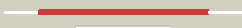
































Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0052 (-)_57407_57970
Date	Tue Jul 23 14:50:08 BST 2019
Unique Job ID	eaf2e06099e89d4f

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ewnA_	 Alignment		100.0	35	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
2	c3nooB_	 Alignment		100.0	34	PDB header: lyase Chain: B: PDB Molecule: thij/pfpi family protein; PDBTitle: crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
3	c3mgkA_	 Alignment		100.0	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: intracellular protease/amidase related enzyme (thij) PDBTitle: crystal structure of probable protease/amidase from clostridium2 acetobutylicum atcc 824
4	c3bhnA_	 Alignment		100.0	21	PDB header: unknown function Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
5	c3graA_	 Alignment		100.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, arac family; PDBTitle: crystal structure of arac family transcriptional regulator from2 pseudomonas putida
6	c3er6D_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative transcriptional regulator protein; PDBTitle: crystal structure of a putative transcriptional regulator protein from2 vibrio parahaemolyticus
7	c3ot1B_	 Alignment		100.0	20	PDB header: structural genomics Chain: B: PDB Molecule: 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate PDBTitle: crystal structure of vc2308 protein
8	c4e08B_	 Alignment		100.0	20	PDB header: motor protein Chain: B: PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta
9	d1p5fa_	 Alignment		100.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
10	c4xllB_	 Alignment		100.0	20	PDB header: unknown function Chain: B: PDB Molecule: dj-1 family protein; PDBTitle: toxoplasma gondii dj-1, oxidized
11	d1q2ia_	 Alignment		100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl

12	d2ab0a1	Alignment		100.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
13	c3efeC	Alignment		100.0	18	PDB header: chaperone Chain: C: PDB Molecule: thij/pfpi family protein; PDBTitle: the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
14	c4hcaA	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi domain protein; PDBTitle: crystal structure of thij/pfpi domain protein from brachyspira2 murdochii
15	c4y0nB	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein sav1875; PDBTitle: sav1875
16	c4k2hG	Alignment		100.0	20	PDB header: unknown function Chain: G: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of c103a mutant of dj-1 superfamily protein stm19312 from salmonella typhimurium
17	c3f5dA	Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ydea; PDBTitle: crystal structure of a protein of unknown function from bacillus2 subtilis
18	d2fexa1	Alignment		100.0	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
19	c4ge0C	Alignment		100.0	24	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein c22e12.03c; PDBTitle: schizosaccharomyces pombe dj-1 t114p mutant
20	d1oi4a1	Alignment		100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
21	c3fseB	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
22	c3uk7B	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
23	c3cneD	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
24	c2vrnA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: protease i; PDBTitle: the structure of the stress response protein dr1199 from deinococcus2 radiodurans: a member of the dj-1 superfamily
25	c3kkIA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
26	d1sy7a1	Alignment	not modelled	99.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
27	c4iruA	Alignment	not modelled	99.9	15	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
28	d1u9ca	Alianment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like

						Family: DJ-1/Pfpl
29	c4p5pA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpl family protein; PDBTitle: x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
30	c1sy7B	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
31	d1qvwa	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
32	c3n7tA	Alignment	not modelled	99.9	18	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
33	c4i2nC	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: C: PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
34	d1vhqa	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
35	c5xr2D	Alignment	not modelled	99.8	23	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
36	d1n57a	Alignment	not modelled	99.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
37	c3l3bA	Alignment	not modelled	99.7	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
38	d1p80a1	Alignment	not modelled	99.6	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
39	c1p81A	Alignment	not modelled	98.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
40	d1t3ta2	Alignment	not modelled	97.6	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	d2nv0a1	Alignment	not modelled	97.5	32	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
42	d1ka9h	Alignment	not modelled	97.4	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
43	d1q7ra	Alignment	not modelled	97.2	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
44	c2issF	Alignment	not modelled	97.1	22	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
45	d1o1ya	Alignment	not modelled	97.1	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
46	c3ej6D	Alignment	not modelled	96.9	18	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
47	d2abwa1	Alignment	not modelled	96.9	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	c3l7nA	Alignment	not modelled	96.8	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
49	c2ywjA	Alignment	not modelled	96.8	15	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
50	d2a9va1	Alignment	not modelled	96.7	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
51	c3d54D	Alignment	not modelled	96.6	21	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
52	c3l83A	Alignment	not modelled	96.5	25	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
53	c2ad5B	Alignment	not modelled	96.4	22	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
54	d1k9vf	Alignment	not modelled	96.3	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

55	c4gudA	Alignment	not modelled	96.3	13	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
56	c5n9mA	Alignment	not modelled	96.2	15	PDB header: transferase Chain: A: PDB Molecule: cobyrinic acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from <i>Staphylococcus aureus</i> involved in peptidoglycan amidation
57	c6fqB_E	Alignment	not modelled	96.2	13	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from <i>Streptococcus pneumoniae</i> r6
58	c2iufA	Alignment	not modelled	96.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the structures of penicillium vitale catalase: resting state, oxidised state (compound i) and complex with 3-aminotriazole
59	c2ywdA	Alignment	not modelled	95.9	19	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
60	c3nvaB	Alignment	not modelled	95.8	16	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from <i>Sulfolobus solfataricus</i>
61	c5u03C	Alignment	not modelled	95.8	22	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
62	c1jvnB	Alignment	not modelled	95.7	16	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel through a (beta/alpha) ₈ barrel joins two active sites
63	c4zdiE	Alignment	not modelled	95.7	24	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
64	c3r74B	Alignment	not modelled	95.7	23	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (ad)c2 synthase phze from <i>Burkholderia lata</i> 383
65	d1s1ma1	Alignment	not modelled	95.7	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
66	c1keeH	Alignment	not modelled	95.7	15	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate synthetase by the antibiotic acivicin
67	d1w18a1	Alignment	not modelled	95.6	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
68	d1a9xb2	Alignment	not modelled	95.5	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
69	c3l4eA	Alignment	not modelled	95.5	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from <i>Listeria monocytogenes</i> egd-e
70	d1qdlb	Alignment	not modelled	95.5	27	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
71	d1jvna2	Alignment	not modelled	95.4	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
72	c2w7tA	Alignment	not modelled	95.3	22	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: <i>Trypanosoma brucei</i> ctps - glutaminase domain with bound acivicin
73	d1vcoa1	Alignment	not modelled	95.2	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
74	c3fijD	Alignment	not modelled	94.8	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
75	d1l1qb	Alignment	not modelled	94.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
76	d1gpma2	Alignment	not modelled	94.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
77	c1vcnA	Alignment	not modelled	94.2	11	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
78	c6a4tB	Alignment	not modelled	93.9	18	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from <i>Deinococcus radiodurans</i> r1
79	d1fyea	Alignment	not modelled	93.8	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
80	c6surA	Alignment	not modelled	93.6	17	PDB header: transferase Chain: A: PDB Molecule: glutaminase;

80	c0qulA	Alignment	not modelled	93.8	17	PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
81	d1i7qb	Alignment	not modelled	93.5	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
82	c2v4uA	Alignment	not modelled	92.3	22	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
83	c2lxnA	Alignment	not modelled	90.8	19	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit a; PDBTitle: solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
84	c1t3tA	Alignment	not modelled	90.4	20	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
85	d2ghra1	Alignment	not modelled	90.2	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
86	c2ywcC	Alignment	not modelled	89.8	26	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
87	c5tw7E	Alignment	not modelled	86.0	20	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
88	c2h2wA	Alignment	not modelled	84.6	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
89	c1gpmD	Alignment	not modelled	83.4	16	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
90	c2vpiA	Alignment	not modelled	81.6	15	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
91	c3uowB	Alignment	not modelled	81.2	17	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
92	c3en0A	Alignment	not modelled	80.5	16	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
93	c6mtgB	Alignment	not modelled	78.9	16	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
94	d1i9xa	Alignment	not modelled	76.4	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
95	c1i9xA	Alignment	not modelled	76.4	13	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
96	c3tqiB	Alignment	not modelled	76.1	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
97	c4i8fA	Alignment	not modelled	74.6	19	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
98	c2vx0B	Alignment	not modelled	69.7	11	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
99	c3rgwS	Alignment	not modelled	61.8	6	PDB header: oxidoreductase/oxidoreductase Chain: S: PDB Molecule: membrane-bound hydrogenase (nife) small subunit hoxk; PDBTitle: crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
100	c1h2aS	Alignment	not modelled	59.5	16	PDB header: oxidoreductase Chain: S: PDB Molecule: hydrogenase; PDBTitle: single crystals of hydrogenase from desulfovibrio vulgaris
101	d1wuis1	Alignment	not modelled	57.5	16	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
102	c5douC	Alignment	not modelled	57.5	19	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
103	c3myrE	Alignment	not modelled	57.3	21	PDB header: oxidoreductase Chain: E: PDB Molecule: hydrogenase (nife) small subunit hyda; PDBTitle: crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
104	c6ehqT	Alignment	not modelled	54.9	13	PDB header: oxidoreductase Chain: T: PDB Molecule: hydrogenase-2 small chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
						PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase

105	c5dotA_	Alignment	not modelled	53.9	19	[ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
106	d1cc1s_	Alignment	not modelled	50.0	20	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
107	c5xf9G_	Alignment	not modelled	49.6	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
108	d1frfs_	Alignment	not modelled	48.8	12	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
109	c4gd3T_	Alignment	not modelled	45.1	6	PDB header: oxidoreductase/electron transport Chain: T: PDB Molecule: hydrogenase-1 small chain; PDBTitle: structure of e. coli hydrogenase-1 in complex with cytochrome b
110	c4iciA_	Alignment	not modelled	44.7	11	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of a putative flavoprotein (bacegg_01620) from bacteroides eggerthii dsm 20697 at 1.40 a resolution
111	c2wpaA_	Alignment	not modelled	42.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [nifese] hydrogenase, small subunit; PDBTitle: structure of the oxidised, as-isolated nifese hydrogenase from d.2 vulgaris hildenborough
112	d1e3da_	Alignment	not modelled	41.8	17	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
113	c3k1bA_	Alignment	not modelled	41.7	9	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
114	d1yq9a1	Alignment	not modelled	39.0	14	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
115	c2xv4S_	Alignment	not modelled	36.0	14	PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase iii subunit rpc3; PDBTitle: structure of human rpc62 (partial)
116	c3zfsB_	Alignment	not modelled	35.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: f420-reducing hydrogenase, subunit gamma; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
117	c3edoA_	Alignment	not modelled	35.6	10	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fmn (yp_193882.1)2 from lactobacillus acidophilus ncfm at 1.20 a resolution
118	c5odiE_	Alignment	not modelled	34.1	20	PDB header: oxidoreductase Chain: E: PDB Molecule: methyl-viologen reducing hydrogenase, subunit g; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus cocrystallized with com-sh
119	c4j8pA_	Alignment	not modelled	31.0	9	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of a putative flavoprotein (bacuni_04544) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
120	c6cfwj_	Alignment	not modelled	28.8	10	PDB header: membrane protein Chain: J: PDB Molecule: probable membrane-bound hydrogenase subunit mbhj; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase