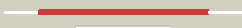























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1901_cinA_2147669_2148961
Date	Fri Aug 2 13:30:52 BST 2019
Unique Job ID	446a7896c9b41124

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4uuwA_	 Alignment		100.0	35	PDB header: biosynthetic protein Chain: A; PDB Molecule: cina-like protein; PDBTitle: competence or damage-inducible protein cina from thermus thermophilus
2	c6mr3C_	 Alignment		100.0	33	PDB header: structural genomics Chain: C; PDB Molecule: putative competence-damage inducible protein; PDBTitle: crystal structure of the competence-damaged protein (cina) superfamily2 protein from streptococcus mutans
3	c5kolA_	 Alignment		100.0	30	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the competence-damaged protein (cina) superfamily2 protein eck1530/ec0983 from escherichia coli
4	c5vu3A_	 Alignment		100.0	35	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: competence damage-inducible protein a; PDBTitle: crystal structure of the competence-damaged protein (cina) superfamily2 protein ecl_02051 from enterobacter cloacae
5	c5kvkA_	 Alignment		100.0	36	PDB header: unknown function Chain: A; PDB Molecule: protein kp700603; PDBTitle: crystal structure of the competence-damaged protein (cina) superfamily2 protein kp700603 from klebsiella pneumoniae 700603
6	d2a9sa1	 Alignment		100.0	36	Fold: Anticodon-binding domain-like Superfamily: CinA-like Family: CinA-like
7	c3kbqA_	 Alignment		100.0	35	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
8	c2pjkA_	 Alignment		100.0	23	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	d1mkza_	 Alignment		100.0	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
10	c3rfqC_	 Alignment		100.0	27	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
11	d1y5ea1	 Alignment		99.9	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like

12	c4lhbC_	Alignment		99.9	22	PDB header: transferase Chain: C: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of tungsten cofactor synthesizing protein moab from <i>pyrococcus furiosus</i>
13	d1uuya_	Alignment		99.9	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
14	c2is8A_	Alignment		99.9	29	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from <i>thermus thermophilus</i> hb8
15	d2fts3	Alignment		99.9	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
16	d1jja_	Alignment		99.9	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
17	d2f7wa1	Alignment		99.9	27	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
18	c2q4rB_	Alignment		99.9	25	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
19	d2q2ca1	Alignment		99.9	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
20	d2nqra3	Alignment		99.9	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
21	c2qq1A_	Alignment	not modelled	99.9	26	PDB header: structural protein Chain: A: PDB Molecule: molybdenum cofactor biosynthesis mog; PDBTitle: crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from <i>aquifex aeolicus</i> vf5
22	c4xcwF_	Alignment	not modelled	99.9	26	PDB header: transferase Chain: F: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of molybdenum cofactor biosynthesis protein moga2 from <i>helicobacter pylori</i> str. j99
23	c2nqgA_	Alignment	not modelled	99.9	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
24	c2fu3A_	Alignment	not modelled	99.9	23	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
25	d1uz5a3	Alignment	not modelled	99.9	25	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
26	d1di6a_	Alignment	not modelled	99.9	25	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
27	c5g2rA_	Alignment	not modelled	99.9	24	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from <i>2 arabidopsis thaliana</i>
28	c1uz5A_	Alignment	not modelled	99.9	26	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from <i>pyrococcus horikoshii</i>
						Fold: Molybdenum cofactor biosynthesis proteins

29	d1wu2a3	Alignment	not modelled	99.8	19	Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
30	d1xi8a3	Alignment	not modelled	99.6	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
31	c1wu2B_	Alignment	not modelled	99.6	21	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
32	c3wvbA_	Alignment	not modelled	97.4	24	PDB header: hydrolase Chain: A: PDB Molecule: upf0254 protein mj1251; PDBTitle: hcgf from methanocaldococcus jannaschii
33	d1wl8a1	Alignment	not modelled	93.3	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
34	d2a9va1	Alignment	not modelled	89.5	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	d1gpma2	Alignment	not modelled	86.4	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
36	c4yccC_	Alignment	not modelled	83.9	9	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
37	d1ka9h_	Alignment	not modelled	83.1	30	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
38	c1z0zC_	Alignment	not modelled	82.7	31	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
39	d1z0sa1	Alignment	not modelled	82.1	31	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
40	c3l3bA_	Alignment	not modelled	82.0	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
41	c5n2iC_	Alignment	not modelled	81.5	22	PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
42	c4rshB_	Alignment	not modelled	81.2	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: structure of a putative lipolytic protein of g-d-s-l family from2 desulfitobacterium hafniense dcb-2
43	c3ckyA_	Alignment	not modelled	79.6	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
44	d1a9xb2	Alignment	not modelled	79.3	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
45	c3a9rA_	Alignment	not modelled	77.9	23	PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
46	c2f1kD_	Alignment	not modelled	77.5	15	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
47	d1vhqa_	Alignment	not modelled	77.5	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/PfpI
48	c5t8xA_	Alignment	not modelled	77.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
49	c4ky3A_	Alignment	not modelled	77.2	19	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
50	c2lssF_	Alignment	not modelled	76.8	28	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
51	d1i36a2	Alignment	not modelled	76.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
52	c4fq5B_	Alignment	not modelled	74.5	17	PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
53	d1k9vf_	Alignment	not modelled	74.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
54	c2bonB_	Alignment	not modelled	73.9	15	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)

55	c3vzdB	Alignment	not modelled	73.4	20	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
56	c6qurA	Alignment	not modelled	72.2	23	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
57	c3c1nA	Alignment	not modelled	71.7	15	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
58	d2bona1	Alignment	not modelled	71.4	15	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
59	d1qf6a1	Alignment	not modelled	71.2	16	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
60	c5zxID	Alignment	not modelled	69.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
61	c3orsD	Alignment	not modelled	69.5	9	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
62	c4q7qA	Alignment	not modelled	69.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: the crystal structure of a possible lipase from chitinophaga pinensis2 dsm 2588
63	c2v6bB	Alignment	not modelled	68.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
64	c2pv7B	Alignment	not modelled	68.5	21	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
65	c1np3B	Alignment	not modelled	68.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
66	c6a4tB	Alignment	not modelled	66.6	29	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
67	c3l4eA	Alignment	not modelled	66.3	20	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
68	c3kkIA	Alignment	not modelled	65.9	17	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
69	c3c7cB	Alignment	not modelled	65.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
70	d1l7da1	Alignment	not modelled	65.1	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
71	d2naca2	Alignment	not modelled	65.0	14	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
72	c4werA	Alignment	not modelled	64.2	24	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
73	d2cdqa1	Alignment	not modelled	63.8	21	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
74	c3cq9C	Alignment	not modelled	63.5	17	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
75	c4ei8A	Alignment	not modelled	63.4	14	PDB header: replication Chain: A: PDB Molecule: plasmid replication protein repx; PDBTitle: crystal structure of bacillus cereus tubz, apo-form
76	c2e85B	Alignment	not modelled	62.9	17	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
77	d2p1ra1	Alignment	not modelled	62.7	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
78	d2f1ka2	Alignment	not modelled	62.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
79	c2pkkA	Alignment	not modelled	62.2	29	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of m tuberculosis adenosine kinase

						complexed with 2-2 fluoro adenosine
80	d1pjca1	Alignment	not modelled	61.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
81	d1nyra1	Alignment	not modelled	61.5	17	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
82	c2dc1A	Alignment	not modelled	61.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
83	d1vcoa1	Alignment	not modelled	60.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
84	d2qv7a1	Alignment	not modelled	59.8	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
85	c2fqxA	Alignment	not modelled	59.3	23	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
86	c1wziA	Alignment	not modelled	59.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for alteration of cofactor specificity of malate2 dehydrogenase from thermus flavus
87	d2hmfa1	Alignment	not modelled	58.2	15	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
88	c2v65A	Alignment	not modelled	57.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase a chain; PDBTitle: apo ldh from the psychrophile c. gunnari
89	c3ktnA	Alignment	not modelled	57.1	26	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase, pfkb family; PDBTitle: crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
90	d1i7qb	Alignment	not modelled	57.1	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
91	c3n7tA	Alignment	not modelled	57.0	24	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis
92	c1i36A	Alignment	not modelled	56.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases
93	c5yeiG	Alignment	not modelled	56.7	20	PDB header: transferase Chain: G: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
94	c3en0A	Alignment	not modelled	56.5	22	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
95	d2nv0a1	Alignment	not modelled	56.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
96	c2qhpA	Alignment	not modelled	55.6	13	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
97	c5ojlA	Alignment	not modelled	55.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]jazepine
98	d1jaya	Alignment	not modelled	55.3	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
99	c3h5lB	Alignment	not modelled	55.1	17	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
100	c5xr2D	Alignment	not modelled	54.9	17	PDB header: chaperone Chain: D: PDB Molecule: protein/nucleic acid deglycase hcha; PDBTitle: sav0551
101	d1q7ra	Alignment	not modelled	54.5	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
102	d1vjga	Alignment	not modelled	54.4	19	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Hypothetical protein alr1529
103	c6qssA	Alignment	not modelled	53.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of ignicoccus islandicus malate dehydrogenase co-2 crystallized with 10 mm tb-xo4
104	c2xecD	Alignment	not modelled	53.6	14	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
105	c2ywiA	Alignment	not modelled	53.5	24	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii

106	d2jgra1	Alignment	not modelled	53.3	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
107	c3qbeA	Alignment	not modelled	53.0	26	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: crystal structure of the 3-dehydroquininate synthase (arob) from2 mycobacterium tuberculosis
108	c1ta9A	Alignment	not modelled	52.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
109	c5a9tA	Alignment	not modelled	52.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
110	d1qvwa	Alignment	not modelled	51.6	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
111	c2ys6A	Alignment	not modelled	50.6	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
112	c3s99A	Alignment	not modelled	50.5	18	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
113	c3me1C	Alignment	not modelled	50.2	16	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
114	c3s40C	Alignment	not modelled	50.2	26	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
115	c3ihkC	Alignment	not modelled	50.2	17	PDB header: transferase Chain: C: PDB Molecule: thiamin pyrophosphokinase; PDBTitle: crystal structure of thiamin pyrophosphokinase from s.mutans,2 northeast structural genomics consortium target smr83
116	c4lhsA	Alignment	not modelled	50.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gds1-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
117	c3fn4A	Alignment	not modelled	49.6	18	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
118	d1fmfa	Alignment	not modelled	48.3	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
119	d1wu7a1	Alignment	not modelled	47.6	22	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
120	d1pgja2	Alignment	not modelled	47.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain