

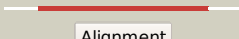

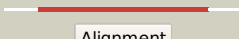












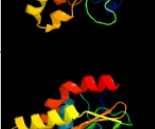






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0984_(moaB2)_1100464_1101009
Date	Wed Jul 31 22:05:05 BST 2019
Unique Job ID	e003f8ec4ed91b74

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfqC_	 Alignment		100.0	96	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
2	c2qq1A_	 Alignment		100.0	30	PDB header: structural protein Chain: A: PDB Molecule: molybdenum cofactor biosynthesis mog; PDBTitle: crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
3	c2is8A_	 Alignment		100.0	36	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab2; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
4	d1uuya_	 Alignment		100.0	33	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
5	c2g4rB_	 Alignment		100.0	38	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
6	d1mkza_	 Alignment		100.0	28	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
7	d2f7wa1	 Alignment		100.0	31	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
8	c2pjkA_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
9	c4xcwF_	 Alignment		100.0	29	PDB header: transferase Chain: F: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
10	d1y5ea1	 Alignment		100.0	36	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
11	d1ljlja_	 Alignment		100.0	31	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like

12	c4lhbC_	Alignment		100.0	30	PDB header: transferase Chain: C: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
13	d2g2ca1	Alignment		100.0	25	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
14	d1di6a_	Alignment		100.0	28	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
15	c5g2rA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
16	c2nqqA_	Alignment		100.0	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
17	c3kbqA_	Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
18	d2nqra3	Alignment		100.0	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
19	c2fu3A_	Alignment		100.0	15	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
20	d2ftsa3	Alignment		99.9	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
21	c4uuwA_	Alignment	not modelled	99.9	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: cina-like protein; PDBTitle: competence or damage-inducible protein cina from thermus thermophilus
22	c1uz5A_	Alignment	not modelled	99.9	19	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
23	d1uz5a3	Alignment	not modelled	99.9	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
24	d1wu2a3	Alignment	not modelled	99.9	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
25	c1wu2B_	Alignment	not modelled	99.9	16	PDB header: structural genomics,biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis moea protein; PDBTitle: crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
26	d1xi8a3	Alignment	not modelled	99.8	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
27	c2xecD_	Alignment	not modelled	95.3	19	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
28	c5xr2D_	Alignment	not modelled	91.8	21	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
						PDB header: isomerase

29	c4fq5B_	Alignment	not modelled	91.5	14	Chain: B; PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
30	c2eezG_	Alignment	not modelled	91.4	19	PDB header: oxidoreductase Chain: G; PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
31	c4yccC_	Alignment	not modelled	90.9	12	PDB header: hydrolase Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
32	dli7qb_	Alignment	not modelled	90.5	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
33	dli1qb_	Alignment	not modelled	88.6	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
34	c3ce9A_	Alignment	not modelled	87.3	13	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from 2 clostridium acetobutylicum at 2.37 a resolution
35	c6qurA_	Alignment	not modelled	87.0	18	PDB header: transferase Chain: A; PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
36	c3onoA_	Alignment	not modelled	86.5	15	PDB header: isomerase Chain: A; PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpiB from 2 vibrio parahaemolyticus
37	c3he8A_	Alignment	not modelled	85.9	22	PDB header: isomerase Chain: A; PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
38	c3p2yA_	Alignment	not modelled	85.9	18	PDB header: oxidoreductase Chain: A; PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
39	d2naca2	Alignment	not modelled	85.4	22	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
40	c4i2nC_	Alignment	not modelled	84.4	20	PDB header: hydrolase Chain: C; PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio2 cholerae
41	d1yq9a1	Alignment	not modelled	83.8	17	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
42	c2ppwA_	Alignment	not modelled	83.5	16	PDB header: isomerase Chain: A; PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpiB from streptococcus pneumoniae
43	d1qcza_	Alignment	not modelled	83.2	11	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
44	d1o1xa_	Alignment	not modelled	83.0	20	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
45	d1a9xb2	Alignment	not modelled	82.7	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
46	d1nn4a_	Alignment	not modelled	81.8	31	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
47	d1wl8a1	Alignment	not modelled	81.5	8	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	d1o2da_	Alignment	not modelled	81.1	26	Fold: Dehydroquinase-like Superfamily: Dehydroquinase-like Family: Iron-containing alcohol dehydrogenase
49	c4lfnD_	Alignment	not modelled	81.0	20	PDB header: isomerase Chain: D; PDB Molecule: galactose-6-phosphate isomerase subunit b; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with 2 d-ribose
50	d1qf6a1	Alignment	not modelled	80.2	16	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
51	c1ta9A_	Alignment	not modelled	79.5	17	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
52	d1n57a_	Alignment	not modelled	78.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
53	c4pevB_	Alignment	not modelled	78.8	24	PDB header: solute-binding protein Chain: B; PDB Molecule: membrane lipoprotein family protein; PDBTitle: crystal structure of abc transporter system solute-binding proteins2 from aeropyrum pernix k1
54	c4gd3T_	Alignment	not modelled	78.3	10	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
55	c6a4tB_	Alignment	not modelled	78.0	28	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
56	c3s5pA_	Alignment	not modelled	77.9	22	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
57	c5zxD_	Alignment	not modelled	77.8	26	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
58	c6c76A_	Alignment	not modelled	77.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducers in an orthorhombic crystal form
59	d1jq5a_	Alignment	not modelled	77.5	25	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
60	c3en0A_	Alignment	not modelled	77.4	11	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
61	c6fxsA_	Alignment	not modelled	77.4	22	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase, putative; PDBTitle: structure of trypanosoma brucei type b ribose 5-phosphate isomerase
62	d2bona1	Alignment	not modelled	77.3	21	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
63	c3vzdB_	Alignment	not modelled	77.1	20	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
64	c3bfjK_	Alignment	not modelled	77.0	28	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
65	c4dioB_	Alignment	not modelled	76.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium melloti
66	c6fxwA_	Alignment	not modelled	76.6	22	PDB header: isomerase Chain: A: PDB Molecule: putative ribose 5-phosphate isomerase; PDBTitle: structure of leishmania infantum type b ribose 5-phosphate isomerase
67	c3m1pA_	Alignment	not modelled	76.6	24	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
68	c3k7pA_	Alignment	not modelled	76.6	24	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
69	d2vvpA1	Alignment	not modelled	76.3	22	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
70	c3lm8D_	Alignment	not modelled	75.9	21	PDB header: transferase Chain: D: PDB Molecule: thiamine pyrophosphokinase; PDBTitle: crystal structure of thiamine pyrophosphokinase from bacillus2 subtilis, northeast structural genomics consortium target sr677
71	c3fn4A_	Alignment	not modelled	75.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
72	c2bonB_	Alignment	not modelled	75.5	23	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
73	c4fr2A_	Alignment	not modelled	75.2	17	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
74	c3c5yD_	Alignment	not modelled	75.2	21	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
75	d2qv7a1	Alignment	not modelled	74.9	12	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
76	c4werA_	Alignment	not modelled	74.7	20	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein; PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583
77	c6mu0A_	Alignment	not modelled	74.5	22	PDB header: isomerase Chain: A: PDB Molecule: probable ribose-5-phosphate isomerase b; PDBTitle: crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
78	d1gpma2	Alignment	not modelled	74.4	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
79	c3rgwS_	Alignment	not modelled	74.3	10	PDB header: oxidoreductase/oxidoreductase Chain: S: PDB Molecule: membrane-bound hydrogenase (nife) small subunit hoxx; PDBTitle: crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel

						iron-sulfur3 cluster
80	c2an1D_	Alignment	not modelled	74.2	27	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
81	c2rirA_	Alignment	not modelled	73.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
82	c3okfA_	Alignment	not modelled	73.6	16	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
83	c4mcaB_	Alignment	not modelled	72.6	23	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
84	c3louB_	Alignment	not modelled	72.4	15	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
85	c3l4eA_	Alignment	not modelled	71.0	15	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
86	c5z5eB_	Alignment	not modelled	70.8	10	PDB header: ligase Chain: B: PDB Molecule: neq417; PDBTitle: crystal structure of the glycyl-trna synthetase (glyrs) in2 nanoarchaeum equitans
87	d1pjca1	Alignment	not modelled	70.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
88	c2wpaA_	Alignment	not modelled	70.7	19	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
89	d1dxya2	Alignment	not modelled	69.7	17	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
90	c4r3uD_	Alignment	not modelled	69.6	24	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
91	d1nyra1	Alignment	not modelled	68.1	13	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
92	c2f17A_	Alignment	not modelled	68.1	25	PDB header: transferase Chain: A: PDB Molecule: thiamin pyrophosphokinase 1; PDBTitle: mouse thiamin pyrophosphokinase in a ternary complex with2 pyrithiamin pyrophosphate and amp at 2.5 angstrom
93	c4lfmA_	Alignment	not modelled	67.6	22	PDB header: isomerase Chain: A: PDB Molecule: galactose-6-phosphate isomerase subunit a; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-psicose
94	c5eksB_	Alignment	not modelled	67.4	20	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from acinetobacter baumannii in2 complex with nad
95	c6ehqT_	Alignment	not modelled	67.4	17	PDB header: oxidoreductase Chain: T: PDB Molecule: hydrogenase-2 small chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
96	c3meIC_	Alignment	not modelled	67.3	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: thiamin pyrophosphokinase family protein; PDBTitle: crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
97	c6dspB_	Alignment	not modelled	67.3	18	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrB; PDBTitle: lsrB from clostridium saccharobutylicum in complex with ai-2
98	d2g4ca1	Alignment	not modelled	67.1	12	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
99	c3cq9C_	Alignment	not modelled	67.1	22	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein lp_1622; PDBTitle: crystal structure of the lp_1622 protein from lactobacillus plantarum.2 northeast structural genomics consortium target lpr114
100	c3r74B_	Alignment	not modelled	66.6	25	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase paze from burkholderia lata 383
101	d2p1ra1	Alignment	not modelled	66.6	26	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
102	c2fqxA_	Alignment	not modelled	66.1	15	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
103	c5mvrA_	Alignment	not modelled	65.8	12	PDB header: transferase Chain: A: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
						Fold: HydA/Nqo6-like

104	d1e3da_	Alignment	not modelled	65.6	12	Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
105	d1vlja_	Alignment	not modelled	65.6	20	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
106	d2a9va1	Alignment	not modelled	65.1	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
107	c3kk1A_	Alignment	not modelled	65.0	20	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
108	c4ix1B_	Alignment	not modelled	64.5	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
109	c6cy1B_	Alignment	not modelled	64.4	17	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
110	c3ox4D_	Alignment	not modelled	63.6	20	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
111	c2qy9A_	Alignment	not modelled	63.6	15	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
112	c1keeH_	Alignment	not modelled	63.4	19	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
113	c3o11B_	Alignment	not modelled	62.5	13	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
114	c2yxba_	Alignment	not modelled	62.3	21	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
115	c4wzza_	Alignment	not modelled	61.9	17	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
116	c3b9qa_	Alignment	not modelled	61.6	17	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
117	c3h51B_	Alignment	not modelled	61.5	9	PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc transporter; PDBTitle: crystal structure of a putative branched-chain amino acid abc2 transporter from silicibacter pomeroyi
118	d1qdlb_	Alignment	not modelled	61.3	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
119	c3clhA_	Alignment	not modelled	60.8	22	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
120	d1l7da1	Alignment	not modelled	60.5	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain