















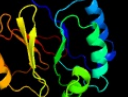






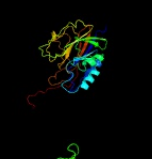
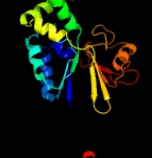

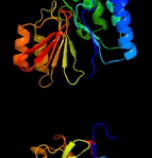

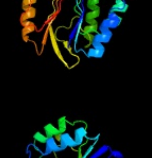
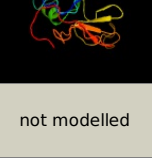


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3683 (-)_4124595_4125554
Date	Fri Aug 9 18:20:37 BST 2019
Unique Job ID	f88ddf248d12787c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xmoB_	 Alignment		99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
2	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
3	c4fcxB_	 Alignment		99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad32; PDBTitle: s.pombe mre11 apoenzym
4	c3t1iC_	 Alignment		99.8	19	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
5	c4fbkB_	 Alignment		99.8	20	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
6	d2yvta1	 Alignment		99.8	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
7	d1uf3a_	 Alignment		99.8	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
8	c4ykeA_	 Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: mre11; PDBTitle: crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
9	c3ib7A_	 Alignment		99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
10	d1ii7a_	 Alignment		99.8	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
11	c3auzA_	 Alignment		99.8	17	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese

12	c2hy1A	Alignment		99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
13	d2hy1a1	Alignment		99.8	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
14	c2q8uA	Alignment		99.7	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
15	c3qfnA	Alignment		99.7	17	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
16	c4ltyD	Alignment		99.7	16	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
17	d3d03a1	Alignment		99.7	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
18	c3rl4A	Alignment		99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
19	c3qg5D	Alignment		99.7	20	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	c6nvoA	Alignment		99.7	25	PDB header: dna binding protein Chain: A: PDB Molecule: nuclease mpe; PDBTitle: crystal structure of pseudomonas putida nuclease mpe
21	c5wlyA	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: e. coli lpxh- 8 mutations
22	c5karA	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3b; PDBTitle: murine acid sphingomyelinase-like phosphodiesterase 3b (smpdl3b)
23	c5ebbA	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3a; PDBTitle: structure of human sphingomyelinase phosphodiesterase like 3a2 (smpdl3a) with zn2+
24	c5b4bB	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: B: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: crystal structure of lpxh with lipid x in spacegroup c2
25	d2nxfA1	Alignment	not modelled	99.7	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
26	c5k8kA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: structure of the haemophilus influenzae lpxh-lipid x complex
27	d1xzwa2	Alignment	not modelled	99.7	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
28	d1s3la	Alignment	not modelled	99.7	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfCE-like

29	c1s3mA	Alignment	not modelled	99.7	22	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
30	d1xm7a	Alignment	not modelled	99.6	24	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
31	d2z1aa2	Alignment	not modelled	99.6	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
32	c3rqzC	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
33	c1oidA	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
34	c2z1aA	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
35	d1usha2	Alignment	not modelled	99.6	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
36	d2qfra2	Alignment	not modelled	99.6	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
37	d1nnwa	Alignment	not modelled	99.5	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
38	c5ficD	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: D: PDB Molecule: sphingomyelin phosphodiesterase; PDBTitle: open form of murine acid sphingomyelinase in presence of lipid
39	d2a22a1	Alignment	not modelled	99.5	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
40	d1su1a	Alignment	not modelled	99.5	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
41	c1su1A	Alignment	not modelled	99.5	23	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
42	c5xceB	Alignment	not modelled	99.5	24	PDB header: transport protein Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of wild type vps29 from entamoeba histolytica
43	c5w8mD	Alignment	not modelled	99.4	20	PDB header: endocytosis Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of chaetomium thermophilum vps29
44	d1z2wa1	Alignment	not modelled	99.4	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
45	c3qfkA	Alignment	not modelled	99.4	16	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
46	c5h7wB	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: B: PDB Molecule: venom 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from venom of naja atra
47	d1lutea	Alignment	not modelled	99.4	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
48	d1qhwa	Alignment	not modelled	99.4	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
49	c1qhwa	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone
50	c3tghA	Alignment	not modelled	99.4	14	PDB header: cell invasion Chain: A: PDB Molecule: glideosome-associated protein 50; PDBTitle: gap50 the anchor in the inner membrane complex of plasmodium
51	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
52	c3zu0A	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadm)
53	c1kbpB	Alignment	not modelled	99.3	12	PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
54	c2kknA	Alignment	not modelled	99.3	28	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

55	c3ivdA	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in complex with2 uridine
56	d3c9fa2	Alignment	not modelled	99.3	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
57	c1xzwB	Alignment	not modelled	99.2	11	PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
58	d3ck2a1	Alignment	not modelled	99.2	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
59	c3zk4A	Alignment	not modelled	99.2	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
60	c2wdfA	Alignment	not modelled	99.1	27	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
61	c3gveB	Alignment	not modelled	99.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
62	d1g5ba	Alignment	not modelled	99.1	11	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
63	c3iyfB	Alignment	not modelled	99.1	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
64	c4j6oA	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of the phosphatase domain of c. thermocellum2 (bacterial) pnkp
65	c3c9fB	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
66	c4b2oB	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: B: PDB Molecule: yymb phosphodiesterase; PDBTitle: crystal structure of bacillus subtilis yymb, a global2 regulator of late adaptive responses.
67	c5iheB	Alignment	not modelled	98.9	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)
68	d1t71a	Alignment	not modelled	98.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
69	c2qjcA	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
70	d2z06a1	Alignment	not modelled	98.8	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
71	c2dfjA	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
72	d1t70a	Alignment	not modelled	98.7	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
73	c5vjwA	Alignment	not modelled	98.6	24	PDB header: hydrolase Chain: A: PDB Molecule: rhizobiales-like phosphatase 2; PDBTitle: arabidopsis thaliana rhizobiales-like phosphatase 2 complexed with2 tungstate
74	c2zbmA	Alignment	not modelled	98.1	20	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
75	c4pehC	Alignment	not modelled	98.1	18	PDB header: hydrolase/rna Chain: C: PDB Molecule: rna lariat debranching enzyme, putative; PDBTitle: dbr1 in complex with synthetic linear rna
76	c6hv9B	Alignment	not modelled	97.9	25	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon subunit b; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
77	c5vbnE	Alignment	not modelled	97.9	19	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
78	d3c5wc1	Alignment	not modelled	97.8	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
79	d1jk7a	Alignment	not modelled	97.8	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
80	c3e0jG	Alignment	not modelled	97.6	24	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
81	c5jpfA	Alignment	not modelled	97.6	12 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
82	d1s95a	Alignment	not modelled	97.5	13 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
83	c2jogA	Alignment	not modelled	97.4	15 PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
84	c2yeqA	Alignment	not modelled	97.4	15 PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase d; PDBTitle: structure of phod
85	d1s70a	Alignment	not modelled	97.2	12 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
86	c1wao4	Alignment	not modelled	97.1	13 PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
87	c5jttA	Alignment	not modelled	97.1	10 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
88	c3floG	Alignment	not modelled	97.0	10 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
89	c1auiA	Alignment	not modelled	97.0	17 PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
90	d1auiA	Alignment	not modelled	97.0	17 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
91	c3icfB	Alignment	not modelled	96.9	15 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
92	d2p6ba1	Alignment	not modelled	96.9	14 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
93	c2p6bC	Alignment	not modelled	96.8	17 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
94	c4y97E	Alignment	not modelled	96.4	15 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
95	c4il1A	Alignment	not modelled	95.5	14 PDB header: hydrolase Chain: A: PDB Molecule: calmodulin, calcineurin subunit b type 1, serine/threonine- PDBTitle: crystal structure of the rat calcineurin
96	c4r3uD	Alignment	not modelled	81.2	8 PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
97	d1ccwa	Alignment	not modelled	79.5	13 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
98	c5khaA	Alignment	not modelled	77.0	13 PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
99	c4zhtB	Alignment	not modelled	77.0	21 PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcnac 2-epimerase
100	d3bula2	Alignment	not modelled	74.9	14 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
101	d1fmfa	Alignment	not modelled	74.8	9 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
102	c2yxbA	Alignment	not modelled	73.8	10 PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
103	c1y80A	Alignment	not modelled	72.9	12 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
104	c1xrsB	Alignment	not modelled	70.9	10 PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
105	d2gupa2	Alignment	not modelled	70.9	18 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
106	d1xrsb1	Alignment	not modelled	69.7	12 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain

					Family: Cobalamin (vitamin B12)-binding domain
107	d7reqa2	Alignment	not modelled	68.4	18 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
108	d1xc3a2	Alignment	not modelled	66.2	13 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
109	c4ldaF_	Alignment	not modelled	65.1	9 PDB header: transcription Chain: F; PDB Molecule: tadz; PDBTitle: crystal structure of a chey-like protein (tadz) from pseudomonas2 aeruginosa pao1 at 2.70 a resolution
110	c5ccfA_	Alignment	not modelled	64.2	19 PDB header: transferase Chain: A; PDB Molecule: adp-dependent glucokinase; PDBTitle: structure of mouse adp-dependent glucokinase
111	c5ul4A_	Alignment	not modelled	63.5	12 PDB header: metal binding protein Chain: A; PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
112	c5wb4H_	Alignment	not modelled	60.3	6 PDB header: transferase Chain: H; PDB Molecule: n-acetylglucosaminyldiphosphoundecaprenol n-acetyl-beta-d- PDBTitle: crystal structure of the tara wall teichoic acid glycosyltransferase
113	c4jgiB_	Alignment	not modelled	59.9	14 PDB header: protein binding Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
114	d2aa4a2	Alignment	not modelled	56.6	15 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
115	c4hh3C_	Alignment	not modelled	55.7	12 PDB header: flavoprotein/transcription Chain: C; PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
116	c1xc3A_	Alignment	not modelled	54.9	13 PDB header: transferase Chain: A; PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
117	c2i2xD_	Alignment	not modelled	54.8	14 PDB header: transferase Chain: D; PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
118	c3aufA_	Alignment	not modelled	52.7	21 PDB header: transferase Chain: A; PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
119	d1z6ra3	Alignment	not modelled	52.6	7 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
120	c2ei9A_	Alignment	not modelled	50.9	19 PDB header: gene regulation Chain: A; PDB Molecule: non-ltr retrotransposon r1bmks orf2 protein; PDBTitle: crystal structure of r1bm endonuclease domain