Phyre2

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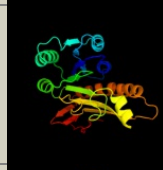
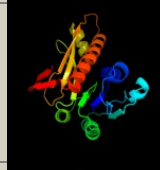
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jkxa_	Alignment		100.0	100	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
2	c3tqrA_	Alignment		100.0	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
3	c3louB_	Alignment		100.0	25	**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
4	c2ywrA_	Alignment		100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
5	c3o1lB_	Alignment		100.0	26	**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
6	c3n0vD_	Alignment		100.0	23	**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
7	c3obiC_	Alignment		100.0	24	**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
8	c3nrbD_	Alignment		100.0	25	**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
9	c3p9xB_	Alignment		100.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
10	d1meoa_	Alignment		100.0	41	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
11	c3kcqA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum

12	c3dcjA_	Alignment		100.0	35	**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
13	c1z7eC_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
14	c3tqqA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
15	c1yrwA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
16	d2blna2	Alignment		100.0	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
17	c1fmtA_	Alignment		100.0	19	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
18	c3q0iA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
19	c1s3iA_	Alignment		100.0	19	**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
20	c3rfoA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
21	d1fmta2	Alignment	not modelled	100.0	20	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
22	d1s3ia2	Alignment	not modelled	100.0	19	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
23	d2bw0a2	Alignment	not modelled	100.0	20	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
24	c1zghA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
25	d1zgha2	Alignment	not modelled	100.0	12	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
26	c1nvmB_	Alignment	not modelled	95.1	26	**PDB header:**lyase/oxidoreductase **Chain:** B: **PDB Molecule:**acetaldehyde dehydrogenase (acylating); **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
27	d1nvmb1	Alignment	not modelled	93.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	d1r0ka2	Alignment	not modelled	92.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
29	d1q0qa2	Alignment	not modelled	92.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-

						terminal domain
30	c2ho3D_	Alignment	not modelled	92.4	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
31	c3q2kB_	Alignment	not modelled	92.1	14	**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
32	c3ceaA_	Alignment	not modelled	92.0	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
33	c3a14B_	Alignment	not modelled	91.9	10	**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
34	c3dtyA_	Alignment	not modelled	91.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
35	c3rbvA_	Alignment	not modelled	91.5	14	**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
36	c2o48X_	Alignment	not modelled	91.2	17	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
37	c3db2C_	Alignment	not modelled	91.0	15	**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
38	c1r0lD_	Alignment	not modelled	90.8	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
39	c2nvwB_	Alignment	not modelled	90.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
40	c3v5nA_	Alignment	not modelled	89.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
41	d1b74a1	Alignment	not modelled	89.8	27	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
42	c1zh8B_	Alignment	not modelled	89.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
43	d1o6ca_	Alignment	not modelled	89.3	9	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
44	c3ezyB_	Alignment	not modelled	88.9	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
45	c3moiA_	Alignment	not modelled	88.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
46	c1b74A_	Alignment	not modelled	88.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
47	c2jfzB_	Alignment	not modelled	88.3	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
48	d2nvwa1	Alignment	not modelled	88.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	c3btuD_	Alignment	not modelled	87.5	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
50	d2d13a1	Alignment	not modelled	87.0	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
51	c3e9mC_	Alignment	not modelled	86.9	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
52	c3ec7C_	Alignment	not modelled	86.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
53	c2jcyA_	Alignment	not modelled	85.9	22	**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
54	c1xeaD_	Alignment	not modelled	85.9	18	**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
55	c2p2sA_	Alignment	not modelled	85.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
56	c3m2tA_	Alignment	not modelled	85.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
57	c2q4eB_	Alignment	not modelled	84.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
58	c3ot5D_	Alignment	not modelled	84.6	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
59	d1zh8a1	Alignment	not modelled	84.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	d2czca2	Alignment	not modelled	84.1	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	c1ni5A_	Alignment	not modelled	83.7	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
62	c3e18A_	Alignment	not modelled	83.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
63	c2glxD_	Alignment	not modelled	81.1	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
64	c2p2gD_	Alignment	not modelled	80.0	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
65	d1f0ka_	Alignment	not modelled	79.0	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
66	c1tltB_	Alignment	not modelled	78.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
67	c3nbmA_	Alignment	not modelled	78.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
68	c3ketA_	Alignment	not modelled	77.8	15	**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
69	c1h6dL_	Alignment	not modelled	77.3	12	**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
70	c2q8nB_	Alignment	not modelled	77.3	9	**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	c3evnA_	Alignment	not modelled	77.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
72	c3nt5B_	Alignment	not modelled	76.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
73	c2eghA_	Alignment	not modelled	75.4	16	**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
74	d1rrma_	Alignment	not modelled	75.3	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
75	c3euwB_	Alignment	not modelled	75.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
76	d1v4va_	Alignment	not modelled	74.9	9	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
77	c1ofgF_	Alignment	not modelled	74.8	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase;

						PDBTitle: glucose-fructose oxidoreductase
78	d1ru8a_	Alignment	not modelled	74.4	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
79	c3au9A_	Alignment	not modelled	74.4	21	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
80	c3bfjK_	Alignment	not modelled	74.1	16	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
81	d1iira_	Alignment	not modelled	73.9	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
82	c3ip3D_	Alignment	not modelled	73.7	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
83	d1vlva2	Alignment	not modelled	73.6	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
84	d1ni5a1	Alignment	not modelled	73.4	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
85	c3nklA_	Alignment	not modelled	72.1	13	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
86	c2e21A_	Alignment	not modelled	71.8	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.
87	c2l18A_	Alignment	not modelled	70.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
88	d1ydwa1	Alignment	not modelled	68.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
89	d1rrva_	Alignment	not modelled	68.3	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
90	d1xeaa1	Alignment	not modelled	68.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
91	c3gfgB_	Alignment	not modelled	68.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
92	c1ml4A_	Alignment	not modelled	67.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
93	c3ox4D_	Alignment	not modelled	66.8	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
94	d1t1ra2	Alignment	not modelled	66.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	c2gzmB_	Alignment	not modelled	64.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
96	c3gd5D_	Alignment	not modelled	64.4	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
97	c3rh0A_	Alignment	not modelled	63.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
98	c3kuxA_	Alignment	not modelled	63.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
99	d1txga2	Alignment	not modelled	63.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
100	d1e9yb2	Alignment	not modelled	62.4	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
101	c2l2qA_	Alignment	not modelled	60.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
102	d1o8bb1	Alignment	not modelled	60.1	32	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
						PDB header:isomerase

103	c2jfnA_	Alignment	not modelled	58.2	21	**Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
104	d1jl3a_	Alignment	not modelled	57.9	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
105	c3a2kB_	Alignment	not modelled	57.3	17	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
106	d2aeea1	Alignment	not modelled	57.3	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
107	c2hmaA_	Alignment	not modelled	56.6	20	**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
108	c3uuwB_	Alignment	not modelled	56.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase with nad(p)-binding rossmann-fold **PDBTitle:** 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
109	d1wy5a1	Alignment	not modelled	55.7	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
110	c2dt5A_	Alignment	not modelled	55.4	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
111	c3rf7A_	Alignment	not modelled	55.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
112	c2jfoB_	Alignment	not modelled	54.8	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
113	d1ml4a2	Alignment	not modelled	54.6	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
114	c3do5A_	Alignment	not modelled	54.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
115	c2derA_	Alignment	not modelled	53.0	24	**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
116	c2dy0A_	Alignment	not modelled	52.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
117	d1ejxc2	Alignment	not modelled	51.5	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
118	c3lq1A_	Alignment	not modelled	51.4	18	**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
119	d1m1nb_	Alignment	not modelled	51.2	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
120	c2jjmH_	Alignment	not modelled	51.2	9	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.