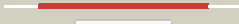



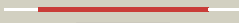

























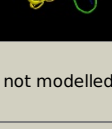


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0865_(mog)_963393_963875
Date	Fri Jul 26 01:50:45 BST 2019
Unique Job ID	c6ec1669cb41e0f5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g4rB_	 Alignment		100.0	100	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
2	c2is8A_	 Alignment		100.0	41	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
3	c2qq1A_	 Alignment		100.0	32	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
4	d2f7wa1	 Alignment		100.0	36	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
5	d1uuya_	 Alignment		100.0	34	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
6	c3rfqC_	 Alignment		100.0	38	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
7	c4xcwF_	 Alignment		100.0	32	PDB header: transferase Chain: F: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
8	d1jlja_	 Alignment		100.0	30	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
9	c2pjkA_	 Alignment		100.0	27	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
10	c4lhbC_	 Alignment		100.0	29	PDB header: transferase Chain: C: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
11	d1y5ea1	 Alignment		100.0	29	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like

12	d2g2ca1	Alignment		100.0	26	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
13	d1mkza_	Alignment		100.0	28	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	c3kbqA_	Alignment		100.0	20	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
16	d2ftsa3	Alignment		100.0	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
17	d2nqra3	Alignment		100.0	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
18	c2nqqa_	Alignment		100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
19	c5g2rA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
20	c2fu3A_	Alignment		100.0	21	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
21	c4uuwA_	Alignment	not modelled	100.0	20	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	18	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	17	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	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
27	d1i7qb_	Alignment	not modelled	95.1	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
28	d1i1qb_	Alignment	not modelled	93.6	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
						Fold: Flavodoxin-like

29	d1gpm2	Alignment	not modelled	93.5	15	Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
30	c6qurA	Alignment	not modelled	91.4	17	PDB header: transferase Chain: A: PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
31	d1wl8a1	Alignment	not modelled	90.1	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
32	d1fmfa	Alignment	not modelled	89.3	20	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
33	d1yq9a1	Alignment	not modelled	87.9	15	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
34	c4rshB	Alignment	not modelled	87.3	13	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
35	c3ce9A	Alignment	not modelled	85.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
36	c4pevB	Alignment	not modelled	85.1	12	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
37	c4gd3T	Alignment	not modelled	85.1	11	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
38	d1qf6a1	Alignment	not modelled	84.4	13	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
39	c2lpmA	Alignment	not modelled	84.3	20	PDB header: transcription regulator Chain: A: PDB Molecule: two-component response regulator; PDBTitle: chemical shift and structure assignments for sma0114
40	c3rgwS	Alignment	not modelled	84.1	16	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
41	c4lhsA	Alignment	not modelled	83.4	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
42	c4r3uD	Alignment	not modelled	83.2	18	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
43	c3onoA	Alignment	not modelled	82.6	12	PDB header: isomerase Chain: A: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpb from2 vibrio parahaemolyticus
44	d1pjca1	Alignment	not modelled	81.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
45	c6a4tB	Alignment	not modelled	80.8	19	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
46	c4yccC	Alignment	not modelled	80.1	10	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
47	d1vcoa1	Alignment	not modelled	79.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	c2vptA	Alignment	not modelled	79.6	22	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: clostridium thermocellum family 3 carbohydrate esterase
49	c2yxbA	Alignment	not modelled	79.1	25	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
50	c1ta9A	Alignment	not modelled	79.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
51	c1z0zC	Alignment	not modelled	78.9	23	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
52	c2an1D	Alignment	not modelled	78.8	20	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
53	c2ppwA	Alignment	not modelled	78.5	13	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
54	d1z0sa1	Alignment	not modelled	78.3	23	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like

55	d1s1ma1	Alignment	not modelled	78.0	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
56	c3l4eA	Alignment	not modelled	78.0	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase I mo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
57	c2wpaA	Alignment	not modelled	77.2	20	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
58	d2a9va1	Alignment	not modelled	77.2	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
59	c4gudA	Alignment	not modelled	75.3	17	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
60	c6ehqT	Alignment	not modelled	75.2	17	PDB header: oxidoreductase Chain: T: PDB Molecule: hydrogenase-2 small chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
61	d1cc1s	Alignment	not modelled	75.1	23	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
62	c2xmoB	Alignment	not modelled	75.0	22	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
63	d1vjga	Alignment	not modelled	74.9	13	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Hypothetical protein alr1529
64	c1w25B	Alignment	not modelled	74.7	22	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pld in complex with c-digmp
65	c3c5yD	Alignment	not modelled	74.5	14	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
66	d1nyra1	Alignment	not modelled	74.3	16	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
67	c1np3B	Alignment	not modelled	74.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxyhydroxy acid isomerase reductase from pseudomonas aeruginosa
68	c3myrE	Alignment	not modelled	73.8	20	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
69	c2xecD	Alignment	not modelled	72.2	13	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
70	c2eezG	Alignment	not modelled	71.9	17	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
71	d2g4ca1	Alignment	not modelled	71.9	12	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
72	d1dlja3	Alignment	not modelled	71.5	4	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain Family: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
73	d1ka9h	Alignment	not modelled	71.1	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
74	c3en0A	Alignment	not modelled	70.9	15	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
75	c4ix1B	Alignment	not modelled	70.8	17	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
76	d1e8ca2	Alignment	not modelled	70.6	12	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
77	c3r74B	Alignment	not modelled	70.3	27	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 phze from burkholderia lata 383
78	c3dc7B	Alignment	not modelled	69.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein lp_3323; PDBTitle: crystal structure of the protein q88sr8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109.
79	d1qdlb	Alignment	not modelled	69.6	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
						Fold: Flavodoxin-like

80	d2naca2	Alignment	not modelled	69.5	21	Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
81	d1a9xb2	Alignment	not modelled	69.5	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
82	c4lfnD	Alignment	not modelled	69.2	24	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
83	c2w7tA	Alignment	not modelled	68.9	16	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
84	d1bg6a2	Alignment	not modelled	68.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	d1xhfa1	Alignment	not modelled	68.8	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
86	c2rirA	Alignment	not modelled	68.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
87	c3s40C	Alignment	not modelled	67.8	15	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
88	c4q7qA	Alignment	not modelled	67.8	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
89	c3he8A	Alignment	not modelled	67.6	26	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
90	c4fq5B	Alignment	not modelled	67.4	11	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
91	c2ywcC	Alignment	not modelled	67.0	21	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
92	c5zxID	Alignment	not modelled	66.7	16	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glDA from e.coli
93	c5yvmA	Alignment	not modelled	66.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
94	c2hqba	Alignment	not modelled	66.4	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comK gene; PDBTitle: crystal structure of a transcriptional activator of comK2 gene from bacillus halodurans
95	c2pmfA	Alignment	not modelled	66.3	18	PDB header: ligase Chain: A: PDB Molecule: glycyl-trna synthetase; PDBTitle: the crystal structure of a human glycyl-trna synthetase mutant
96	d1wuis1	Alignment	not modelled	64.4	14	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
97	d2b4aa1	Alignment	not modelled	64.3	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	d1q7ra	Alignment	not modelled	64.1	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
99	c4mcaB	Alignment	not modelled	64.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
100	c4a7pA	Alignment	not modelled	63.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
101	c3vzdB	Alignment	not modelled	63.1	13	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
102	d1e3da	Alignment	not modelled	63.1	17	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
103	c3r0ja	Alignment	not modelled	63.1	26	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
104	d1hc7a1	Alignment	not modelled	63.0	14	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
105	c4e12A	Alignment	not modelled	62.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase PDB header: transferase

106	c2qv7A_	Alignment	not modelled	62.6	16	Chain: A; PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
107	c2g04B_	Alignment	not modelled	62.1	20	PDB header: isomerase Chain: B; PDB Molecule: probable fatty-acid-coa racemase far; PDBTitle: crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
108	c3s99A_	Alignment	not modelled	61.8	15	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
109	d3bzwa1	Alignment	not modelled	61.3	17	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: BT2961-like
110	c3bzwa_	Alignment	not modelled	61.3	17	PDB header: hydrolase Chain: A; PDB Molecule: putative lipase; PDBTitle: crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
111	c4ypoB_	Alignment	not modelled	61.1	14	PDB header: oxidoreductase Chain: B; PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
112	c3pfnB_	Alignment	not modelled	60.7	15	PDB header: transferase Chain: B; PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
113	c3p2yA_	Alignment	not modelled	60.5	13	PDB header: oxidoreductase Chain: A; PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
114	d1nn4a_	Alignment	not modelled	60.1	26	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
115	d1jq5a_	Alignment	not modelled	60.1	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
116	d2auna2	Alignment	not modelled	60.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
117	c1keeH_	Alignment	not modelled	59.3	23	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
118	c3d54D_	Alignment	not modelled	59.0	14	PDB header: ligase Chain: D; PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
119	d1frfs_	Alignment	not modelled	58.9	15	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
120	c3kkIA_	Alignment	not modelled	58.7	24	PDB header: hydrolase Chain: A; PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae