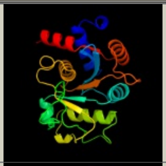
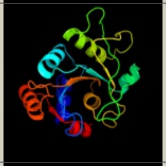
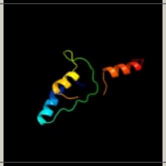
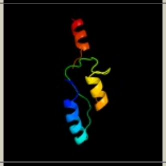
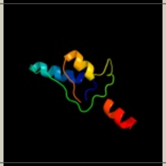
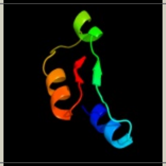
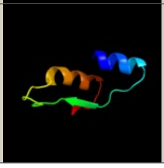
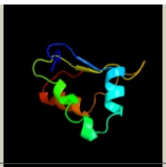
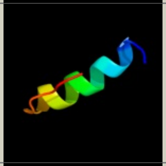
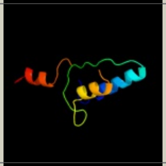
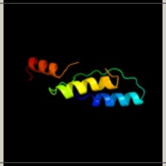
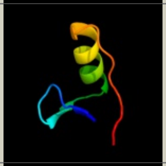
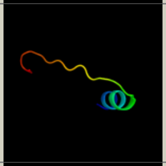
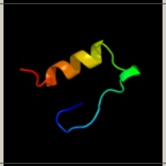
Email	l.a.kelley@imperial.ac.uk
Description	P0A7J0
Date	Thu Jan 5 11:05:45 GMT 2012
Unique Job ID	5e17918f389f11e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g57a_	Alignment		100.0	100	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
2	d1k4ia_	Alignment		100.0	46	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
3	d1snna_	Alignment		100.0	31	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
4	d1tksa_	Alignment		100.0	49	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
5	c3mioA_	Alignment		100.0	48	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
6	d1lh0a_	Alignment		93.3	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
7	c3n2lA_	Alignment		87.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
8	d1y0na_	Alignment		82.9	34	**Fold:**YehU-like **Superfamily:**YehU-like **Family:**YehU-like
9	c3mjdA_	Alignment		76.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
10	d1ohwa_	Alignment		72.9	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
11	d1js3a_	Alignment		68.7	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase

12	d1ko7a1	Alignment		59.8	16	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
13	c3p04A_	Alignment		49.2	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
14	c2przB_	Alignment		48.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
15	c3p04B_	Alignment		46.3	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
16	c2wnsB_	Alignment		41.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
17	d1tifa_	Alignment		41.5	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Translation initiation factor IF3, N-terminal domain **Family:**Translation initiation factor IF3, N-terminal domain
18	c2uvpB_	Alignment		38.7	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hoba; **PDBTitle:** crystal structure of hoba (hp1230)from helicobacter pylori
19	d1oeyj_	Alignment		38.6	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
20	c3bcxA_	Alignment		37.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
21	c3qw4B_	Alignment	not modelled	36.4	19	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
22	c2p1zA_	Alignment	not modelled	32.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
23	c3nuiA_	Alignment	not modelled	31.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate transaminase; **PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17
24	c3jszA_	Alignment	not modelled	30.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
25	c3hmuA_	Alignment	not modelled	30.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi
26	c3k40B_	Alignment	not modelled	30.4	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase; **PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
27	c2okkA_	Alignment	not modelled	30.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glutamate decarboxylase 2; **PDBTitle:** the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
28	c2ordA_	Alignment	not modelled	29.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution

29	c2eo5A_	Alignment	not modelled	29.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**419aa long hypothetical aminotransferase; **PDBTitle:** crystal structure of 4-aminobutyrate aminotransferase from sulfolobus2 tokodaii strain7
30	c2l09A_	Alignment	not modelled	28.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**asr4154 protein; **PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
31	c3oksB_	Alignment	not modelled	28.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-aminobutyrate transaminase; **PDBTitle:** crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
32	d1hrua_	Alignment	not modelled	28.0	12	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
33	c2cjdA_	Alignment	not modelled	27.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-lysine-epsilon aminotransferase; **PDBTitle:** lysine aminotransferase from m. tuberculosis in external2 aldimine form
34	c3dezA_	Alignment	not modelled	26.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
35	c3l44A_	Alignment	not modelled	26.1	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase 1; **PDBTitle:** crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
36	d1h8ba_	Alignment	not modelled	25.2	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
37	d1yqea1	Alignment	not modelled	24.8	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
38	c3m3hA_	Alignment	not modelled	24.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
39	c2jisA_	Alignment	not modelled	24.1	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase; **PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
40	c3fcrA_	Alignment	not modelled	23.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
41	d1sffa_	Alignment	not modelled	23.2	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
42	d1fc4a_	Alignment	not modelled	23.0	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
43	c2gfqC_	Alignment	not modelled	22.4	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
44	c1t3mA_	Alignment	not modelled	22.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
45	d1j20a1	Alignment	not modelled	22.0	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
46	d1fvpa_	Alignment	not modelled	21.9	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
47	c3bs8A_	Alignment	not modelled	21.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
48	c2w8wA_	Alignment	not modelled	20.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
49	d2aeea1	Alignment	not modelled	20.8	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
50	c3ndnC_	Alignment	not modelled	20.7	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
51	c3nx3A_	Alignment	not modelled	20.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
52	d1vbga2	Alignment	not modelled	19.6	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
53	c2pb2B	Alignment	not modelled	19.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetylornithine/succinyldiaminopimelate aminotransferase;

53	c2pbzB_	Alignment	not modelled	19.5	17	**PDBTitle:** structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
54	d1vkma_	Alignment	not modelled	19.3	20	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
55	c3n5mD_	Alignment	not modelled	18.8	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystals structure of a bacillus anthracis aminotransferase
56	c3iuuA_	Alignment	not modelled	18.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of putative metallopeptidase (yp_676511.1) from2 mesorhizobium sp. bnc1 at 2.13 a resolution
57	c2gezE_	Alignment	not modelled	18.5	11	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
58	c1apyA_	Alignment	not modelled	18.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartylglucosaminidase; **PDBTitle:** human aspartylglucosaminidase
59	c2yzkC_	Alignment	not modelled	18.2	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
60	c2k89A_	Alignment	not modelled	18.0	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phospholipase a-2-activating protein; **PDBTitle:** solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
61	c2jyaA_	Alignment	not modelled	17.8	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
62	c2kg4A_	Alignment	not modelled	17.4	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible protein **PDBTitle:** three-dimensional structure of human gadd45alpha in2 solution by nmr
63	c2iz6A_	Alignment	not modelled	17.2	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
64	c3i5tB_	Alignment	not modelled	16.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
65	c2cb1A_	Alignment	not modelled	16.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
66	c3dxvA_	Alignment	not modelled	16.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase; **PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
67	d1y0ba1	Alignment	not modelled	15.8	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d2ctza1	Alignment	not modelled	15.7	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
69	c2kruA_	Alignment	not modelled	15.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** solution nmr structure of the pcp_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)
70	c3c19A_	Alignment	not modelled	15.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mk0293; **PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19
71	c2qmaB_	Alignment	not modelled	15.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diaminobutyrate-pyruvate transaminase and l-2,4- **PDBTitle:** crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
72	d1k7ja_	Alignment	not modelled	15.1	10	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
73	c3a8uX_	Alignment	not modelled	15.1	27	**PDB header:**transferase **Chain:** X: **PDB Molecule:**omega-amino acid--pyruvate aminotransferase; **PDBTitle:** crystal structure of omega-amino acid:pyruvate aminotransferase
74	c1s97D_	Alignment	not modelled	15.1	21	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
75	d2bwna1	Alignment	not modelled	15.1	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
76	d1ru4a_	Alignment	not modelled	14.9	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate transeliminase

77	c1ko7B_	Alignment	not modelled	14.8	15	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution
78	d1zoda1	Alignment	not modelled	14.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
79	c1zczA_	Alignment	not modelled	13.9	22	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
80	d2byla1	Alignment	not modelled	13.8	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
81	d1kl1a_	Alignment	not modelled	13.6	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
82	d1zcza2	Alignment	not modelled	13.6	22	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
83	d1vl2a1	Alignment	not modelled	13.4	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
84	c3hs2H_	Alignment	not modelled	13.1	19	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
85	c1kblA_	Alignment	not modelled	13.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
86	d1pkxa2	Alignment	not modelled	12.7	19	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
87	c2zakB_	Alignment	not modelled	12.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
88	d1knxa1	Alignment	not modelled	12.6	15	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
89	d1jx4a2	Alignment	not modelled	12.6	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
90	c2vyoA_	Alignment	not modelled	12.5	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
91	c1k97A_	Alignment	not modelled	12.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
92	d2gz1a2	Alignment	not modelled	12.2	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
93	c1w17A_	Alignment	not modelled	11.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
94	d1h6za2	Alignment	not modelled	11.7	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
95	c3tqxA_	Alignment	not modelled	11.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-amino-3-ketobutyrate coenzyme a ligase; **PDBTitle:** structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
96	c1pixB_	Alignment	not modelled	11.6	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutaconyl-coa decarboxylase a subunit; **PDBTitle:** crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
97	d1l1qa_	Alignment	not modelled	11.3	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
98	c3ervA_	Alignment	not modelled	11.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative c39-like peptidase; **PDBTitle:** crystal structure of an putative c39-like peptidase from2 bacillus anthracis
99	d1g8ma2	Alignment	not modelled	11.0	22	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC