial; <b>PDBTitle:</b> homocitrate synthase lys4 bound to 2-og
74	<a href="#">d1vyua2</a>	Alignment	not modelled	18.2	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
75	<a href="#">c1pggB_</a>	Alignment	not modelled	18.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin h2 synthase-1; <b>PDBTitle:</b> prostaglandin h2 synthase-1 complexed with 1-(4-iodobenzoyl)-5-2 methoxy-2-methylindole-3-acetic acid (iodoindomethacin), trans model
76	<a href="#">c1ht8B_</a>	Alignment	not modelled	18.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin h2 synthase-1; <b>PDBTitle:</b> the 2.7 angstrom resolution model of ovine cox-1 complexed with2 alclofenac
77	<a href="#">c3kvoB_</a>	Alignment	not modelled	18.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxysteroid dehydrogenase-like protein 2; <b>PDBTitle:</b> crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsd12)
78	<a href="#">c1y2iC_</a>	Alignment	not modelled	17.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein s0862; <b>PDBTitle:</b> crystal structure of mcsg target apc27401 from shigella2 flexneri
79	<a href="#">d1y2ia_</a>	Alignment	not modelled	17.2	11	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> YbqQ-like

					<b>Family:</b> YbjQ-like
80	<a href="#">c2w91A_</a>	Alignment	not modelled	16.8	26 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase d; <b>PDBTitle:</b> structure of a streptococcus pneumoniae family 85 glycoside2 hydrolase, endo-d.
81	<a href="#">c2oyuP_</a>	Alignment	not modelled	16.7	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> prostaglandin g/h synthase 1; <b>PDBTitle:</b> indomethacin-(s)-alpha-ethyl-ethanolamide bound to cyclooxygenase-1
82	<a href="#">c2qr6A_</a>	Alignment	not modelled	16.6	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imp dehydrogenase/gmp reductase; <b>PDBTitle:</b> crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
83	<a href="#">c3qr0A_</a>	Alignment	not modelled	16.5	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase c-beta (plc-beta); <b>PDBTitle:</b> crystal structure of s. officinalis plc21
84	<a href="#">c1zfjA_</a>	Alignment	not modelled	16.1	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
85	<a href="#">d1o70a2</a>	Alignment	not modelled	16.1	9 <b>Fold:</b> FAS1 domain <b>Superfamily:</b> FAS1 domain <b>Family:</b> FAS1 domain
86	<a href="#">c3mdoB_</a>	Alignment	not modelled	15.7	15 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
87	<a href="#">c2a7rD_</a>	Alignment	not modelled	15.7	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> gmp reductase 2; <b>PDBTitle:</b> crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
88	<a href="#">c3gaff_</a>	Alignment	not modelled	15.2	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 7-alpha-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
89	<a href="#">d2cu0a1</a>	Alignment	not modelled	14.9	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
90	<a href="#">c2kheA_</a>	Alignment	not modelled	14.9	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> toxin-like protein; <b>PDBTitle:</b> solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
91	<a href="#">d1w6ua_</a>	Alignment	not modelled	14.8	20 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
92	<a href="#">d1uzma1</a>	Alignment	not modelled	14.6	21 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
93	<a href="#">d1q4ga1</a>	Alignment	not modelled	14.4	14 <b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Myeloperoxidase-like
94	<a href="#">d1pvna1</a>	Alignment	not modelled	14.2	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
95	<a href="#">d2jn4a1</a>	Alignment	not modelled	14.1	21 <b>Fold:</b> NifT/FixU barrel-like <b>Superfamily:</b> NifT/FixU-like <b>Family:</b> NifT/FixU
96	<a href="#">c2jn4A_</a>	Alignment	not modelled	14.1	21 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein fixu, nift; <b>PDBTitle:</b> solution nmr structure of protein rp4601 from2 rhodopseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
97	<a href="#">d1zfja1</a>	Alignment	not modelled	14.0	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
98	<a href="#">c3rihB_</a>	Alignment	not modelled	14.0	28 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase or reductase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
99	<a href="#">c1d2vD_</a>	Alignment	not modelled	14.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> myeloperoxidase; <b>PDBTitle:</b> crystal structure of bromide-bound human myeloperoxidase isoform c at2 ph 5.5