Phyre^2

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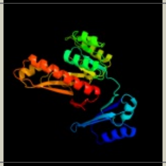
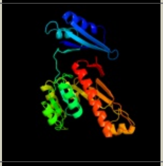
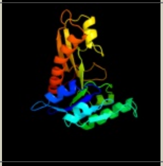
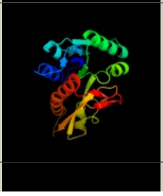
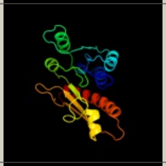
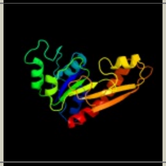
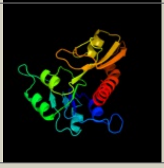
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3louB_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
2	c3o1lB_	Alignment		100.0	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
3	c3obiC_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
4	c3n0vD_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
5	c3nrbD_	Alignment		100.0	39	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
6	c2ywrA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
7	d1jkxa_	Alignment		100.0	26	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
8	c3p9xB_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
9	c3tqrA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
10	c3dcjA_	Alignment		100.0	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
11	d1meoa_	Alignment		100.0	29	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase

12	c3kcqA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
13	d1fmta2	Alignment		100.0	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
14	d2blna2	Alignment		100.0	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
15	c1z7eC_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
16	c1fmtA_	Alignment		100.0	19	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
17	d1s3ia2	Alignment		100.0	18	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
18	c3tqqA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
19	c1yrwA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
20	d2bw0a2	Alignment		100.0	17	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
21	c3q0iA_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
22	c3rfoA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
23	c1s3iA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
24	d1zgha2	Alignment	not modelled	100.0	17	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
25	c1zghA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
26	d1zpva1	Alignment	not modelled	99.4	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
27	c1u8sB_	Alignment	not modelled	99.3	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
28	d1u8sa1	Alignment	not modelled	99.0	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
29	c2nviB	Alignment	not modelled	99.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein;

29	[illegible]	Alignment	not modelled	99.0	11	**PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
30	d1u8sa2	Alignment	not modelled	98.8	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
31	c3p96A_	Alignment	not modelled	97.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
32	c1y7pB_	Alignment	not modelled	97.4	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
33	c3ibwA_	Alignment	not modelled	97.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
34	d1ygya3	Alignment	not modelled	97.1	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
35	d1sc6a3	Alignment	not modelled	96.9	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
36	c1ygyA_	Alignment	not modelled	96.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
37	d2fgca2	Alignment	not modelled	96.2	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
38	c2fgcA_	Alignment	not modelled	95.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
39	c3a14B_	Alignment	not modelled	94.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
40	d1ru8a_	Alignment	not modelled	94.7	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
41	c2f1fA_	Alignment	not modelled	94.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
42	d2pc6a2	Alignment	not modelled	93.9	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
43	d2d13a1	Alignment	not modelled	93.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
44	d1f0ka_	Alignment	not modelled	93.7	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
45	c2pc6C_	Alignment	not modelled	93.2	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
46	d1xi8a3	Alignment	not modelled	92.9	23	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
47	c2e21A_	Alignment	not modelled	92.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
48	c2hmaA_	Alignment	not modelled	92.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
49	d2f06a1	Alignment	not modelled	92.5	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
50	d2f1fa1	Alignment	not modelled	92.5	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
51	c2derA_	Alignment	not modelled	91.0	12	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
52	d1wy5a1	Alignment	not modelled	90.5	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
53	d1r0ka2	Alignment	not modelled	90.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						PDB header:cell cycle

54	c1ni5A_	Alignment	not modelled	90.5	15	**Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
55	c2jcyA_	Alignment	not modelled	90.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
56	c3bl5E_	Alignment	not modelled	90.0	9	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
57	d1ni5a1	Alignment	not modelled	89.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
58	c2fu3A_	Alignment	not modelled	89.6	15	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
59	d2ftsa3	Alignment	not modelled	89.5	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
60	c3l76B_	Alignment	not modelled	88.5	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
61	d1wu2a3	Alignment	not modelled	88.3	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
62	d2f06a2	Alignment	not modelled	87.4	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
63	c3a2kB_	Alignment	not modelled	86.8	13	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
64	c1ofgF_	Alignment	not modelled	86.7	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
65	d1q0qa2	Alignment	not modelled	86.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c1h6dL_	Alignment	not modelled	86.5	10	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
67	c2nvwB_	Alignment	not modelled	86.5	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
68	c2nqqA_	Alignment	not modelled	86.2	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
69	d1phza1	Alignment	not modelled	86.0	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
70	c2q8nB_	Alignment	not modelled	85.8	16	**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
71	c2qmxB_	Alignment	not modelled	85.6	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
72	c3mwbA_	Alignment	not modelled	85.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
73	c3luyA_	Alignment	not modelled	84.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
74	d1jsca3	Alignment	not modelled	83.9	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
75	d1uz5a3	Alignment	not modelled	83.5	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
76	c3e18A_	Alignment	not modelled	83.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
77	c3q2kB_	Alignment	not modelled	82.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
78	c1uz5A_	Alignment	not modelled	82.4	11	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
79	c3mtjA_	Alignment	not modelled	81.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
						PDB header:structural genomics, unknown function

80	c2f06B_	Alignment	not modelled	80.0	13	**Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
81	c3lq1A_	Alignment	not modelled	80.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
82	c2o48X_	Alignment	not modelled	79.4	13	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
83	c3ceaA_	Alignment	not modelled	78.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
84	c2pjkA_	Alignment	not modelled	77.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
85	d2hmfa3	Alignment	not modelled	77.0	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
86	d1ozha3	Alignment	not modelled	76.9	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
87	c3e9mC_	Alignment	not modelled	75.8	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
88	c2is8A_	Alignment	not modelled	75.5	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
89	d1y5ea1	Alignment	not modelled	74.9	12	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
90	d2f7wa1	Alignment	not modelled	74.9	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
91	c3gd5D_	Alignment	not modelled	74.4	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
92	c2vxoB_	Alignment	not modelled	73.9	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
93	d1ybha3	Alignment	not modelled	73.6	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
94	d1vh3a_	Alignment	not modelled	73.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
95	d1h6da1	Alignment	not modelled	72.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	c3ketA_	Alignment	not modelled	72.1	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
97	c1xeaD_	Alignment	not modelled	71.9	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
98	d1jlja_	Alignment	not modelled	71.8	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
99	c3moiA_	Alignment	not modelled	71.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
100	d1tq8a_	Alignment	not modelled	71.0	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
101	c3db2C_	Alignment	not modelled	70.8	4	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
102	c1evjC_	Alignment	not modelled	69.8	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
103	c1zh8B_	Alignment	not modelled	69.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
104	d2hmfa2	Alignment	not modelled	69.4	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like

						Family: Aspartokinase allosteric domain-like
105	d3bula2	Alignment	not modelled	69.2	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
106	d2djia3	Alignment	not modelled	68.8	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
107	d1mvla_	Alignment	not modelled	68.6	14	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
108	c1mvlA_	Alignment	not modelled	68.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
109	d1vl2a1	Alignment	not modelled	68.5	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
110	c1jscA_	Alignment	not modelled	68.3	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
111	d2qmwa2	Alignment	not modelled	68.0	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
112	d2nqra3	Alignment	not modelled	66.6	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
113	c2eghA_	Alignment	not modelled	65.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
114	d1a9xa4	Alignment	not modelled	65.6	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
115	c2ho3D_	Alignment	not modelled	65.6	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
116	c2glxD_	Alignment	not modelled	62.8	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
117	d2nvwa1	Alignment	not modelled	62.7	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
118	d1q6za3	Alignment	not modelled	61.5	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
119	c3rbvA_	Alignment	not modelled	61.1	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
120	c2ag1A_	Alignment	not modelled	61.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet