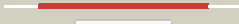


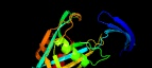
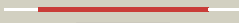


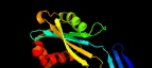

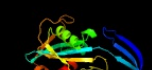



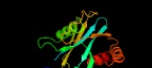



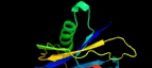

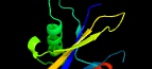

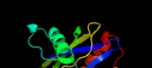

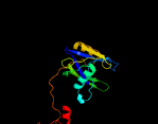









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1700_(-)_1925589_1926212
Date	Fri Aug 2 13:30:30 BST 2019
Unique Job ID	b9e8e2ea0a2cadbc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mqea_	 Alignment		100.0	97	Fold: Nudix Superfamily: Nudix Family: MutT-like
2	c5c7tB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: nudf protein; PDBTitle: crystal structure of the bdellovibrio bacteriovorus nucleoside2 diphosphate sugar hydrolase in complex with adp-ribose
3	d1vhza_	 Alignment		100.0	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
4	d1g0sa_	 Alignment		100.0	24	Fold: Nudix Superfamily: Nudix Family: MutT-like
5	c2yvoA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of ndx2 in complex with mg2+ and amp from thermus2 thermophilus hb8
6	d1viua_	 Alignment		100.0	23	Fold: Nudix Superfamily: Nudix Family: MutT-like
7	c3bm4B_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: adp-sugar pyrophosphatase; PDBTitle: crystal structure of human adp-ribose pyrophosphatase nudt5 in complex2 with magnesium and ampcpr
8	d1v8ya_	 Alignment		100.0	38	Fold: Nudix Superfamily: Nudix Family: MutT-like
9	c2w4eA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
10	c3q91D_	 Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: uridine diphosphate glucose pyrophosphatase; PDBTitle: crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
11	d1sjya_	 Alignment		99.9	18	Fold: Nudix Superfamily: Nudix Family: MutT-like

12	c6o3pA	Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
13	c5gg7A	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family protein; PDBTitle: crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
14	c3fjyB	Alignment		99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
15	d2fkba1	Alignment		99.8	17	Fold: Nudix Superfamily: Nudix Family: !PP isomerase-like
16	d1vk6a2	Alignment		99.8	20	Fold: Nudix Superfamily: Nudix Family: NADH pyrophosphatase
17	d2o5fa1	Alignment		99.8	15	Fold: Nudix Superfamily: Nudix Family: !PP isomerase-like
18	d2b0va1	Alignment		99.8	15	Fold: Nudix Superfamily: Nudix Family: MutT-like
19	c5lopA	Alignment		99.8	15	PDB header: rna binding protein Chain: A: PDB Molecule: klla0f23980p; PDBTitle: structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
20	c2jvbA	Alignment		99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: mrna-decapping enzyme subunit 2; PDBTitle: solution structure of catalytic domain of ydcp2
21	c5mp0D	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: D: PDB Molecule: m7gpppn-mrna hydrolase; PDBTitle: human m7gpppn-mrna hydrolase (dcp2, nudt20) catalytic domain
22	c4jztA	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: dgtp pyrophosphohydrolase; PDBTitle: crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
23	c2gb5B	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
24	c3dkuB	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of nudix hydrolase orf153, ymfb, from escherichia2 coli k-1
25	c4kyxA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase mutt; PDBTitle: crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
26	c2rrkA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: ctp pyrophosphohydrolase; PDBTitle: solution structure of the e. coli orf135 protein
27	c3gg6A	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 18; PDBTitle: crystal structure of the nudix domain of human nudt18
28	c4zbpC	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase 7; PDBTitle: crystal structure of the ampccpr-bound atnudt7
29	d1nqza	Alignment	not modelled	99.8	22	Fold: Nudix Superfamily: Nudix

						Family: MutT-like
30	c2r5wA_	Alignment	not modelled	99.8	21	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenylyltransferase; PDBTitle: crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
31	c2kdvA_	Alignment	not modelled	99.8	26	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
32	c3h95A_	Alignment	not modelled	99.8	24	PDB header: gene regulation Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 6; PDBTitle: crystal structure of the nudix domain of nudt6
33	c2fvvA_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: diphosphoinositol polyphosphate phosphohydrolase 1; PDBTitle: human diphosphoinositol polyphosphate phosphohydrolase 1
34	d2fvva1	Alignment	not modelled	99.8	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
35	c3hhjA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: crystal structure of mutator mutt from bartonella henselae
36	c3grnB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: mutt related protein; PDBTitle: crystal structure of mutt protein from methanosarcina mazei go1
37	d1vcda1	Alignment	not modelled	99.7	21	Fold: Nudix Superfamily: Nudix Family: MutT-like
38	c4dywA_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt nudix hydrolase from burkholderia2 pseudomallei
39	d1ryaa_	Alignment	not modelled	99.7	16	Fold: Nudix Superfamily: Nudix Family: GDP-mannose mannosyl hydrolase NudD
40	d1jkna_	Alignment	not modelled	99.7	20	Fold: Nudix Superfamily: Nudix Family: MutT-like
41	c5zrhA_	Alignment	not modelled	99.7	26	PDB header: hydrolase Chain: A: PDB Molecule: putative mutator protein mutt2/nudix hydrolase; PDBTitle: m. smegmatis antimutator protein mutt2 in complex with cmp
42	c2o1cB_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: B: PDB Molecule: datp pyrophosphohydrolase; PDBTitle: structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
43	c2pq1B_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: ap4a hydrolase; PDBTitle: crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
44	c5gp0F_	Alignment	not modelled	99.7	25	PDB header: hydrolase Chain: F: PDB Molecule: nudix hydrolase 1; PDBTitle: crystal structure of geraniol-nudx1 complex
45	c3id9B_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
46	c3exqA_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: nudix family hydrolase; PDBTitle: crystal structure of a nudix family hydrolase from2 lactobacillus brevis
47	c3cngC_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
48	c3gwyA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: putative ctp pyrophosphohydrolase; PDBTitle: crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
49	c5bonC_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: C: PDB Molecule: probable 8-oxo-dgtp diphosphatase nudt15; PDBTitle: crystal structure of human nudt15 (mth2)
50	c3o8sA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribose pyrophosphatase; PDBTitle: crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
51	d2a6ta2	Alignment	not modelled	99.7	19	Fold: Nudix Superfamily: Nudix Family: mRNA decapping enzyme-like
52	c5x1xA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: solution nmr structure of dna mismatch repair protein mutt (family2 nudix hydrolase) from methicillin resistant staphylococcus aureus 252
53	d1ppva_	Alignment	not modelled	99.7	12	Fold: Nudix Superfamily: Nudix Family: IPP isomerase-like
54	d1ktga_	Alignment	not modelled	99.7	20	Fold: Nudix Superfamily: Nudix

						Family:MutT-like
55	c3sonB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical nudix hydrolase; PDBTitle: crystal structure of a putative nudix hydrolase (lmoF2365_2679) from <i>listeria monocytogenes</i> str. 4b f2365 at 1.70 a resolution
56	c3ef5A_	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
57	c2qkmF_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
58	d1hzta_	Alignment	not modelled	99.7	12	Fold: Nudix Superfamily: Nudix Family: !PP isomerase-like
59	d2azwa1	Alignment	not modelled	99.7	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
60	d1puna_	Alignment	not modelled	99.7	18	Fold: Nudix Superfamily: Nudix Family: MutT-like
61	d1irya_	Alignment	not modelled	99.7	22	Fold: Nudix Superfamily: Nudix Family: MutT-like
62	c2qjoB_	Alignment	not modelled	99.7	17	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nmh adenylyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nmh adenylyltransferase/adp ribose 2 pyrophosphatase (nadm) complexed with adprp and nad from <i>synechocystis</i> sp.
63	c4v14A_	Alignment	not modelled	99.7	28	PDB header: hydrolase Chain: A: PDB Molecule: mutator mutt protein; PDBTitle: structure and function analysis of mutt from the 2 psychrophile fish pathogen <i>alivibrio salmonicida</i> and the 3 mesophile <i>vibrio cholerae</i>
64	c3gz8C_	Alignment	not modelled	99.7	19	PDB header: dna binding protein Chain: C: PDB Molecule: mutt/nudix family protein; PDBTitle: cocrystal structure of nudix domain of <i>shewanella oneidensis</i> nrtr2 complexed with adp ribose
65	d2b06a1	Alignment	not modelled	99.7	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
66	c3i9xA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mutt/nudix family protein from <i>listeria innocua</i>
67	d1xsba_	Alignment	not modelled	99.7	19	Fold: Nudix Superfamily: Nudix Family: MutT-like
68	c5lf8A_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 17; PDBTitle: human nucleoside diphosphate-linked moiety x motif 17 (nudt17)
69	d2fb1a2	Alignment	not modelled	99.7	15	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
70	c5cfiC_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: C: PDB Molecule: bis(5'-nucleosyl)-tetraphosphatase (diadenosine ap4a2 hydrolase PDBTitle: structural and functional attributes of malaria parasite ap4a2 hydrolase
71	c2pqvA_	Alignment	not modelled	99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family protein from <i>streptococcus2 pneumoniae</i>
72	c3q4iA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase (mutt/nudix family protein); PDBTitle: crystal structure of cdp-chase in complex with gd3+
73	c3r03B_	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: B: PDB Molecule: nudix hydrolase; PDBTitle: the crystal structure of nudix hydrolase from <i>rhodospirillum rubrum</i>
74	c4hfqB_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of udp-x diphosphatase
75	c3e57A_	Alignment	not modelled	99.6	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein tm1382; PDBTitle: crystal structure of tm1382, a putative nudix hydrolase
76	c4ilqA_	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: A: PDB Molecule: ct771; PDBTitle: 2.60a resolution structure of ct771 from <i>chlamydia trachomatis</i>
77	c2yyhC_	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: C: PDB Molecule: 8-oxo-dgtpase domain; PDBTitle: crystal structure of nudix family protein from <i>aquifex aeolicus</i>
78	c3n77B_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside triphosphatase nudi; PDBTitle: crystal structure of idp01880, putative ntp pyrophosphohydrolase of <i>salmonella typhimurium</i> lt2
79	c3f08B_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: B: PDB Molecule: mutator mutt protein;

79	c3kzB_	Alignment	not modelled	99.0	19	PDBTitle: crystal structure of mmutator mutt protein from bacillus halodurans PDB header: hydrolase
80	c3fcmA_	Alignment	not modelled	99.6	14	Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a nudix hydrolase from clostridium perfringens
81	c3edsA_	Alignment	not modelled	99.6	28	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
82	c5t3pB_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal coenzyme a diphosphatase nudt7; PDBTitle: crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
83	c3f6aA_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family; PDBTitle: crystal structure of a hydrolase, nudix family from2 clostridium perfringens
84	c3gz6A_	Alignment	not modelled	99.5	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of shewanella oneidensis nrtr complexed with a 27mer2 dna
85	d1k2ea_	Alignment	not modelled	99.5	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
86	c2fb1A_	Alignment	not modelled	99.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0354 from bacteroides thetaiotaomicron
87	c2i6kA_	Alignment	not modelled	99.5	12	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 1; PDBTitle: crystal structure of human type i ipp isomerase complexed with a2 substrate analog
88	d2fmla2	Alignment	not modelled	99.5	17	Fold: Nudix Superfamily: Nudix Family: BT0354 N-terminal domain-like
89	c3f13A_	Alignment	not modelled	99.5	24	PDB header: hydrolase Chain: A: PDB Molecule: putative nudix hydrolase family member; PDBTitle: crystal structure of putative nudix hydrolase family member from2 chromobacterium violaceum
90	c3rh7A_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
91	c2pnyA_	Alignment	not modelled	99.4	15	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
92	c2fmB_	Alignment	not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family protein from enterococcus2 faecalis
93	d1x51a1	Alignment	not modelled	99.3	14	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
94	c3dupB_	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
95	c1rrqA_	Alignment	not modelled	99.3	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
96	c3qsjA_	Alignment	not modelled	99.2	26	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
97	d1q33a_	Alignment	not modelled	99.2	16	Fold: Nudix Superfamily: Nudix Family: MutT-like
98	d1rrqa2	Alignment	not modelled	99.1	21	Fold: Nudix Superfamily: Nudix Family: MutY C-terminal domain-like
99	d1u20a1	Alignment	not modelled	99.1	17	Fold: Nudix Superfamily: Nudix Family: MutT-like
100	c4v1aj_	Alignment	not modelled	99.1	19	PDB header: ribosome Chain: J: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
101	c2j8qB_	Alignment	not modelled	99.0	17	PDB header: nuclear protein Chain: B: PDB Molecule: cleavage and polyadenylation specificity factor 5; PDBTitle: crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
102	c5f9A_	Alignment	not modelled	99.0	13	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 22; PDBTitle: crystal structure of human nudt22
103	c3couA_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
104	c3kvhA_	Alignment	not modelled	97.8	16	PDB header: rna binding protein Chain: A: PDB Molecule: protein syndesmos; PDBTitle: crystal structure of human protein syndesmos (nudt16-

						like protein)
105	c1vw46_	Alignment	not modelled	95.7	26	PDB header: ribosome Chain: 6: PDB Molecule: 54s ribosomal protein l17, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
106	c3p5tE_	Alignment	not modelled	90.9	22	PDB header: rna binding protein Chain: E: PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
107	c4ktbA_	Alignment	not modelled	81.2	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of possible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
108	c5mu7B_	Alignment	not modelled	49.7	11	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit delta-like protein; PDBTitle: crystal structure of the beta/delta-copi core complex
109	c5a1vP_	Alignment	not modelled	47.1	16	PDB header: transport protein Chain: P: PDB Molecule: coatomer subunit delta; PDBTitle: the structure of the cop1 coat linkage i
110	c1w63T_	Alignment	not modelled	34.9	14	PDB header: endocytosis Chain: T: PDB Molecule: adapter-related protein complex 1 sigma 1a subunit; PDBTitle: ap1 clathrin adaptor core
111	d1gw5s_	Alignment	not modelled	31.3	16	Fold: Profilin-like Superfamily: SNARE-like Family: Clathrin coat assembly domain
112	c5nzvN_	Alignment	not modelled	29.4	16	PDB header: transport protein Chain: N: PDB Molecule: coatomer subunit delta; PDBTitle: the structure of the cop1 coat linkage iv
113	c2hf6A_	Alignment	not modelled	26.0	30	PDB header: protein transport Chain: A: PDB Molecule: coatomer subunit zeta-1; PDBTitle: solution structure of human zeta-cop
114	d2dxx3	Alignment	not modelled	24.2	18	Fold: Pentein, beta/alpha-propeller Superfamily: Pentein Family: Peptidylarginine deiminase Pad4, catalytic C-terminal domain
115	c6ce1A_	Alignment	not modelled	22.9	18	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-3; PDBTitle: crystal structure of peptidyl arginine deiminase type iii (padi3)
116	c5a1yH_	Alignment	not modelled	21.8	17	PDB header: transport protein Chain: H: PDB Molecule: coatomer subunit delta; PDBTitle: the structure of the cop1 coat linkage iv