

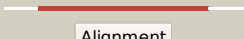

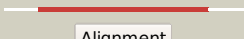

















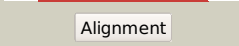
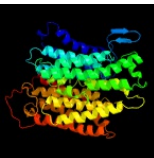






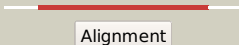

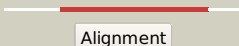

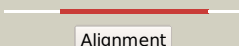



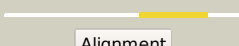

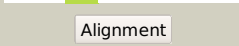
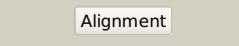
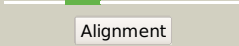
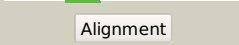

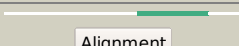

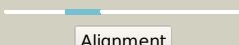


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3157_(nuoM)_3524129_3525790
Date	Thu Aug 8 16:20:34 BST 2019
Unique Job ID	e674f2eb255959f1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoM_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: M; PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c3rkoL_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-quinone oxidoreductase subunit l; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c4heaT_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: T; PDB Molecule: nadh-quinone oxidoreductase subunit 12; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
4	c6humD_	 Alignment		100.0	28	PDB header: proton transport Chain: D; PDB Molecule: nad(p)h-quinone oxidoreductase chain 4 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
5	c6humF_	 Alignment		100.0	22	PDB header: proton transport Chain: F; PDB Molecule: nadh dehydrogenase subunit 5; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
6	c6gcs4_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: 4; PDB Molecule: nd4 subunit (nu4m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
7	c6gcs5_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: 5; PDB Molecule: nd5 subunit (nu5m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
8	c4he8M_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: M; PDB Molecule: nadh-quinone oxidoreductase subunit 13; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
9	c6cfwH_	 Alignment		100.0	23	PDB header: membrane protein Chain: H; PDB Molecule: monovalent cation/h+ antiporter subunit d; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
10	c6humB_	 Alignment		100.0	18	PDB header: proton transport Chain: B; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
11	c5ldwL_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: structure of mammalian respiratory complex i, class1

12	c6g2jL_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: mouse mitochondrial complex i in the active state
13	c3rkoN_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-quinone oxidoreductase subunit n; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
14	c5ldwM_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class1
15	c4he8I_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh-quinone oxidoreductase subunit 14; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
16	c6gcs2_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: 2: PDB Molecule: nd2 subunit (nu2m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
17	c5xtdi_	 Alignment		100.0	17	PDB header: oxidoreductase/electron transport Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: cryo-em structure of human respiratory complex i
18	c6g2jN_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: mouse mitochondrial complex i in the active state
19	c5ldwN_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: structure of mammalian respiratory complex i, class1
20	c6cfwM_	 Alignment		75.2	13	PDB header: membrane protein Chain: M: PDB Molecule: mbh13 nadh dehydrogenase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
21	c6gcsL_	 Alignment	not modelled	65.6	13	PDB header: oxidoreductase Chain: L: PDB Molecule: nd4l subunit (nulm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
22	c6gcs1_	 Alignment	not modelled	57.7	16	PDB header: oxidoreductase Chain: 1: PDB Molecule: nd1 subunit (nu1m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
23	c6g2jK_	 Alignment	not modelled	55.9	10	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: mouse mitochondrial complex i in the active state
24	c6humE_	 Alignment	not modelled	54.7	16	PDB header: proton transport Chain: E: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 4l; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
25	c4heaK_	 Alignment	not modelled	43.0	14	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit 11; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
26	c5lc5H_	 Alignment	not modelled	42.2	12	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class2
27	c6cfwG_	 Alignment	not modelled	40.9	10	PDB header: membrane protein Chain: G: PDB Molecule: monovalent cation/h+ antiporter subunit c; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
28	c3rkoK_	 Alignment	not modelled	38.2	12	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory

						complex i from2 e. coli at 3.0 angstrom resolution
29	c5ldwK_	Alignment	not modelled	37.3	8	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class1
30	c5lc5K_	Alignment	not modelled	37.3	8	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class2
31	d1a6qa1	Alignment	not modelled	30.4	17	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
32	c2l3iA_	Alignment	not modelled	24.7	42	PDB header: antimicrobial protein Chain: A: PDB Molecule: aoxki4a, antimicrobial peptide in spider venom; PDBTitle: ooxki4a, spider derived antimicrobial peptide
33	c4x84C_	Alignment	not modelled	21.4	18	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
34	c4p6vE_	Alignment	not modelled	18.9	17	PDB header: oxidoreductase Chain: E: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit e; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
35	d1o8bb1	Alignment	not modelled	18.1	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
36	c6humA_	Alignment	not modelled	13.3	12	PDB header: proton transport Chain: A: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
37	c5ldwb_	Alignment	not modelled	11.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class1
38	c5lc5b_	Alignment	not modelled	11.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
39	c5o31b_	Alignment	not modelled	11.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: mitochondrial complex i in the deactive state
40	c5ldxb_	Alignment	not modelled	11.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class3.
41	c5lnkm_	Alignment	not modelled	11.4	29	PDB header: oxidoreductase Chain: M: PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i
42	d1s1qa_	Alignment	not modelled	11.1	31	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
43	c5n9yB_	Alignment	not modelled	9.7	18	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
44	c4he8H_	Alignment	not modelled	9.3	14	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-quinone oxidoreductase subunit 8; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
45	c6odmK_	Alignment	not modelled	9.3	33	PDB header: viral protein Chain: K: PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
46	c4lnsA_	Alignment	not modelled	9.0	13	PDB header: ligase Chain: A: PDB Molecule: asparagine synthetase a; PDBTitle: crystal structure of asparagine synthetase a (asna) from trypanosoma2 brucei
47	d1oqwa_	Alignment	not modelled	8.6	17	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
48	c3sokB_	Alignment	not modelled	8.5	13	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
49	c4ddpA_	Alignment	not modelled	8.4	27	PDB header: membrane protein Chain: A: PDB Molecule: beclin-1; PDBTitle: crystal structure of beclin 1 evolutionarily conserved domain(ecd)
50	c4j15A_	Alignment	not modelled	8.3	25	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna ligase, cytoplasmic; PDBTitle: crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
51	c6btmD_	Alignment	not modelled	8.1	14	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
52	c5dfzD_	Alignment	not modelled	8.0	36	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
53	d1n9wa2	Alignment	not modelled	7.8	25	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
54	c3vp7A_	Alignment	not modelled	7.8	36	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 30;

						PDBTitle: crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
55	c4k0eA_	Alignment	not modelled	7.7	11	PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
56	c1n9wA_	Alignment	not modelled	7.7	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
57	c3bjuB_	Alignment	not modelled	7.2	38	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna synthetase
58	c3r24A_	Alignment	not modelled	7.1	33	PDB header: transferase, viral protein Chain: A: PDB Molecule: 2'-o-methyl transferase; PDBTitle: crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible
59	c4ex5A_	Alignment	not modelled	7.0	13	PDB header: transferase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
60	d1r6ra_	Alignment	not modelled	7.0	15	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
61	c1r6rA_	Alignment	not modelled	7.0	15	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
62	c5elnC_	Alignment	not modelled	7.0	25	PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
63	c3c25A_	Alignment	not modelled	6.9	83	PDB header: hydrolase/dna Chain: A: PDB Molecule: noti restriction endonuclease; PDBTitle: crystal structure of noti restriction endonuclease bound to cognate2 dna
64	c5vl1D_	Alignment	not modelled	6.9	13	PDB header: ligase Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine
65	c4o2dB_	Alignment	not modelled	6.9	13	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase; PDBTitle: crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
66	c5hgqD_	Alignment	not modelled	6.8	38	PDB header: ligase/ligase inhibitor Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: loa loa lysyl-trna synthetase in complex with cladosporin.
67	c4upaA_	Alignment	not modelled	6.7	13	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp
68	c6hu9n_	Alignment	not modelled	6.6	12	PDB header: oxidoreductase/electron transport Chain: N: PDB Molecule: cytochrome b; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
69	d2gf4a1	Alignment	not modelled	6.6	27	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Vng1086c-like Family: Vng1086c-like
70	c1b8aB_	Alignment	not modelled	6.6	25	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
71	c3mesB_	Alignment	not modelled	6.6	31	PDB header: transferase Chain: B: PDB Molecule: choline kinase; PDBTitle: crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
72	c6pqhA_	Alignment	not modelled	6.5	13	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of asparagine-trna ligase from elizabethkingia sp.2 ccug 26117
73	c2kncA_	Alignment	not modelled	6.5	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
74	c1wydB_	Alignment	not modelled	6.4	38	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfobolus tokodaii
75	c6ns0A_	Alignment	not modelled	6.2	25	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from chlamydia trachomatis2 complexed with l-lysine and cladosporin
76	c6iu3A_	Alignment	not modelled	6.2	14	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
77	c1x55A_	Alignment	not modelled	6.1	13	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase; PDBTitle: crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
78	c2xgtB_	Alignment	not modelled	6.1	0	PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
79	c1e22A_	Alignment	not modelled	6.1	38	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-ppc

80	d2pila_	Alignment	not modelled	6.1	14	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
81	c5ynpA_	Alignment	not modelled	6.1	22	PDB header: transferase Chain: A: PDB Molecule: nsp16 protein; PDBTitle: crystal structure of mers-cov nsp16/nsp10 complex bound to sinefungin2 and m7gpppa
82	c4h02B_	Alignment	not modelled	6.0	25	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of p. falciparum lysyl-trna synthetase
83	c5o60M_	Alignment	not modelled	5.9	40	PDB header: ribosome Chain: M: PDB Molecule: 50s ribosomal protein l15; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
84	c5zg8A_	Alignment	not modelled	5.8	13	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase; PDBTitle: crystal structure of ttnrs
85	c5xixD_	Alignment	not modelled	5.8	0	PDB header: ligase Chain: D: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the canonical domain of human asparaginyl-trna synthetase
86	c6od8A_	Alignment	not modelled	5.7	13	PDB header: ligase Chain: A: PDB Molecule: putative aspartyl-trna synthetase; PDBTitle: crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin
87	c1asyA_	Alignment	not modelled	5.7	25	PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
88	c2voyK_	Alignment	not modelled	5.7	23	PDB header: hydrolase Chain: K: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
89	c3fq6A_	Alignment	not modelled	5.6	26	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
90	c4up8A_	Alignment	not modelled	5.5	13	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase apo2 form
91	c5t59D_	Alignment	not modelled	5.4	31	PDB header: cell cycle Chain: D: PDB Molecule: klla0f02343p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
92	c3na2C_	Alignment	not modelled	5.3	33	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
93	c6j5ib_	Alignment	not modelled	5.2	13	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
94	c6e3yE_	Alignment	not modelled	5.2	7	PDB header: signaling protein Chain: E: PDB Molecule: receptor activity-modifying protein 1; PDBTitle: cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor
95	c3e9hB_	Alignment	not modelled	5.2	13	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
96	c3m4qA_	Alignment	not modelled	5.2	0	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnrs)
97	c2ks1B_	Alignment	not modelled	5.2	13	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
98	d1u7ga_	Alignment	not modelled	5.1	10	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter
99	c1vw48_	Alignment	not modelled	5.0	36	PDB header: ribosome Chain: 8: PDB Molecule: 54s ribosomal protein l13, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit