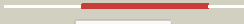



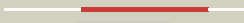





















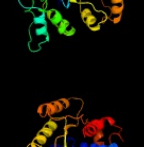


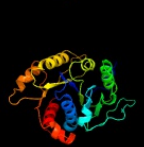
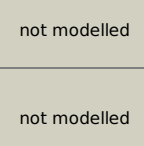


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0530 (-) _620910_622127
Date	Fri Jul 26 01:50:08 BST 2019
Unique Job ID	ca451f868ba1bbdf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2afhe1	 Alignment		100.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
2	d1cp2a_	 Alignment		100.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
3	c3endA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
4	c3ea0B_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
5	c4rz3B_	 Alignment		100.0	19	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
6	c511jA_	 Alignment		100.0	18	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
7	d1iona_	 Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
8	c3q91B_	 Alignment		100.0	18	PDB header: cell cycle, hydrolase Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
9	d1g3qa_	 Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
10	d1hyqa_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
11	c1hyqA_	 Alignment		100.0	23	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus

12	c6iucC_	Alignment		100.0	17	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
13	c3ez6B_	Alignment		100.0	17	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
14	c2ozeA_	Alignment		100.0	12	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
15	c3kjqB_	Alignment		100.0	21	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
16	c3fkqA_	Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
17	c6nonB_	Alignment		100.0	17	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
18	c2bekB_	Alignment		100.0	24	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
19	c4v02B_	Alignment		100.0	24	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
20	c3vx3A_	Alignment		100.0	21	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
21	c6g2gA_	Alignment	not modelled	100.0	19	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
22	c2ph1A_	Alignment	not modelled	100.0	18	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
23	c3k9gA_	Alignment	not modelled	100.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
24	c3cioA_	Alignment	not modelled	100.0	17	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
25	c3la6P_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
26	c3ezfA_	Alignment	not modelled	100.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
27	c2xj9B_	Alignment	not modelled	100.0	17	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
28	c3pg5A_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics

					consortium target cdr78 PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
29	c4pfsA_	Alignment	not modelled	100.0	21
30	c2wojD_	Alignment	not modelled	100.0	14
31	c4ru8C_	Alignment	not modelled	99.9	19
32	c2vedA_	Alignment	not modelled	99.9	18
33	c4dzzB_	Alignment	not modelled	99.9	14
34	c2wooC_	Alignment	not modelled	99.9	17
35	c3zq6D_	Alignment	not modelled	99.9	22
36	d1byia_	Alignment	not modelled	99.9	15
37	d1ihua2	Alignment	not modelled	99.9	18
38	c3ug7D_	Alignment	not modelled	99.9	19
39	c5zmfA_	Alignment	not modelled	99.9	20
40	c6bs3A_	Alignment	not modelled	99.9	16
41	c5bwkA_	Alignment	not modelled	99.9	18
42	c6bs5B_	Alignment	not modelled	99.9	21
43	c3cwqB_	Alignment	not modelled	99.9	23
44	d1ihua1	Alignment	not modelled	99.9	19
45	c3ibgF_	Alignment	not modelled	99.9	15
46	c3io3A_	Alignment	not modelled	99.9	14
47	c1ii0A_	Alignment	not modelled	99.9	20
48	c3of5A_	Alignment	not modelled	99.9	9
49	c2qmoA_	Alignment	not modelled	99.9	14
50	c3igfB_	Alignment	not modelled	99.8	13
51	c3fmfA_	Alignment	not modelled	99.8	19
52	c5l3qB_	Alignment	not modelled	99.4	15
53	c2qy9A_	Alignment	not modelled	99.4	16

54	c1zu4A_	Alignment	not modelled	99.4	17	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2_group p21212
55	c1vmaA_	Alignment	not modelled	99.3	19	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
56	c5l3rC_	Alignment	not modelled	99.3	20	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
57	c2og2A_	Alignment	not modelled	99.3	21	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
58	c3b9qA_	Alignment	not modelled	99.2	17	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
59	c2yhsA_	Alignment	not modelled	99.2	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
60	c5gafi_	Alignment	not modelled	99.2	17	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
61	c6cy1B_	Alignment	not modelled	99.2	19	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
62	c3dm5A_	Alignment	not modelled	99.2	16	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
63	c2j37W_	Alignment	not modelled	99.2	15	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
64	c2cnwF_	Alignment	not modelled	99.2	20	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsyt; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsyt
65	c2iy3A_	Alignment	not modelled	99.2	15	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
66	c2j7pA_	Alignment	not modelled	99.2	16	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsyt
67	c5l3sF_	Alignment	not modelled	99.2	15	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsyt; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsyt
68	c2q9cA_	Alignment	not modelled	99.1	19	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: structure of ftsyt:gmppnp with mgcl complex
69	c2v3cC_	Alignment	not modelled	99.1	15	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
70	c1qzwC_	Alignment	not modelled	99.1	16	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
71	c4ak9A_	Alignment	not modelled	99.1	20	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsyt from physcomitrella patens
72	c3dmdA_	Alignment	not modelled	98.9	15	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
73	c2j289_	Alignment	not modelled	98.9	18	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
74	c2px0D_	Alignment	not modelled	98.5	14	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
75	d1vmaa2	Alignment	not modelled	98.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	d1qzxa3	Alignment	not modelled	98.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c1j8yF_	Alignment	not modelled	98.1	15	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
78	c4xc8B_	Alignment	not modelled	98.1	17	PDB header: isomerase Chain: B: PDB Molecule: isobutyryl-coa mutase fused; PDBTitle: isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
						Fold: P-loop containing nucleoside triphosphate hydrolases

79	d1j8yf2	Alignment	not modelled	98.0	16	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	d2qm8a1	Alignment	not modelled	97.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	c4ohvA	Alignment	not modelled	97.8	19	PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
82	c2npiB	Alignment	not modelled	97.8	12	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
83	c5hcnA	Alignment	not modelled	97.8	14	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
84	c4a0gC	Alignment	not modelled	97.7	16	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
85	c4nkrB	Alignment	not modelled	97.7	14	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
86	c2h5eB	Alignment	not modelled	97.7	20	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
87	c2recB	Alignment	not modelled	97.6	20	PDB header: helicase PDB COMPND:
88	d2qy9a2	Alignment	not modelled	97.6	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
89	c3tr5C	Alignment	not modelled	97.5	14	PDB header: translation Chain: C: PDB Molecule: peptide chain release factor 3; PDBTitle: structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
90	c1xjqA	Alignment	not modelled	97.5	15	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
91	c2f1rA	Alignment	not modelled	97.5	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
92	d1okkd2	Alignment	not modelled	97.4	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
93	d1nlfa	Alignment	not modelled	97.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
94	d1nija1	Alignment	not modelled	97.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
95	c2vyeA	Alignment	not modelled	97.4	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
96	c3cr8C	Alignment	not modelled	97.4	14	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
97	c1xp8A	Alignment	not modelled	97.4	21	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
98	c6qelB	Alignment	not modelled	97.3	16	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
99	c4zc0A	Alignment	not modelled	97.3	10	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
100	d1yrba1	Alignment	not modelled	97.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
101	c1xnjB	Alignment	not modelled	97.3	15	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
102	c2zroA	Alignment	not modelled	97.2	21	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
103	d1ls1a2	Alignment	not modelled	97.2	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
104	c4nmnA	Alignment	not modelled	97.2	15	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
105	d1xjca	Alignment	not modelled	97.2	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

106	c4zciA_	Alignment	not modelled	97.2	19	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
107	d1x6va3	Alignment	not modelled	97.2	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
108	c6bbmA_	Alignment	not modelled	97.2	16	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
109	c2dy1A_	Alignment	not modelled	97.1	15	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
110	c4fn5A_	Alignment	not modelled	97.1	19	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
111	c2ywfA_	Alignment	not modelled	97.0	22	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
112	d2dy1a2	Alignment	not modelled	97.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
113	d1mo6a1	Alignment	not modelled	97.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
114	c3bgwD_	Alignment	not modelled	97.0	9	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
115	c5dn8A_	Alignment	not modelled	97.0	28	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
116	c4xgcE_	Alignment	not modelled	97.0	18	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
117	c4a1fB_	Alignment	not modelled	96.9	10	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
118	c4wiaA_	Alignment	not modelled	96.9	11	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
119	c1d2eA_	Alignment	not modelled	96.9	19	PDB header: rna binding protein Chain: A: PDB Molecule: elongation factor tu (ef-tu); PDBTitle: crystal structure of mitochondrial ef-tu in complex with gdp
120	c1fnnB_	Alignment	not modelled	96.8	21	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum