Phyre2

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Description	P0ACE0
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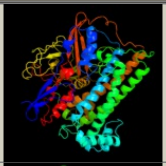
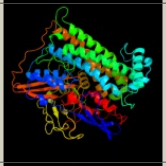
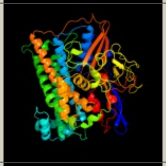
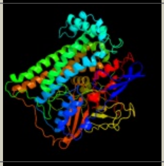
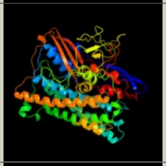
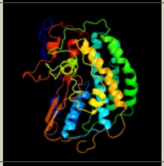
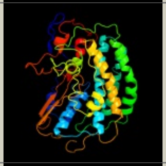
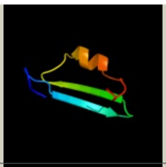
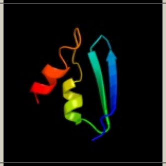
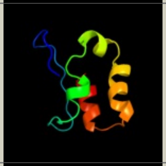
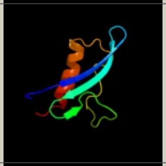
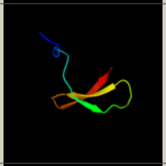
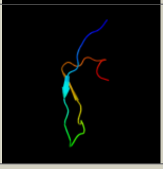
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3myrB_	Alignment		100.0	50	**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	d1frfl_	Alignment		100.0	45	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
3	d1wuil1	Alignment		100.0	44	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
4	d1yq9h1	Alignment		100.0	45	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
5	d1e3db_	Alignment		100.0	44	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
6	c1h2aL_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
7	d1cc1l_	Alignment		100.0	36	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
8	c2wpnB_	Alignment		100.0	39	**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	21	**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	21	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
11	d1ffvc1	Alignment		79.9	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	d1vqza1	Alignment		74.9	7	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
13	c1vqzA_	Alignment		73.3	6	**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
14	d1x2ga1	Alignment		71.1	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
15	d1t3qc1	Alignment		57.8	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
16	d1yeya2	Alignment		56.9	10	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
17	d1n62c1	Alignment		52.1	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
18	c1xx3A_	Alignment		51.4	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
19	c2dgyA_	Alignment		50.0	8	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
20	d2gskb1	Alignment		49.6	25	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
21	d1o12a1	Alignment	not modelled	48.2	33	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
22	d1u07a_	Alignment	not modelled	45.4	25	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
23	d1jdfa2	Alignment	not modelled	44.8	10	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
24	d1v97a4	Alignment	not modelled	44.7	4	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
25	d1jroa3	Alignment	not modelled	44.4	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
26	c2oqkA_	Alignment	not modelled	43.6	14	**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
27	d1iyxa2	Alignment	not modelled	42.6	21	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
28	c2e5aA_	Alignment	not modelled	41.8	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp

29	d1rm6b1	Alignment	not modelled	41.6	5	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
30	d1w6ta2	Alignment	not modelled	41.5	26	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
31	c3o6uB_	Alignment	not modelled	41.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein cpe2226; **PDBTitle:** crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
32	c2qq4A_	Alignment	not modelled	40.9	21	**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
33	d1jt8a_	Alignment	not modelled	40.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
34	c3mkcA_	Alignment	not modelled	39.2	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**racemase; **PDBTitle:** crystal structure of a putative racemase
35	c2grxC_	Alignment	not modelled	38.9	25	**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
36	d1vk9a_	Alignment	not modelled	38.8	27	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Hypothetical protein TM1506
37	c2dnwA_	Alignment	not modelled	36.9	11	**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
38	d1su0b_	Alignment	not modelled	36.5	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
39	d2ntka1	Alignment	not modelled	36.3	23	**Fold:**Ntn hydrolase-like **Superfamily:**Archaeal IMP cyclohydrolase PurO **Family:**Archaeal IMP cyclohydrolase PurO
40	c1grjA_	Alignment	not modelled	33.8	14	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
41	d1d7qa_	Alignment	not modelled	33.7	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	d3dm8a1	Alignment	not modelled	32.2	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rpa4348-like
43	d1grja2	Alignment	not modelled	31.3	16	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
44	d1e9ga_	Alignment	not modelled	29.9	29	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
45	d1wfza_	Alignment	not modelled	29.8	28	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
46	c1ufiD_	Alignment	not modelled	29.8	30	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of the dimerization domain of human cenp-b
47	d1ufia_	Alignment	not modelled	29.6	30	**Fold:**ROP-like **Superfamily:**Dimerisation domain of CENP-B **Family:**Dimerisation domain of CENP-B
48	c2k9kA_	Alignment	not modelled	28.1	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
49	d2f23a2	Alignment	not modelled	27.9	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
50	d1xjsa_	Alignment	not modelled	25.4	23	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
51	d1rvka2	Alignment	not modelled	23.5	15	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
52	c2xzn5_	Alignment	not modelled	23.3	57	**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
53	c3u5ga_	Alignment	not modelled	23.3	57	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
54	c3g0kA_	Alignment	not modelled	22.9	20	**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
55	c1x2gB_	Alignment	not modelled	21.6	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
56	c1n62C_	Alignment	not modelled	20.3	19	**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
57	d1ihra_	Alignment	not modelled	20.0	25	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
58	d1zjca1	Alignment	not modelled	19.1	19	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
59	c1y7jA_	Alignment	not modelled	18.7	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)
60	c3f40A_	Alignment	not modelled	18.5	18	**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
61	d2r4qa1	Alignment	not modelled	18.5	24	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
62	d2q22a1	Alignment	not modelled	18.2	32	**Fold:**Ava3019-like **Superfamily:**Ava3019-like **Family:**Ava3019-like
63	c3b4oB_	Alignment	not modelled	17.9	13	**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
64	c2etnA_	Alignment	not modelled	17.7	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
65	c3sc0A_	Alignment	not modelled	17.5	75	**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
66	d2nyga1	Alignment	not modelled	17.3	30	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
67	c3bmbB_	Alignment	not modelled	16.0	18	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
68	d2auwa2	Alignment	not modelled	15.8	11	**Fold:**NE0471 N-terminal domain-like **Superfamily:**NE0471 N-terminal domain-like **Family:**NE0471 N-terminal domain-like
69	c3smaD_	Alignment	not modelled	15.6	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
70	d2chra2	Alignment	not modelled	15.5	24	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
71	c2kzxA_	Alignment	not modelled	15.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
72	c2p4vA_	Alignment	not modelled	15.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
73	c2w3rG_	Alignment	not modelled	15.2	18	**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
74	c2fq2A_	Alignment	not modelled	14.9	17	**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
75	c2nytB_	Alignment	not modelled	14.4	67	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
76	c3hk4B_	Alignment	not modelled	13.9	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
77	d2e1ba2	Alignment	not modelled	13.8	31	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**AlaX-like
78	d1ah9a_	Alignment	not modelled	13.7	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
79	c2nqlB_	Alignment	not modelled	13.6	24	**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
80	c3e4fB_	Alignment	not modelled	13.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
81	c2dvyA_	Alignment	not modelled	13.1	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease pabi; **PDBTitle:** crystal structure of restriction endonucleases pabi
82	c2auwB_	Alignment	not modelled	13.1	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
83	c3n6jA_	Alignment	not modelled	12.9	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from actinobacillus succinogenes 130z
84	c3gkaB_	Alignment	not modelled	12.9	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
85	d1gsma2	Alignment	not modelled	12.9	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
86	c2l9fA_	Alignment	not modelled	12.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
87	c2kboA_	Alignment	not modelled	12.4	56	**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
88	c3f14A_	Alignment	not modelled	12.1	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
89	c2l4bA_	Alignment	not modelled	12.1	8	**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
90	d1h9aa2	Alignment	not modelled	12.1	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
91	d1t8ka_	Alignment	not modelled	12.0	19	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
92	c3bjsB_	Alignment	not modelled	11.5	18	**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
93	c1t3qF_	Alignment	not modelled	11.4	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
94	d2etna2	Alignment	not modelled	11.2	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
95	c2kciA_	Alignment	not modelled	11.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acyl carrier protein; **PDBTitle:** solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
96	d1z1sa1	Alignment	not modelled	11.1	25	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
97	c3nxlD_	Alignment	not modelled	10.9	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** crystal structure of glucarate dehydratase from burkholderia cepacia2 complexed with magnesium
98	c2pn0D_	Alignment	not modelled	10.7	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
99	c3fgyB_	Alignment	not modelled	10.6	0	**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