Phyre2

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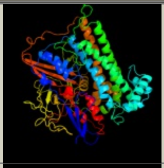
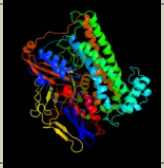
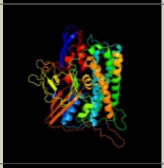
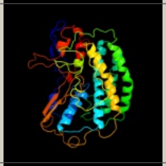
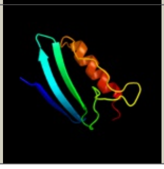
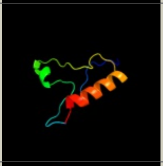
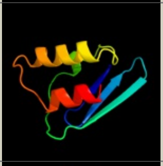
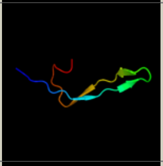
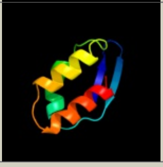
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3myrB_	Alignment		100.0	54	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
2	d1e3db_	Alignment		100.0	45	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
3	d1frfl_	Alignment		100.0	45	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
4	c1h2aL_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
5	d1wuil1	Alignment		100.0	43	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
6	d1yq9h1	Alignment		100.0	46	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
7	d1cc1l_	Alignment		100.0	34	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
8	c2wpnB_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
9	c2fug4_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** 4: **PDB Molecule:**nadh-quinone oxidoreductase chain 4; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
10	d2fug41	Alignment		100.0	22	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
11	d1ffvc1	Alignment		74.7	18	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like

12	d1yeya2	Alignment		63.2	11	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
13	d1v97a4	Alignment		56.0	6	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
14	d1t3qc1	Alignment		55.0	10	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
15	d1iyxa2	Alignment		52.6	21	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
16	d1vqza1	Alignment		52.1	22	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
17	c1vqzA_	Alignment		49.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
18	d1n62c1	Alignment		47.1	21	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
19	c1xx3A_	Alignment		46.9	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
20	d1jdfa2	Alignment		46.3	11	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
21	c2dgyA_	Alignment	not modelled	45.8	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
22	d1rvka2	Alignment	not modelled	42.5	16	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
23	d1jroa3	Alignment	not modelled	39.9	19	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
24	c2grxC_	Alignment	not modelled	39.2	18	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
25	d2ntka1	Alignment	not modelled	37.3	27	**Fold:**Ntn hydrolase-like **Superfamily:**Archaeal IMP cyclohydrolase PurO **Family:**Archaeal IMP cyclohydrolase PurO
26	d1x2ga1	Alignment	not modelled	35.7	22	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
27	d2gskb1	Alignment	not modelled	35.5	18	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
28	d2gjxa2	Alignment	not modelled	34.8	29	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**beta-N-acetylhexosaminidase domain
29	c1ufiD	Alignment	not modelled	33.9	20	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**major centromere autoantigen b;

29	c1ufiD_	Alignment	not modelled	33.9	20	**PDBTitle:** crystal structure of the dimerization domain of human cenp-b
30	d1ufia_	Alignment	not modelled	33.7	20	**Fold:**ROP-like **Superfamily:**Dimerisation domain of CENP-B **Family:**Dimerisation domain of CENP-B
31	d1u07a_	Alignment	not modelled	33.5	21	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
32	c2oqkA_	Alignment	not modelled	31.0	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
33	c2dnwA_	Alignment	not modelled	30.7	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
34	d1wfza_	Alignment	not modelled	28.9	20	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
35	c2xzn5_	Alignment	not modelled	27.3	43	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
36	c3u5ga_	Alignment	not modelled	27.1	43	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
37	c3b42B_	Alignment	not modelled	24.2	26	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0935
38	d1hcza2	Alignment	not modelled	23.4	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
39	c3sc0A_	Alignment	not modelled	23.0	63	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methylmalonic aciduria and homocystinuria type c protein; **PDBTitle:** crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
40	d1nowa2	Alignment	not modelled	23.0	21	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**beta-N-acetylhexosaminidase domain
41	d2chra2	Alignment	not modelled	23.0	26	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
42	d2cbia3	Alignment	not modelled	22.7	18	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**Hyaluronidase N-terminal domain-like
43	d1rm6b1	Alignment	not modelled	22.1	19	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
44	c3j0iF_	Alignment	not modelled	21.6	33	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**phikz029; **PDBTitle:** fitting of the phikz gp29pr structure into the cryo-em density map of2 the phikz polysheath
45	c3g0kA_	Alignment	not modelled	21.3	24	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
46	c3nxlD_	Alignment	not modelled	21.3	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** crystal structure of glucarate dehydratase from burkholderia cepacia2 complexed with magnesium
47	c1y7jA_	Alignment	not modelled	21.1	67	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**agouti signaling protein; **PDBTitle:** nmr structure family of human agouti signalling protein (80-2 132: q115y, s124y)
48	c3b4oB_	Alignment	not modelled	21.1	27	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein a/b; **PDBTitle:** crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
49	c2k9kA_	Alignment	not modelled	20.9	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
50	c2e5aA_	Alignment	not modelled	18.7	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
51	c3f40A_	Alignment	not modelled	18.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at3 1.27 a resolution
52	d1qbaa4	Alignment	not modelled	17.4	25	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**beta-N-acetylhexosaminidase domain
53	c1n62C_	Alignment	not modelled	17.3	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh),

						n-2 butylisocyanide-bound state
54	d1h9aa2	Alignment	not modelled	16.7	12	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
55	d1d7qa_	Alignment	not modelled	15.9	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
56	d1qkia2	Alignment	not modelled	15.8	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
57	c2nytB_	Alignment	not modelled	15.7	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
58	d1jt8a_	Alignment	not modelled	15.2	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
59	c1grjA_	Alignment	not modelled	15.0	10	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
60	d2q22a1	Alignment	not modelled	14.8	36	**Fold:**Ava3019-like **Superfamily:**Ava3019-like **Family:**Ava3019-like
61	c3bjsB_	Alignment	not modelled	14.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of a member of enolase superfamily from polaromonas2 sp. js666
62	c3hk4B_	Alignment	not modelled	14.7	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mlr7391 protein; **PDBTitle:** crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
63	c2l4bA_	Alignment	not modelled	14.5	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
64	c2fq2A_	Alignment	not modelled	14.0	14	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
65	c2kboA_	Alignment	not modelled	13.5	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g; **PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
66	d1ihra_	Alignment	not modelled	13.5	18	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
67	c3ff0A_	Alignment	not modelled	13.2	36	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**phenazine biosynthesis protein phzb 2; **PDBTitle:** crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
68	c2l9fA_	Alignment	not modelled	12.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
69	d1jpma2	Alignment	not modelled	12.8	18	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
70	d3dm8a1	Alignment	not modelled	12.7	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rpa4348-like
71	c2v3jA_	Alignment	not modelled	12.5	20	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**essential for mitotic growth 1; **PDBTitle:** the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
72	d1t8ka_	Alignment	not modelled	12.5	22	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
73	d2choa3	Alignment	not modelled	12.3	11	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**Hyaluronidase N-terminal domain-like
74	c1x3oA_	Alignment	not modelled	12.2	21	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
75	c3b47A_	Alignment	not modelled	12.0	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0582
76	c3f14A_	Alignment	not modelled	11.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_680363.1) from cytophaga hutchinsonii atcc 33406 at 1.45 a3 resolution
77	c2w3rG_	Alignment	not modelled	11.5	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
78	c2nqlB_	Alignment	not modelled	11.5	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens

79	c1puoA_	Alignment	not modelled	11.4	17	**PDB header:**allergen **Chain:** A: **PDB Molecule:**major allergen i polypeptide, fused chain 2, **PDBTitle:** crystal structure of fel d 1- the major cat allergen
80	c1qkiE_	Alignment	not modelled	11.4	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
81	c1j73C_	Alignment	not modelled	11.4	22	**PDB header:**hormone/growth factor **Chain:** C: **PDB Molecule:**insulin a; **PDBTitle:** crystal structure of an unstable insulin analog with native activity.
82	c1j73A_	Alignment	not modelled	11.4	22	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin a; **PDBTitle:** crystal structure of an unstable insulin analog with native activity.
83	d2gdqa2	Alignment	not modelled	11.4	16	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
84	d2bs2b2	Alignment	not modelled	11.3	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
85	c3fq9A_	Alignment	not modelled	11.2	22	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin; **PDBTitle:** design of an insulin analog with enhanced receptor-binding2 selectivity. rationale, structure, and therapeutic3 implications
86	c3fq9C_	Alignment	not modelled	11.2	22	**PDB header:**hormone **Chain:** C: **PDB Molecule:**insulin; **PDBTitle:** design of an insulin analog with enhanced receptor-binding2 selectivity. rationale, structure, and therapeutic3 implications
87	d1r9pa_	Alignment	not modelled	11.1	16	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
88	c2bhlB_	Alignment	not modelled	11.1	24	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
89	c3ewnA_	Alignment	not modelled	11.1	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
90	d2e1ba2	Alignment	not modelled	11.0	36	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**AlaX-like
91	d2r4qa1	Alignment	not modelled	10.7	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
92	c2qq4A_	Alignment	not modelled	10.6	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
93	d1grja2	Alignment	not modelled	10.6	10	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
94	c3gwnA_	Alignment	not modelled	10.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-linked sulfhydryl oxidase r596; **PDBTitle:** crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
95	c3grdA_	Alignment	not modelled	10.4	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-superfamily protein; **PDBTitle:** crystal structure of ntf2-superfamily protein with unknown2 function (np_977240.1) from bacillus cereus atcc 10987 at3 1.25 a resolution
96	c3fgyB_	Alignment	not modelled	10.3	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein (bxe_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
97	d1o98a1	Alignment	not modelled	10.3	42	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
98	c3bboL_	Alignment	not modelled	10.3	11	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
99	d1n62a2	Alignment	not modelled	10.2	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins