
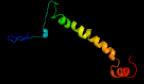
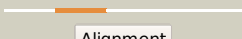
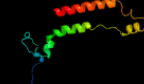
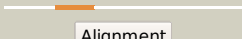
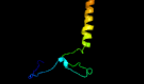
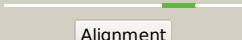

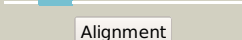
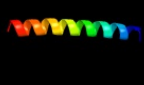
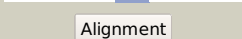

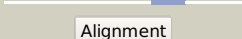

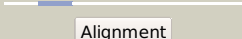
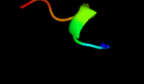
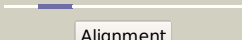
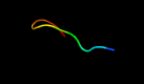
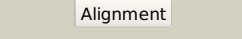

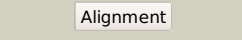

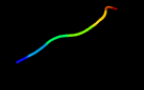


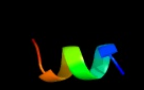




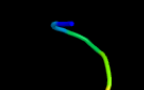


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0537c_(-)_628301_629734
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	628e7adc6bc3ca5c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yewl_	 Alignment		83.9	19	PDB header: oxidoreductase, membrane protein Chain: I; PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
2	c3rfri_	 Alignment		83.0	19	PDB header: oxidoreductase Chain: I; PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
3	c3rgbA_	 Alignment		80.9	19	PDB header: oxidoreductase Chain: A; PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
4	c4uisB_	 Alignment		51.5	15	PDB header: hydrolase Chain: B; PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex
5	c5a63D_	 Alignment		33.1	21	PDB header: hydrolase Chain: D; PDB Molecule: gamma-secretase subunit pen-2; PDBTitle: cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
6	c3w3fB_	 Alignment		26.5	29	PDB header: biosynthetic protein Chain: B; PDB Molecule: uncharacterized protein blr2150; PDBTitle: crystal structure of ent-kaurene synthase bjks from bradyrhizobium2 japonicum
7	d2p7tc1	 Alignment		25.1	47	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
8	c4pw1B_	 Alignment		20.0	67	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (clolep_02462)2 from clostridium leptum dsm 753 at 2.10 a resolution
9	c6h9iB_	 Alignment		18.9	55	PDB header: rna binding protein Chain: B; PDB Molecule: csf5; PDBTitle: csf5, crispr-cas type iv cas6 crrna endonuclease
10	c3chxE_	 Alignment		18.7	23	PDB header: membrane protein Chain: E; PDB Molecule: pmob; PDBTitle: crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
11	c3nglA_	 Alignment		15.8	100	PDB header: oxidoreductase, hydrolase Chain: A; PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum

12	c5nhsB_	Alignment		15.5	100	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
13	c4o65A_	Alignment		15.4	38	PDB header: oxidoreductase Chain: A: PDB Molecule: putative archaeal ammonia monoxygenase subunit b; PDBTitle: crystal structure of the cupredoxin domain of amob from nitrosocaldus2 yellowstonii
14	c1a4iB_	Alignment		14.5	100	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
15	d1kjna_	Alignment		14.4	36	Fold: Hypothetical protein MTH777 (MT0777) Superfamily: Hypothetical protein MTH777 (MT0777) Family: Hypothetical protein MTH777 (MT0777)
16	c2c2xB_	Alignment		14.4	86	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
17	c5zf1A_	Alignment		14.2	100	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate dehydrogenase; PDBTitle: molecular structure of a novel 5,10-methylenetetrahydrofolate2 dehydrogenase from the silkworm, bombyx mori
18	c1b0aA_	Alignment		14.0	100	PDB header: oxidoreductase,hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
19	c5z70B_	Alignment		13.5	20	PDB header: hydrolase Chain: B: PDB Molecule: oleate hydratase; PDBTitle: crystal strcure of oleate hydratase from stenotrophomonas sp. kctc2 12332
20	c4cxA_	Alignment		13.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: c-1-tetrahydrofolate synthase, cytoplasmic, putative; PDBTitle: the crystal structure of trypanosoma brucei n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor and inhibitor
21	c4b4uB_	Alignment	not modelled	12.8	100	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of acinetobacter baumannii n5,2 n10-methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor
22	c3p2oB_	Alignment	not modelled	12.6	100	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
23	c4a5oB_	Alignment	not modelled	12.5	100	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
24	c3l07B_	Alignment	not modelled	12.5	100	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
25	c3p2oA_	Alignment	not modelled	12.3	100	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
26	c5tc4A_	Alignment	not modelled	12.3	100	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional methylenetetrahydrofolate PDBTitle: crystal structure of human mitochondrial methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase (mthfd2) in complex with ly345899 and3 cofactors
27	d1kshb_	Alignment	not modelled	12.3	53	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
						Fold: NAD(P)-binding Rossmann-fold domains

28	d1b0aa1	Alignment	not modelled	11.7	100	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
29	d1xtda2	Alignment	not modelled	11.7	46	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
30	c6apeA	Alignment	not modelled	11.7	86	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
31	c4a26B	Alignment	not modelled	11.5	100	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
32	c4ak2A	Alignment	not modelled	11.0	29	PDB header: heparin-binding protein Chain: A: PDB Molecule: bt 4661; PDBTitle: structure of bt4661, a suse-like surface located polysaccharide2 binding protein from the bacteroides thetaiotaomicron heparin3 utilisation locus
33	d1a34a	Alignment	not modelled	10.6	43	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Satellite viruses Family: Satellite viruses
34	c5odoA	Alignment	not modelled	10.0	20	PDB header: lyase Chain: A: PDB Molecule: isomerase; PDBTitle: crystal structure of the oleate hydratase of rhodococcus erythropolis
35	c4uirB	Alignment	not modelled	9.9	25	PDB header: lyase Chain: B: PDB Molecule: oleate hydratase; PDBTitle: structure of oleate hydratase from elizabethkingia2 meningoseptica
36	c6gcs3	Alignment	not modelled	9.8	20	PDB header: oxidoreductase Chain: 3: PDB Molecule: nd3 subunit (nu3m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
37	d1a4ia1	Alignment	not modelled	9.6	100	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
38	c2mi2A	Alignment	not modelled	9.4	30	PDB header: transport protein Chain: A: PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
39	c4gokG	Alignment	not modelled	9.2	47	PDB header: signaling protein Chain: G: PDB Molecule: protein unc-119 homolog a; PDBTitle: the crystal structure of arl2gppnhp in complex with unc119a
40	c2kr6A	Alignment	not modelled	9.2	19	PDB header: hydrolase Chain: A: PDB Molecule: presenilin-1; PDBTitle: solution structure of presenilin-1 ctf subunit
41	c2mckA	Alignment	not modelled	8.9	43	PDB header: hydrolase Chain: A: PDB Molecule: polyprotein; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus cr6 ns1/2 protein
42	c3rkoE	Alignment	not modelled	8.1	28	PDB header: oxidoreductase Chain: E: PDB Molecule: nahd-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
43	c3rkoA	Alignment	not modelled	8.1	28	PDB header: oxidoreductase Chain: A: PDB Molecule: nahd-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
44	c2mcdA	Alignment	not modelled	7.4	43	PDB header: hydrolase Chain: A: PDB Molecule: murine norovirus 1; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus ns1/2 d94e mutant
45	c2k5cA	Alignment	not modelled	7.3	17	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
46	c4m5bA	Alignment	not modelled	7.2	20	PDB header: membrane protein Chain: A: PDB Molecule: cobalamin biosynthesis protein cbim; PDBTitle: crystal structure of a truncated transition metal transporter
47	c4m5cA	Alignment	not modelled	7.2	20	PDB header: membrane protein Chain: A: PDB Molecule: cobalamin biosynthesis protein cbim; PDBTitle: crystal structure of an truncated transition metal transporter
48	c6mwqB	Alignment	not modelled	7.2	36	PDB header: lyase/fluorescent protein Chain: B: PDB Molecule: darpin, muscle-type aldolase chimeric fusion; PDBTitle: single particle cryoem structure of a darpin-aldolase platform in2 complex with gfp
49	c1n93X	Alignment	not modelled	7.1	30	PDB header: viral protein Chain: X: PDB Molecule: p40 nucleoprotein; PDBTitle: crystal structure of the borna disease virus nucleoprotein
50	d1n93x	Alignment	not modelled	7.1	30	Fold: P40 nucleoprotein Superfamily: P40 nucleoprotein Family: P40 nucleoprotein
51	c3kihC	Alignment	not modelled	6.9	40	PDB header: sugar binding protein Chain: C: PDB Molecule: 5-bladed beta-propeller lectin; PDBTitle: the crystal structures of two fragments truncated from 5-bladed beta-2 propeller lectin, tachylectin-2 (lib2-d2-15)
52	c5d6hB	Alignment	not modelled	6.8	50	PDB header: chaperone/protein transport Chain: B: PDB Molecule: csua/b; PDBTitle: crystal structure of csuc-csua/b chaperone-major subunit pre-assembly2 complex from csu biofilm-mediating pili of acinetobacter baumannii
53	d1ro7a	Alignment	not modelled	6.7	37	Fold: Alpha-2,3/8-sialyltransferase CstII Superfamily: Alpha-2,3/8-sialyltransferase CstII

						Family: Alpha-2,3/8-sialyltransferase CstII
54	c3qheB	Alignment	not modelled	6.6	100	PDB header: signaling protein/splicing Chain: B: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: crystal structure of the complex between the armadillo repeat domain2 of adenomatous polyposis coli and the tyrosine-rich domain of sam68
55	d1ztda1	Alignment	not modelled	6.5	25	Fold: RNase III domain-like Superfamily: RNase III domain-like Family: PF0609-like
56	c2ru8A	Alignment	not modelled	6.5	25	PDB header: replication Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: dnat c-terminal domain
57	d1rzhh1	Alignment	not modelled	6.5	71	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
58	d1droa	Alignment	not modelled	6.4	50	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
59	c3wvbA	Alignment	not modelled	6.4	67	PDB header: hydrolase Chain: A: PDB Molecule: upf0254 protein mj1251; PDBTitle: hcgf from methanocaldococcus jannaschii
60	c5djbD	Alignment	not modelled	6.4	21	PDB header: structural protein Chain: D: PDB Molecule: microcompartments protein; PDBTitle: structure of the haliangium ochraceum bmc-h shell protein
61	c2do6A	Alignment	not modelled	6.4	23	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of rsgi ruh-065, a uba domain from human2 cdna
62	d1jmxg	Alignment	not modelled	6.3	55	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Quinohemoprotein amine dehydrogenase C chain Family: Quinohemoprotein amine dehydrogenase C chain
63	d2c42a2	Alignment	not modelled	6.3	33	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
64	c5wsnC	Alignment	not modelled	6.2	16	PDB header: virus Chain: C: PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
65	c6r7tB	Alignment	not modelled	6.2	32	PDB header: immune system Chain: B: PDB Molecule: melanoma-associated antigen b1; PDBTitle: crystal structure of human melanoma-associated antigen b1 (mageb1) in2 complex with nanobody
66	c3gczA	Alignment	not modelled	6.1	47	PDB header: transferase Chain: A: PDB Molecule: polyprotein; PDBTitle: yokose virus methyltransferase in complex with adomet
67	d1pbyc	Alignment	not modelled	5.9	45	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Quinohemoprotein amine dehydrogenase C chain Family: Quinohemoprotein amine dehydrogenase C chain
68	c1lt1G	Alignment	not modelled	5.9	37	PDB header: de novo protein Chain: G: PDB Molecule: l13g-df1; PDBTitle: sliding helix induced change of coordination geometry in a2 model di-mn(ii) protein
69	c6e3yP	Alignment	not modelled	5.8	62	PDB header: signaling protein Chain: P: PDB Molecule: calcitonin gene-related peptide 1; PDBTitle: cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor
70	c2ekkA	Alignment	not modelled	5.7	18	PDB header: protein binding Chain: A: PDB Molecule: uba domain from e3 ubiquitin-protein ligase PDBTitle: solution structure of ruh-074, a human uba domain
71	c4ou6A	Alignment	not modelled	5.7	25	PDB header: replication/dna Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: crystal structure of dnat84-153-dt10 ssdna complex form 1
72	c2kgIA	Alignment	not modelled	5.4	14	PDB header: chaperone Chain: A: PDB Molecule: mesoderm development candidate 2; PDBTitle: nmr solution structure of mesd
73	c3eeqB	Alignment	not modelled	5.4	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cobalamin biosynthesis protein g homolog; PDBTitle: crystal structure of a putative cobalamin biosynthesis protein g2 homolog from sulfolobus solfataricus
74	d1igna2	Alignment	not modelled	5.4	43	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: DNA-binding domain of rap1
75	d1muka	Alignment	not modelled	5.4	39	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
76	c2wa0A	Alignment	not modelled	5.4	32	PDB header: immune system Chain: A: PDB Molecule: melanoma-associated antigen 4; PDBTitle: crystal structure of the human magea4
77	d2axtk1	Alignment	not modelled	5.4	47	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
78	d1ciya3	Alignment	not modelled	5.3	20	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain
79	c4djhA	Alignment	not modelled	5.3	11	PDB header: hormone receptor/antagonist Chain: A: PDB Molecule: kappa-type opioid receptor, lysozyme; PDBTitle: structure of the human kappa opioid receptor in complex

					with jdtic
80	c1w99A_	Alignment	not modelled	5.2	20 PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry4ba; PDBTitle: mosquito-larvicidal toxin cry4ba from bacillus thuringiensis ssp.2 israelensis
81	c1kzvA_	Alignment	not modelled	5.2	29 PDB header: viral protein Chain: A: PDB Molecule: vpr protein; PDBTitle: structure of human immunodeficiency virus type 1 vpr(34-51)2 peptide in chloroform methanol
82	c1kztA_	Alignment	not modelled	5.2	29 PDB header: viral protein Chain: A: PDB Molecule: vpr protein; PDBTitle: structure of human immunodeficiency virus type 1 vpr(34-51)2 peptide in dpc micelle containing aqueous solution
83	c1kzsA_	Alignment	not modelled	5.2	29 PDB header: viral protein Chain: A: PDB Molecule: vpr protein; PDBTitle: structure of human immunodeficiency virus type 1 vpr(34-51)2 peptide in aqueous tfe solution
84	c6owkA_	Alignment	not modelled	5.2	30 PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry1be, cry1k-like protein PDBTitle: crystal structure of a bacillus thuringiensis cry1b.867 tryptic core2 variant
85	d1bw3a_	Alignment	not modelled	5.2	63 Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: Barwin
86	c3ofgA_	Alignment	not modelled	5.1	22 PDB header: chaperone Chain: A: PDB Molecule: boca/mesd chaperone for ywtd beta-propeller-egf protein 1; PDBTitle: structured domain of caenorhabditis elegans bmy-1
87	c5v6iA_	Alignment	not modelled	5.1	60 PDB header: sugar binding protein Chain: A: PDB Molecule: tmv resistance protein y3; PDBTitle: glycan binding protein y3 from mushroom coprinus comatus possesses2 anti-leukemic activity - pt derivative
88	c6cfzF_	Alignment	not modelled	5.1	26 PDB header: nuclear protein Chain: F: PDB Molecule: dad1,dad1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
89	c6ovbA_	Alignment	not modelled	5.1	10 PDB header: toxin Chain: A: PDB Molecule: active core crystal toxin protein 1d; PDBTitle: crystal structure of a bacillus thuringiensis cry1da tryptic core2 variant