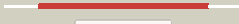
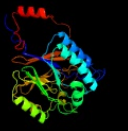


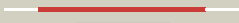




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0805 (-) _898834_899790
Date	Fri Jul 26 01:50:39 BST 2019
Unique Job ID	3dd729e99d2f7f56

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ib7A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
2	d3d03a1	 Alignment		100.0	24	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
3	c2hy1A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
4	d2hy1a1	 Alignment		100.0	100	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
5	c2xmoB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
6	c4ltyD_	 Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
7	c4ykeA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: mre11; PDBTitle: crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
8	c4fcxB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad32; PDBTitle: s.pombe mre11 apoenzym
9	c3av0A_	 Alignment		100.0	17	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
10	c2q8uA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
11	c4fbkB_	 Alignment		100.0	17	PDB header: hydrolase, protein binding Chain: B: PDB Molecule: dna repair and telomere maintenance protein nbs1,dna repair PDBTitle: crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site

12	c3t1iC	Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
13	d2nxfA1	Alignment		100.0	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
14	c3qg5D	Alignment		100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: mre11; PDBTitle: the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
15	c3auzA	Alignment		100.0	18	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
16	c5ebbA	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3a; PDBTitle: structure of human sphingomyelinase phosphodiesterase like 3a2 (smpdl3a) with zn2+
17	c5karA	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3b; PDBTitle: murine acid sphingomyelinase-like phosphodiesterase 3b (smpdl3b)
18	d1ii7a	Alignment		99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
19	d1utea	Alignment		99.9	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
20	d1xzwa2	Alignment		99.9	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
21	c5k8kA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: structure of the haemophilus influenzae lpxh-lipid x complex
22	d2yvta1	Alignment	not modelled	99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
23	c3tghA	Alignment	not modelled	99.9	16	PDB header: cell invasion Chain: A: PDB Molecule: glideosome-associated protein 50; PDBTitle: gap50 the anchor in the inner membrane complex of plasmodium
24	c3zk4A	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: diphosphonucleotide phosphatase 1; PDBTitle: structure of purple acid phosphatase ppd1 isolated from2 yellow lupin (lupinus luteus) seeds
25	d2qfra2	Alignment	not modelled	99.9	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
26	c5b4bB	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: crystal structure of lpxh with lipid x in spacegroup c2
27	d1uf3a	Alignment	not modelled	99.9	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
28	c3rl4A	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
29	c1qhwA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone

30	d1qhwa_	Alignment	not modelled	99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
31	c1xzwB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
32	c1kbpB_	Alignment	not modelled	99.9	17	PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
33	c5wlyA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: e. coli lpxh- 8 mutations
34	c5ficD_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: sphingomyelin phosphodiesterase; PDBTitle: open form of murine acid sphingomyelinase in presence of lipid
35	c3qfnA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
36	d1usha2	Alignment	not modelled	99.8	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
37	d1s3la_	Alignment	not modelled	99.8	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
38	c1s3mA_	Alignment	not modelled	99.8	17	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
39	c5xceB_	Alignment	not modelled	99.8	22	PDB header: transport protein Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of wild type vps29 from entamoeba histolytica
40	d1nnwa_	Alignment	not modelled	99.8	10	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
41	d2a22a1	Alignment	not modelled	99.8	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
42	c3rqzC_	Alignment	not modelled	99.8	25	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
43	c1oidA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
44	d1z2wa1	Alignment	not modelled	99.7	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
45	d1xm7a_	Alignment	not modelled	99.7	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
46	c5w8mD_	Alignment	not modelled	99.7	24	PDB header: endocytosis Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of chaetomium thermophilum vps29
47	c2yeqA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase d; PDBTitle: structure of phod
48	c1su1A_	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yfce; PDBTitle: structural and biochemical characterization of yfce, a phosphoesterase2 from e. coli
49	d1su1a_	Alignment	not modelled	99.7	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
50	c2kknA_	Alignment	not modelled	99.6	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
51	c6nvoA_	Alignment	not modelled	99.6	26	PDB header: dna binding protein Chain: A: PDB Molecule: nuclease mpe; PDBTitle: crystal structure of pseudomonas putida nuclease mpe
52	d3ck2a1	Alignment	not modelled	99.6	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
53	c2z1aA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
54	c3qfkA_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
55	c5iheB_	Alignment	not modelled	99.5	15	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ii small subunit; PDBTitle: d-family dna polymerase - dp1 subunit (3'-5' proof-

						reading2 exonuclease)
56	d2z1aa2	Alignment	not modelled	99.5	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
57	c3ivdA	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in complex with2 uridine
58	c5h7wB	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: venom 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from venom of naja atra
59	c4h1sB	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of a truncated soluble form of human cd73 with ecto-2 5'-nucleotidase activity
60	c2wdfA	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
61	c3zu0A	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadn)
62	c3gveB	Alignment	not modelled	99.3	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
63	d3c9fa2	Alignment	not modelled	99.3	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
64	c3jyfB	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: B: PDB Molecule: 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- PDBTitle: the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
65	d1g5ba	Alignment	not modelled	99.1	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
66	c4pehC	Alignment	not modelled	99.0	15	PDB header: hydrolase/rna Chain: C: PDB Molecule: rna lariat debranching enzyme, putative; PDBTitle: dbr1 in complex with synthetic linear rna
67	c3c9fB	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
68	c4j6oA	Alignment	not modelled	98.8	19	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of the phosphatase domain of c. thermocellum2 (bacterial) pnpk
69	d1t71a	Alignment	not modelled	98.8	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
70	d2z06a1	Alignment	not modelled	98.8	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
71	c4b2oB	Alignment	not modelled	98.8	20	PDB header: hydrolase Chain: B: PDB Molecule: ymdb phosphodiesterase; PDBTitle: crystal structure of bacillus subtilis ymdb, a global2 regulator of late adaptive responses.
72	c2zbmA	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
73	d1t70a	Alignment	not modelled	98.5	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
74	c5vjwA	Alignment	not modelled	98.3	24	PDB header: hydrolase Chain: A: PDB Molecule: rhizobiales-like phosphatase 2; PDBTitle: arabidopsis thaliana rhizobiales-like phosphatase 2 complexed with2 tungstate
75	c2qjcA	Alignment	not modelled	98.2	27	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
76	c2dfjA	Alignment	not modelled	98.2	31	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
77	c3e0jG	Alignment	not modelled	98.1	17	PDB header: transferase Chain: G: PDB Molecule: dna polymerase subunit delta-2; PDBTitle: x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
78	c6hv9B	Alignment	not modelled	98.0	15	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon subunit b; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
79	c5vbnE	Alignment	not modelled	98.0	21	PDB header: transferase Chain: E: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
80	d3c5wc1	Alignment	not modelled	97.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
						Fold: Metallo-dependent phosphatases

81	d1jk7a_	Alignment	not modelled	97.8	17	Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
82	c5jpfA_	Alignment	not modelled	97.7	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine/threonine-protein phosphatase; PDBTitle: serine/threonine phosphatase z1 (candida albicans) binds to inhibitor2 microcystin-lr
83	c3icfB_	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase t; PDBTitle: structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
84	c3floG_	Alignment	not modelled	97.4	16	PDB header: transferase Chain: G: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: crystal structure of the carboxyl-terminal domain of yeast dna2 polymerase alpha in complex with its b subunit
85	d1s95a_	Alignment	not modelled	97.3	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
86	c2jogA_	Alignment	not modelled	97.1	21	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
87	d1s70a_	Alignment	not modelled	97.1	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
88	c1auiA_	Alignment	not modelled	96.7	21	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
89	d1auia_	Alignment	not modelled	96.7	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
90	d2p6ba1	Alignment	not modelled	96.7	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
91	c2p6bC_	Alignment	not modelled	96.7	21	PDB header: hydrolase/hydrolase regulator Chain: C: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha isoform; PDBTitle: crystal structure of human calcineurin in complex with pvivit peptide
92	c1wao4_	Alignment	not modelled	96.3	16	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
93	c4il1A_	Alignment	not modelled	94.5	21	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin, calcineurin subunit b type 1, serine/threonine- PDBTitle: crystal structure of the rat calcineurin
94	c5jitA_	Alignment	not modelled	93.4	15	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine-protein phosphatase 5; PDBTitle: crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
95	c4y97E_	Alignment	not modelled	93.3	21	PDB header: transferase Chain: E: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: crystal structure of human pol alpha b-subunit in complex with c-2 terminal domain of catalytic subunit
96	c1sazA_	Alignment	not modelled	69.2	19	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
97	c3lmaC_	Alignment	not modelled	62.9	19	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6.
98	d1saza2	Alignment	not modelled	62.4	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
99	d1x52a1	Alignment	not modelled	55.8	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
100	c5uvqA_	Alignment	not modelled	55.3	21	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase 3,sphingomyelin PDBTitle: crystal structure of the human neutral sphingomyelinase 2 (nsmase2)2 catalytic domain with insertion deleted and calcium bound
101	d2auna1	Alignment	not modelled	53.8	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LD-carboxypeptidase A C-terminal domain-like Family: LD-carboxypeptidase A C-terminal domain-like
102	d1y5ea1	Alignment	not modelled	52.1	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
103	c6g2dC_	Alignment	not modelled	51.6	25	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
104	c4toiA_	Alignment	not modelled	51.4	23	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s2,ribosomal protein s1; PDBTitle: crystal structure of e.coli ribosomal protein s2 in complex with n-2 terminal domain of s1
105	c3p4iA_	Alignment	not modelled	50.2	26	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium PDB header: ligase

106	c5cskB_	Alignment	not modelled	50.2	22	Chain: B; PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
107	d1o98a2	Alignment	not modelled	50.0	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
108	d1zl0a1	Alignment	not modelled	49.6	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LD-carboxypeptidase A C-terminal domain-like Family: LD-carboxypeptidase A C-terminal domain-like
109	c5nnyA_	Alignment	not modelled	47.6	18	PDB header: hydrolase Chain: A; PDB Molecule: wipb; PDBTitle: crystal structure of the phosphatase domain from the legionella2 effector wipb
110	d1ozha1	Alignment	not modelled	47.0	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
111	c3aj3A_	Alignment	not modelled	46.8	28	PDB header: hydrolase Chain: A; PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
112	c5cslA_	Alignment	not modelled	46.8	22	PDB header: ligase Chain: A; PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
113	c3izcH_	Alignment	not modelled	45.6	15	PDB header: ribosome Chain: H; PDB Molecule: 60s ribosomal protein rpl8 (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
114	c3iz5H_	Alignment	not modelled	44.0	15	PDB header: ribosome Chain: H; PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
115	c1uz5A_	Alignment	not modelled	41.4	26	PDB header: molybdopterin biosynthesis Chain: A; PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
116	c4mm1E_	Alignment	not modelled	41.3	17	PDB header: transferase Chain: E; PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: gggps from methanothermobacter thermautotrophicus
117	d1twda_	Alignment	not modelled	40.9	13	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
118	c1keeH_	Alignment	not modelled	39.8	25	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
119	c3agjD_	Alignment	not modelled	39.8	14	PDB header: translation/hydrolase Chain: D; PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
120	c3agjB_	Alignment	not modelled	39.8	14	PDB header: translation/hydrolase Chain: B; PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex