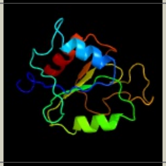
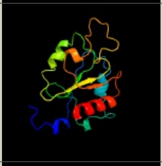
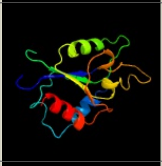
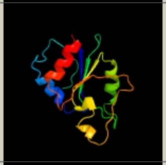
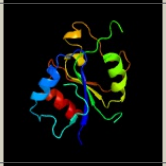
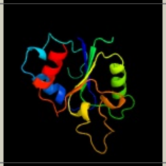
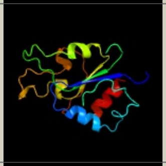
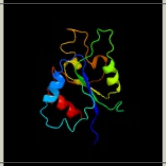
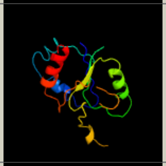
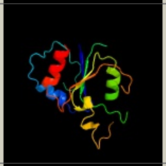
Email	mdejesus@rockefeller.edu
Description	RVBD0082_(-)_89921_90400
Date	Tue Jul 23 14:50:11 BST 2019
Unique Job ID	85ab38ee423928b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gcsK_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**psst subunit (nukm); **PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica
2	c6humK_	Alignment		100.0	38	**PDB header:**proton transport **Chain:** K: **PDB Molecule:**nad(p)h-quinone oxidoreductase subunit k; **PDBTitle:** structure of the photosynthetic complex i from thermosynechococcus2 elongatus
3	c5lc5B_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, **PDBTitle:** structure of mammalian respiratory complex i, class2
4	c6cfwJ_	Alignment		100.0	44	**PDB header:**membrane protein **Chain:** J: **PDB Molecule:**probable membrane-bound hydrogenase subunit mbhj; **PDBTitle:** cryoem structure of a respiratory membrane-bound hydrogenase
5	d2fug61	Alignment		100.0	39	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
6	d1frfs_	Alignment		100.0	22	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
7	c5odiE_	Alignment		100.0	26	**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
8	c5xf9G_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**nad-reducing hydrogenase; **PDBTitle:** crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
9	d1e3da_	Alignment		100.0	19	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
10	c6ehqT_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** T: **PDB Molecule:**hydrogenase-2 small chain; **PDBTitle:** e. coli hydrogenase-2 (as isolated form).
11	d1wuis1	Alignment		100.0	25	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit

12	c1h2aS_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
13	d1cc1s_	Alignment		100.0	24	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
14	c3rgwS_	Alignment		100.0	15	**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
15	d1yq9a1	Alignment		100.0	21	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
16	c3myrE_	Alignment		100.0	26	**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
17	c4gd3T_	Alignment		100.0	22	**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
18	c3zfsB_	Alignment		100.0	20	**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
19	c2wpnA_	Alignment		100.0	23	**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
20	c5aa5D_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nife-hydrogenase small subunit, hofk; **PDBTitle:** actinobacterial-type nife-hydrogenase from ralstonia eutropha h16 at2 2.85 angstrom resolution
21	c4jc0B_	Alignment	not modelled	77.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribosomal protein s12 methylthiotransferase rimo; **PDBTitle:** crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
22	d1e5da1	Alignment	not modelled	44.4	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
23	d1fmfa_	Alignment	not modelled	34.9	19	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
24	c6h0cA_	Alignment	not modelled	34.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** flv1 flavodiiron core from synechocystis sp. pcc6803
25	c2r47C_	Alignment	not modelled	29.5	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
26	d2h1qa1	Alignment	not modelled	29.1	21	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
27	c3npgD_	Alignment	not modelled	28.9	18	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized duf364 family protein; **PDBTitle:** crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
28	c2d3yA_	Alignment	not modelled	28.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus

						thermophilus2 hb8
29	c3rfqC_	Alignment	not modelled	27.4	16	**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
30	d1jlja_	Alignment	not modelled	23.6	9	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
31	c2g4rB_	Alignment	not modelled	23.1	16	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
32	c2wcvI_	Alignment	not modelled	22.3	12	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**l-fucose mutarotase; **PDBTitle:** crystal structure of bacterial fucu
33	d1ycga1	Alignment	not modelled	21.7	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
34	c3rl4A_	Alignment	not modelled	21.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
35	d2f7wa1	Alignment	not modelled	17.2	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
36	c5kojD_	Alignment	not modelled	16.7	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitrogenase femo beta subunit protein nifk; **PDBTitle:** nitrogenase mofep protein in the ids oxidized state
37	d2g2ca1	Alignment	not modelled	16.6	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
38	c3ikbB_	Alignment	not modelled	16.5	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
39	c3pdiG_	Alignment	not modelled	16.1	20	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
40	c2is8A_	Alignment	not modelled	15.9	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
41	c4fo5A_	Alignment	not modelled	14.9	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-like protein; **PDBTitle:** crystal structure of a thioredoxin-like protein (bdi_1100) from2 parabacteroides distasonis atcc 8503 at 2.02 a resolution
42	c5g2rA_	Alignment	not modelled	14.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein cnx1; **PDBTitle:** crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
43	d2dlda1	Alignment	not modelled	13.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
44	d1sqsa_	Alignment	not modelled	13.2	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
45	d1xhja_	Alignment	not modelled	13.2	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
46	d1ogda_	Alignment	not modelled	12.8	16	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
47	c2fu3A_	Alignment	not modelled	12.3	18	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
48	c3e7nB_	Alignment	not modelled	12.2	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**d-ribose high-affinity transport system; **PDBTitle:** crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
49	c3ca8B_	Alignment	not modelled	12.1	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
50	c2nqqA_	Alignment	not modelled	12.1	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
51	d1xwdb1	Alignment	not modelled	11.9	18	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
52	c4xcwF_	Alignment	not modelled	11.8	12	**PDB header:**transferase **Chain:** F: **PDB Molecule:**molybdopterin adenylyltransferase; **PDBTitle:** crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
53	c2xdqB_	Alignment	not modelled	11.4	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-chlb)2 complex
54	c4ptzC_	Alignment	not modelled	11.4	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**fmn reductase ssue; **PDBTitle:** crystal structure of the escherichia coli alkanesulfonate

						fmn2 reductase ssue in fmn-bound form
55	c5n6yD_	Alignment	not modelled	11.3	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitrogenase vanadium-iron protein alpha chain; **PDBTitle:** azotobacter vinelandii vanadium nitrogenase
56	d2djia1	Alignment	not modelled	11.2	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
57	c2z1dA_	Alignment	not modelled	11.0	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
58	c4pfxA_	Alignment	not modelled	10.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (galt1); **PDBTitle:** the highly conserved domain of unknown function 1792 has a distinct2 glycosyltransferase fold
59	d1j4aa1	Alignment	not modelled	10.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
60	c6a4tB_	Alignment	not modelled	10.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase e; **PDBTitle:** crystal structure of peptidase e from deinococcus radiodurans r1
61	c1ychD_	Alignment	not modelled	9.9	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
62	c5v4aB_	Alignment	not modelled	9.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase (duf1792); **PDBTitle:** a new glycosyltransferase (duf1792) from streptococcus sanguinis
63	c4uunA_	Alignment	not modelled	9.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** trichomonas vaginalis lactate dehydrogenase in complex with nadh
64	c4iciA_	Alignment	not modelled	9.6	6	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of a putative flavoprotein (bacegg_01620) from2 bacteroides eggerthii dsm 20697 at 1.40 a resolution
65	d1xjca_	Alignment	not modelled	9.5	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
66	c1pt9B_	Alignment	not modelled	9.5	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
67	c4a34L_	Alignment	not modelled	9.4	16	**PDB header:**isomerase **Chain:** L: **PDB Molecule:**rbsd/fucu transport protein family protein; **PDBTitle:** crystal structure of the fucose mutarotase in complex with2 l-fucose from streptococcus pneumoniae
68	d1rw6a_	Alignment	not modelled	9.2	25	**Fold:**STAT-like **Superfamily:**CAPPD, an extracellular domain of amyloid beta A4 protein **Family:**CAPPD, an extracellular domain of amyloid beta A4 protein
69	c3pdiB_	Alignment	not modelled	9.1	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
70	d2ob5a1	Alignment	not modelled	9.1	16	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
71	c5fyqB_	Alignment	not modelled	8.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent protein deacetylase sirtuin-2; **PDBTitle:** sirt2 in complex with a 13-mer trifluoroacetylated ran peptide
72	c4iloA_	Alignment	not modelled	8.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ct398; **PDBTitle:** 2.12a resolution structure of ct398 from chlamydia trachomatis
73	c2gesA_	Alignment	not modelled	8.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase; **PDBTitle:** pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
74	d1d4oa_	Alignment	not modelled	8.6	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
75	c3d7nA_	Alignment	not modelled	8.6	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
76	d1vmea1	Alignment	not modelled	8.5	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
77	d1civa1	Alignment	not modelled	8.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
78	c3mglA_	Alignment	not modelled	8.4	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate permease family protein; **PDBTitle:** crystal structure of permease family protein from vibrio cholerae
79	c1qfwB_	Alignment	not modelled	8.4	25	**PDB header:**immune system **Chain:** B: **PDB Molecule:**gonadotrophin beta subunit; **PDBTitle:** ternary complex of human chorionic gonadotropin with fv anti alpha2 subunit and fv anti beta subunit

80	d1hcnb_	Alignment	not modelled	8.4	25	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
81	d1m1na_	Alignment	not modelled	8.2	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
82	c2wnyB_	Alignment	not modelled	8.2	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved protein mth689; **PDBTitle:** structure of mth689, a duf54 protein from methanothermobacter2 thermautotrophicus
83	c3aerC_	Alignment	not modelled	8.2	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
84	c2wzlA_	Alignment	not modelled	8.1	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phosphoprotein; **PDBTitle:** the structure of the n-rna binding domain of the mokola2 virus phosphoprotein
85	d2fy6a1	Alignment	not modelled	8.1	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
86	c3lklB_	Alignment	not modelled	8.0	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
87	d1th5a1	Alignment	not modelled	7.9	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
88	c2xdqA_	Alignment	not modelled	7.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-chlb)2 complex
89	d1pnoa_	Alignment	not modelled	7.7	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
90	d2i9be3	Alignment	not modelled	7.7	50	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
91	d2fd6u3	Alignment	not modelled	7.6	50	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
92	c3mvkA_	Alignment	not modelled	7.6	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein fucu; **PDBTitle:** the crystal structure of fucu from bifidobacterium longum to 1.65a
93	d2b0ja2	Alignment	not modelled	7.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
94	d1sc6a1	Alignment	not modelled	7.5	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
95	c5hcdD_	Alignment	not modelled	7.2	71	**PDB header:**immune system **Chain:** D: **PDB Molecule:**rhipicephalus microplus raci2; **PDBTitle:** ternary complex of human complement c5 with ornithodoros moubata omci2 and rhipicephalus microplus raci2
96	c2vzhA_	Alignment	not modelled	7.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
97	c1mldA_	Alignment	not modelled	6.8	15	**PDB header:**oxidoreductase(nad(a)-choh(d)) **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
98	d1uzxa_	Alignment	not modelled	6.8	23	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
99	c5y06A_	Alignment	not modelled	6.8	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**msmeg_4306; **PDBTitle:** structural characterization of msmeg_4306 from mycobacterium smegmatis