Phyre2

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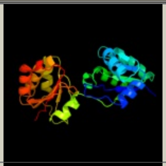
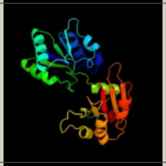
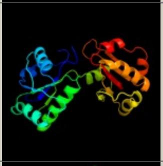
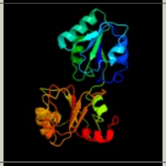
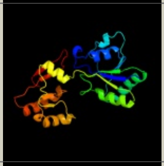
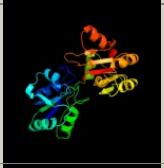
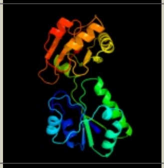
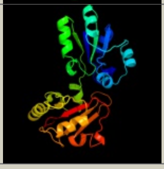
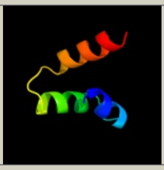
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kwpA_	Alignment		100.0	49	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis
2	d1cbfa_	Alignment		100.0	17	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
3	c1cbfA_	Alignment		100.0	17	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**cobalt-precorrin-4 transmethylase; **PDBTitle:** the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
4	c1pjtB_	Alignment		100.0	20	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
5	c2yboA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
6	d1wyza1	Alignment		100.0	22	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
7	d1s4da_	Alignment		100.0	15	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
8	d1pjqa2	Alignment		100.0	20	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
9	c3ndcB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
10	c2zvbA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-3 c17-methyltransferase; **PDBTitle:** crystal structure of tt0207 from thermus thermophilus hb8
11	d1va0a1	Alignment		100.0	14	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase

12	d1wdea_	Alignment		100.0	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
13	d1ve2a1	Alignment		100.0	21	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
14	c3nutC_	Alignment		100.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**precorrin-3 methylase; **PDBTitle:** crystal structure of the methyltransferase cobj
15	c3nd1B_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6a synthase/cobf protein; **PDBTitle:** crystal structure of precorrin-6a synthase from rhodobacter capsulatus
16	c2qbuA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 methyltransferase; **PDBTitle:** crystal structure of methanothermobacter thermautotrophicus cbil
17	c2e0kA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
18	d1vhva_	Alignment		100.0	13	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
19	d2deka1	Alignment		100.0	21	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
20	c3i4tA_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**diphthine synthase; **PDBTitle:** crystal structure of putative diphthine synthase from2 entamoeba histolytica
21	c2npnA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative cobalamin synthesis related protein; **PDBTitle:** crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
22	c2bb3B_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cobalamin biosynthesis precorrin-6y methylase (cbie); **PDBTitle:** crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
23	d2bb3a1	Alignment	not modelled	100.0	18	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
24	c3fq6A_	Alignment	not modelled	100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
25	c3hh1D_	Alignment	not modelled	100.0	45	**PDB header:**transferase **Chain:** D: **PDB Molecule:**tetrapyrrole methylase family protein; **PDBTitle:** the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum tls
26	d2ezla_	Alignment		85.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
27	c2px0D_	Alignment	not modelled	75.1	15	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf;

						PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
28	c3q3vA_	Alignment	not modelled	73.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
29	c1w78A_	Alignment	not modelled	56.4	14	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
30	c2z1dA_	Alignment	not modelled	51.7	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
31	d1ii7a_	Alignment	not modelled	51.2	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
32	c3navB_	Alignment	not modelled	44.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
33	c3bioB_	Alignment	not modelled	42.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
34	c3l7oB_	Alignment	not modelled	40.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
35	d1ptma_	Alignment	not modelled	39.4	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
36	c2q5cA_	Alignment	not modelled	38.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
37	c2q7xA_	Alignment	not modelled	36.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0052 protein sp_1565; **PDBTitle:** crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
38	c3av0A_	Alignment	not modelled	35.3	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
39	d1t9ba1	Alignment	not modelled	34.4	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
40	d2hzba1	Alignment	not modelled	34.4	10	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
41	d1ybha1	Alignment	not modelled	33.4	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
42	d1sc6a2	Alignment	not modelled	33.4	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
43	d2d59a1	Alignment	not modelled	33.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
44	d1xfia_	Alignment	not modelled	32.9	18	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
45	c2l0kA_	Alignment	not modelled	31.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
46	c2z2uA_	Alignment	not modelled	31.7	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
47	d1gdha2	Alignment	not modelled	30.2	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
48	d2naca2	Alignment	not modelled	30.0	9	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
49	c3mvnA_	Alignment	not modelled	29.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
50	c3rhtB_	Alignment	not modelled	29.3	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
51	d2z67a1	Alignment	not modelled	29.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
						Fold:7-stranded beta/alpha barrel

52	d1v6ta_	Alignment	not modelled	27.4	17	**Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
53	d2o8ra3	Alignment	not modelled	27.4	20	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
54	c3auzA_	Alignment	not modelled	26.7	21	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
55	d2gk3a1	Alignment	not modelled	26.5	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
56	d1xtoa_	Alignment	not modelled	26.4	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Coenzyme PQQ synthesis protein B, PqqB
57	c1gqqA_	Alignment	not modelled	25.0	18	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
58	d1jeyb2	Alignment	not modelled	24.4	9	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku80 subunit N-terminal domain
59	d1f6ya_	Alignment	not modelled	24.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
60	d1q6za1	Alignment	not modelled	23.4	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
61	c3c19A_	Alignment	not modelled	23.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mk0293; **PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19
62	c3hl2D_	Alignment	not modelled	22.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**o-phosphoseryl-trna(sec) selenium transferase; **PDBTitle:** the crystal structure of the human sepsecs-trnasec complex
63	c2q8uA_	Alignment	not modelled	22.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
64	d1ad1a_	Alignment	not modelled	22.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
65	d1ygya2	Alignment	not modelled	22.3	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
66	c2nacA_	Alignment	not modelled	22.3	10	**PDB header:**oxidoreductase(aldehyde(d),nad+(a)) **Chain:** A: **PDB Molecule:**nad-dependent formate dehydrogenase; **PDBTitle:** high resolution structures of holo and apo formate dehydrogenase
67	c1z4hA_	Alignment	not modelled	22.1	13	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
68	c3dmdA_	Alignment	not modelled	21.7	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
69	c3cf4G_	Alignment	not modelled	21.5	13	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
70	d1qbjc_	Alignment	not modelled	21.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
71	d1iuka_	Alignment	not modelled	21.1	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
72	c3iwpK_	Alignment	not modelled	20.9	13	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
73	d1t57a_	Alignment	not modelled	20.7	11	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
74	c3g2bA_	Alignment	not modelled	20.6	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
75	c2yx0A_	Alignment	not modelled	20.2	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
76	d2jfga2	Alignment	not modelled	20.0	21	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
77	d2djia1	Alignment	not modelled	19.9	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain

78	c3canA_	Alignment	not modelled	19.4	21	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
79	c2qasA_	Alignment	not modelled	19.2	20	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of caulobacter crescentus sspb ortholog
80	c2ppvA_	Alignment	not modelled	19.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
81	c3qg5D_	Alignment	not modelled	18.5	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
82	d1jeya2	Alignment	not modelled	18.4	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku70 subunit N-terminal domain
83	d1pvda1	Alignment	not modelled	18.3	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
84	c3ecsD_	Alignment	not modelled	18.2	11	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
85	d1p3y1_	Alignment	not modelled	17.9	5	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
86	c3lqkA_	Alignment	not modelled	17.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
87	c2qazC_	Alignment	not modelled	17.8	20	**PDB header:**hydrolase activator **Chain:** C: **PDB Molecule:**sspb protein; **PDBTitle:** structure of c. crescentus sspb ortholog
88	c3imkA_	Alignment	not modelled	17.5	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
89	c2pjmA_	Alignment	not modelled	16.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
90	c3pfnB_	Alignment	not modelled	16.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
91	c3oa2B_	Alignment	not modelled	16.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
92	c1yirA_	Alignment	not modelled	16.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase
93	d1t6t1_	Alignment	not modelled	16.0	10	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
94	d1qgpa_	Alignment	not modelled	16.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
95	d2ez9a1	Alignment	not modelled	15.6	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
96	c1lc3A_	Alignment	not modelled	15.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
97	d2gxba1	Alignment	not modelled	15.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
98	d2dlda2	Alignment	not modelled	15.0	20	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
99	d2q4qa1	Alignment	not modelled	15.0	16	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like