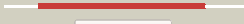



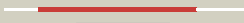




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2795c_(-)_3103947_3104921
Date	Wed Aug 7 12:50:45 BST 2019
Unique Job ID	5fba6ba82890bbee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2yvta1	 Alignment		99.9	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
2	c3ib7A_	 Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
3	c2xmoB_	 Alignment		99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
4	d1uf3a_	 Alignment		99.9	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
5	c3rl4A_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
6	d3d03a1	 Alignment		99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
7	d2hy1a1	 Alignment		99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
8	c2hy1A_	 Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
9	d1nnwa_	 Alignment		99.8	10	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
10	c3qfnA_	 Alignment		99.8	19	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
11	d2nxfa1	 Alignment		99.8	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like

12	c3av0A_	Alignment		99.8	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
13	c4ltyD_	Alignment		99.8	16	PDB header: hydrolase Chain: D; PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
14	c3rqzC_	Alignment		99.8	22	PDB header: hydrolase Chain: C; PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
15	c5k8kA_	Alignment		99.8	11	PDB header: hydrolase Chain: A; PDB Molecule: udp-2,3-diacetylglucosamine hydrolase; PDBTitle: structure of the haemophilus influenzae lpxh-lipid x complex
16	c5ebba_	Alignment		99.8	18	PDB header: hydrolase Chain: A; PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3a; PDBTitle: structure of human sphingomyelinase phosphodiesterase like 3a2 (smpdl3a) with zn2+
17	c3auza_	Alignment		99.8	16	PDB header: recombination Chain: A; PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
18	d2a22a1	Alignment		99.8	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
19	c3qg5D_	Alignment		99.8	18	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
20	d1z2wa1	Alignment		99.8	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
21	c5karA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A; PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3b; PDBTitle: murine acid sphingomyelinase-like phosphodiesterase 3b (smpdl3b)
22	c2q8uA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
23	c5xceB_	Alignment	not modelled	99.8	19	PDB header: transport protein Chain: B; PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of wild type vps29 from entamoeba histolytica
24	c5w8mD_	Alignment	not modelled	99.8	17	PDB header: endocytosis Chain: D; PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of chaetomium thermophilum vps29
25	d1xm7a_	Alignment	not modelled	99.8	24	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
26	d3ck2a1	Alignment	not modelled	99.8	30	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
27	c1s3mA_	Alignment	not modelled	99.7	15	PDB header: phosphodiesterase Chain: A; PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
28	d1s3la_	Alignment	not modelled	99.7	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like

29	c5b4bB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: udp-2,3-diacetylglucosamine hydrolase; PDBTitle: crystal structure of lpxh with lipid x in spacegroup c2
30	d1ii7a_	Alignment	not modelled	99.7	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
31	d1xzw2	Alignment	not modelled	99.7	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
32	c2kknA_	Alignment	not modelled	99.7	26	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
33	c3t1iC_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
34	d1su1a_	Alignment	not modelled	99.7	27	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
35	c1su1A_	Alignment	not modelled	99.7	27	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
36	d2qfra2	Alignment	not modelled	99.7	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
37	c5wlyA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacetylglucosamine hydrolase; PDBTitle: e. coli lpxh- 8 mutations
38	c4ykeA_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: mre11; PDBTitle: crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
39	c4fbkB_	Alignment	not modelled	99.7	15	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
40	c5ficD_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: D: PDB Molecule: sphingomyelin phosphodiesterase; PDBTitle: open form of murine acid sphingomyelinase in presence of lipid
41	c4fcxB_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad32; PDBTitle: s.pombe mre11 apoenzym
42	c3tghA_	Alignment	not modelled	99.6	8	PDB header: cell invasion Chain: A: PDB Molecule: glideosome-associated protein 50; PDBTitle: gap50 the anchor in the inner membrane complex of plasmodium
43	d1qhwa_	Alignment	not modelled	99.6	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
44	c1qhWA_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone
45	c1oidA_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
46	d1usha2	Alignment	not modelled	99.6	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
47	d1g5ba_	Alignment	not modelled	99.6	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
48	c1kbpB_	Alignment	not modelled	99.6	18	PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
49	d1lutea_	Alignment	not modelled	99.6	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
50	c1xzwB_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
51	c5iheB_	Alignment	not modelled	99.5	17	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ii small subunit; PDBTitle: d-family dna polymerase - dp1 subunit (3'-5' proof-reading2 exonuclease)
52	c3qfKA_	Alignment	not modelled	99.4	14	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
53	c3zk4A_	Alignment	not modelled	99.4	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
54	c4j6oA_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of the phosphatase domain of c.

						thermocellum2 (bacterial) pnkp
55	c3ivdA	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in complex with2 uridine
56	c2zbnA	Alignment	not modelled	99.3	23	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
57	c2dfjA	Alignment	not modelled	99.3	21	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
58	c4pehC	Alignment	not modelled	99.3	11	PDB header: hydrolase/rna Chain: C: PDB Molecule: rna lariat debranching enzyme, putative; PDBTitle: dbr1 in complex with synthetic linear rna
59	c2z1aA	Alignment	not modelled	99.3	23	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
60	c2wdfA	Alignment	not modelled	99.2	23	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
61	c6nvoA	Alignment	not modelled	99.2	25	PDB header: dna binding protein Chain: A: PDB Molecule: nuclease mpe; PDBTitle: crystal structure of pseudomonas putida nuclease mpe
62	d2z1aa2	Alignment	not modelled	99.2	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
63	c2qjcA	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
64	c5vjwA	Alignment	not modelled	99.1	23	PDB header: hydrolase Chain: A: PDB Molecule: rhizobiales-like phosphatase 2; PDBTitle: arabidopsis thaliana rhizobiales-like phosphatase 2 complexed with2 tungstate
65	d3c9fa2	Alignment	not modelled	99.1	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
66	c3zu0A	Alignment	not modelled	99.0	21	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadm)
67	c3gveB	Alignment	not modelled	99.0	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
68	c3jyfB	Alignment	not modelled	99.0	18	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
69	c5h7wB	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: B: PDB Molecule: venom 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from venom of naja atra
70	c4h1sB	Alignment	not modelled	98.9	20	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
71	c3c9fB	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
72	c5jpfA	Alignment	not modelled	98.7	13	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
73	d1jk7a	Alignment	not modelled	98.7	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
74	c2yeqA	Alignment	not modelled	98.6	13	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase d; PDBTitle: structure of phod
75	c2jogA	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
76	d1s95a	Alignment	not modelled	98.5	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
77	c5jttA	Alignment	not modelled	98.5	14	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
78	c1wao4	Alignment	not modelled	98.4	16	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
79	c4b2oB	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: B: PDB Molecule: yymb phosphodiesterase; PDBTitle: crystal structure of bacillus subtilis yymb, a global2 regulator of late adaptive responses. Fold: Metallo-dependent phosphatases

80	d3c5wc1	Alignment	not modelled	98.4	17	Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
81	d2p6ba1	Alignment	not modelled	98.4	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
82	c2p6bC_	Alignment	not modelled	98.4	15	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
83	d1s70a_	Alignment	not modelled	98.4	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
84	d1t71a_	Alignment	not modelled	98.4	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
85	c3lcfB_	Alignment	not modelled	98.3	11	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
86	c5vbnE_	Alignment	not modelled	98.3	13	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
87	c1auiA_	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
88	d1auia_	Alignment	not modelled	98.2	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
89	d2z06a1	Alignment	not modelled	98.1	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
90	d1t70a_	Alignment	not modelled	98.1	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
91	c6hv9B_	Alignment	not modelled	98.0	21	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon subunit b; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
92	c4il1A_	Alignment	not modelled	97.6	15	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin, calcineurin subunit b type 1, serine/threonine- PDBTitle: crystal structure of the rat calcineurin
93	c3e0jG_	Alignment	not modelled	97.2	18	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
94	c3floG_	Alignment	not modelled	96.9	13	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
95	c4y97E_	Alignment	not modelled	94.8	18	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	83.0	17	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	d1saza2	Alignment	not modelled	75.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
98	d2qedal	Alignment	not modelled	44.6	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
99	c3qp1A_	Alignment	not modelled	43.1	9	PDB header: transcription Chain: A: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir ligand-binding domain bound to the native2 ligand c6-hsl
100	d1l3la2	Alignment	not modelled	42.4	24	Fold: Profilin-like Superfamily: Pheromone-binding domain of LuxR-like quorum-sensing transcription factors Family: Pheromone-binding domain of LuxR-like quorum-sensing transcription factors
101	c5mjiA_	Alignment	not modelled	41.4	21	PDB header: flavoprotein Chain: A: PDB Molecule: bramp domain protein; PDBTitle: crystal structure of rosb with bound intermediate ohc-rp (8-demethyl-2 8-formylriboflavin-5'-phosphate)
102	c5i4rA_	Alignment	not modelled	39.8	32	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
103	d1ljj_	Alignment	not modelled	34.2	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
104	d3bula2	Alignment	not modelled	33.2	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
105	c5cskB_	Alignment	not modelled	33.1	19	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated

106	d1ozha1	Alignment	not modelled	31.6	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
107	c3bmaC	Alignment	not modelled	28.8	17	PDB header: ligase Chain: C: PDB Molecule: d-alanyl-lipoteichoic acid synthetase; PDBTitle: crystal structure of d-alanyl-lipoteichoic acid synthetase from <i>Streptococcus pneumoniae</i> r6
108	c4zhtB	Alignment	not modelled	28.8	14	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcnaC 2-epimerase
109	d1q6za1	Alignment	not modelled	28.4	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
110	c5cslA	Alignment	not modelled	28.2	19	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
111	c6pfxB	Alignment	not modelled	27.8	14	PDB header: transferase Chain: B: PDB Molecule: d-alanyl transferase dltD; PDBTitle: d-alanyl transferase dltD from <i>Enterococcus faecium</i>
112	c3izcH	Alignment	not modelled	27.8	21	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 <i>Saccharomyces cerevisiae</i> translating 80s ribosome
113	c2yggA	Alignment	not modelled	27.7	36	PDB header: metal binding protein/transport protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: complex of cambr and cam
114	c6g2dC	Alignment	not modelled	27.5	22	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
115	c6o93A	Alignment	not modelled	27.0	21	PDB header: transferase Chain: A: PDB Molecule: d-alanyl transferase dltD; PDBTitle: d-alanyl transferase dltD from <i>Enterococcus faecalis</i>
116	c3j61G	Alignment	not modelled	26.3	26	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8e; PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of <i>Triticum aestivum</i> translating 80s ribosome
117	c3iz5H	Alignment	not modelled	26.3	26	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 <i>Triticum aestivum</i> translating 80s ribosome
118	c3p4iA	Alignment	not modelled	25.9	27	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from <i>Mycobacterium avium</i>
119	c4a1eF	Alignment	not modelled	25.4	23	PDB header: ribosome Chain: F: PDB Molecule: rpl7a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
120	d2f7wa1	Alignment	not modelled	25.0	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like