Phyre^2

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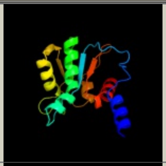
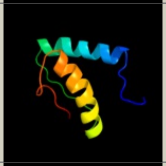
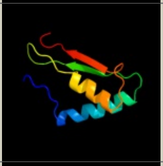
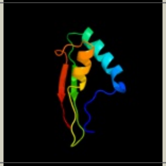
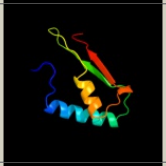
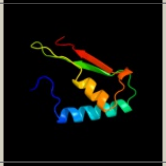
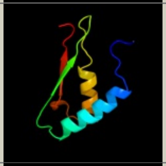
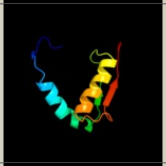
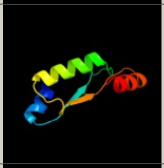
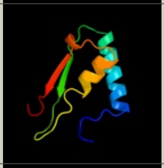
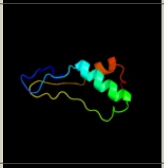
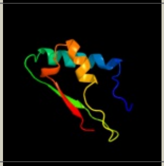
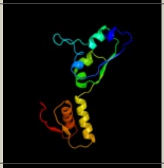
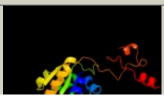
Description	P0AFY2
Date	Thu Jan 5 11:27:33 GMT 2012
Unique Job ID	6324878e7eec15f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ca8B_	Alignment		99.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
2	c3k13A_	Alignment		94.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
3	c2zf8A_	Alignment		93.2	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
4	d2aizp1	Alignment		93.0	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
5	d2hqsc1	Alignment		91.4	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
6	c1r1mA_	Alignment		90.1	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein class 4; **PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis
7	d1r1ma_	Alignment		90.1	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
8	c2kgwA_	Alignment		87.9	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
9	c2l26A_	Alignment		87.1	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
10	c3khnB_	Alignment		87.1	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
11	d1miob_	Alignment		84.3	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein

12	d1p5dx1	Alignment		83.9	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
13	c2h9aB_	Alignment		83.9	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase, iron- **PDBTitle:** corrinoid iron-sulfur protein
14	c2k1sA_	Alignment		82.5	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad; **PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
15	c3rhgA_	Alignment		82.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
16	c3oonA_	Alignment		81.8	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein (tpn50); **PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31
17	d1c7qa_	Alignment		79.0	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
18	c3qi7A_	Alignment		76.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
19	d1qh8b_	Alignment		74.3	9	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
20	c3c04A_	Alignment		73.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
21	c2yciX_	Alignment	not modelled	71.7	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
22	c3tr9A_	Alignment	not modelled	69.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
23	c2rgyA_	Alignment	not modelled	66.4	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
24	c2h9aA_	Alignment	not modelled	66.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
25	c1zzgB_	Alignment	not modelled	65.8	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
26	c3e3mA_	Alignment	not modelled	65.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
27	d1ad1a_	Alignment	not modelled	65.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
28	d2djia3	Alignment		64.3	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)

						**Family:**Pyruvate oxidase and decarboxylase PP module
29	d1f6ya_	Alignment	not modelled	61.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
30	d2nzug1	Alignment	not modelled	61.6	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
31	d3pmga1	Alignment	not modelled	61.2	16	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
32	d1vm8a_	Alignment	not modelled	60.7	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
33	d2nvma1	Alignment	not modelled	59.7	25	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
34	c2xmhB_	Alignment	not modelled	59.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
35	c3i3wB_	Alignment	not modelled	58.5	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
36	d2nlva1	Alignment	not modelled	58.4	35	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
37	c3brqA_	Alignment	not modelled	57.3	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
38	c3cs3A_	Alignment	not modelled	56.2	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
39	d2nwva1	Alignment	not modelled	56.1	35	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
40	c3d7qB_	Alignment	not modelled	54.7	30	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**xisi protein-like; **PDBTitle:** crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
41	c3h5oB_	Alignment	not modelled	54.4	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
42	c3ldtA_	Alignment	not modelled	54.3	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein, ompa family protein; **PDBTitle:** crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila
43	c3m5uA_	Alignment	not modelled	54.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
44	d1jv1a_	Alignment	not modelled	53.6	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
45	c3td4D_	Alignment	not modelled	51.6	13	**PDB header:**membrane protein,peptide binding protein **Chain:** D: **PDB Molecule:**outer membrane protein omp38; **PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
46	c3d8uA_	Alignment	not modelled	51.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
47	c2q8nB_	Alignment	not modelled	50.8	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
48	c3euaD_	Alignment	not modelled	50.4	9	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
49	d2a1fa1	Alignment	not modelled	50.0	13	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
50	d1hm5a_	Alignment	not modelled	49.7	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
51	c1vbkA_	Alignment	not modelled	46.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
52	c3pdiB_	Alignment	not modelled	45.3	11	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
						PDB header:transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine

53	c3oc9A_	Alignment	not modelled	44.8	13	pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
54	d1eyea_	Alignment	not modelled	44.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
55	c2vp8A_	Alignment	not modelled	44.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
56	c3clkB_	Alignment	not modelled	43.2	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum
57	c2fuvB_	Alignment	not modelled	42.1	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
58	c2y5sA_	Alignment	not modelled	42.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
59	d2g6ta1	Alignment	not modelled	39.2	16	**Fold:**CAC2185-like **Superfamily:**CAC2185-like **Family:**CAC2185-like
60	c2r6hC_	Alignment	not modelled	37.9	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
61	c3d7nA_	Alignment	not modelled	37.3	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
62	c3qk7C_	Alignment	not modelled	37.0	12	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
63	c2vefB_	Alignment	not modelled	37.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
64	d2ji7a1	Alignment	not modelled	36.5	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
65	d1t3ta6	Alignment	not modelled	36.2	14	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
66	d1m1nb_	Alignment	not modelled	36.0	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
67	c1ir6A_	Alignment	not modelled	34.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
68	d1ir6a_	Alignment	not modelled	34.1	12	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
69	d1xpja_	Alignment	not modelled	33.5	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
70	d1iata_	Alignment	not modelled	33.2	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
71	c2wu8A_	Alignment	not modelled	33.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
72	c3ff1B_	Alignment	not modelled	32.7	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
73	d3bofa1	Alignment	not modelled	32.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
74	c2kpoA_	Alignment	not modelled	32.3	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x2 fold protein; **PDBTitle:** solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
75	d2djia1	Alignment	not modelled	32.0	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
76	d1ru8a_	Alignment	not modelled	31.1	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
77	c3gv0A_	Alignment	not modelled	29.5	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
78	c3pe3D_	Alignment	not modelled	29.3	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate

79	c2yqsA_	Alignment	not modelled	29.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
80	c3nwyB_	Alignment	not modelled	29.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
81	d1ozha1	Alignment	not modelled	28.8	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
82	c3dbiA_	Alignment	not modelled	28.5	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate
83	d1cqxa3	Alignment	not modelled	28.0	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
84	d1rz3a_	Alignment	not modelled	27.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
85	d2akoa1	Alignment	not modelled	27.2	9	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
86	c3k32D_	Alignment	not modelled	26.6	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
87	c3dwgA_	Alignment	not modelled	26.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase b; **PDBTitle:** crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
88	d1gzda_	Alignment	not modelled	26.4	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
89	c2zvyB_	Alignment	not modelled	26.3	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form ii)
90	d1u0fa_	Alignment	not modelled	26.2	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
91	d1vg0a1	Alignment	not modelled	26.1	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
92	d1ybha1	Alignment	not modelled	26.0	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
93	c3hbmA_	Alignment	not modelled	25.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
94	c3hcwB_	Alignment	not modelled	25.2	9	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor; **PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus
95	d1jqlb_	Alignment	not modelled	25.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
96	d1lvla2	Alignment	not modelled	24.6	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
97	c1tx2A_	Alignment	not modelled	24.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
98	d1tx2a_	Alignment	not modelled	24.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
99	d3lada2	Alignment	not modelled	24.2	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
100	c2xdqA_	Alignment	not modelled	24.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
101	c3ll5C_	Alignment	not modelled	24.1	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyl kinase related protein; **PDBTitle:** crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
102	c2pqmA_	Alignment	not modelled	24.0	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
103	c3mn1B	Alignment	not modelled	23.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase;

		Alignment	not modelled			**PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
104	c2va1A_	Alignment	not modelled	23.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of ump kinase from ureaplasma parvum
105	c3ljkA_	Alignment	not modelled	23.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
106	d1vmea1	Alignment	not modelled	23.0	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
107	c2x5sB_	Alignment	not modelled	22.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
108	c3k9cA_	Alignment	not modelled	21.9	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
109	c1t10A_	Alignment	not modelled	21.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
110	c2cunA_	Alignment	not modelled	21.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
111	c2vsnB_	Alignment	not modelled	21.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
112	c3f0hA_	Alignment	not modelled	21.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
113	c3k4hA_	Alignment	not modelled	21.2	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
114	c3fxaA_	Alignment	not modelled	21.0	8	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
115	c3egcF_	Alignment	not modelled	20.7	15	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative ribose operon repressor; **PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
116	c3p1tB_	Alignment	not modelled	20.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
117	d1ebda2	Alignment	not modelled	20.4	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
118	c3q41B_	Alignment	not modelled	20.2	6	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
119	d1pvda1	Alignment	not modelled	20.1	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
120	c2o2cB_	Alignment	not modelled	20.0	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site