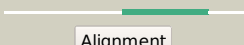

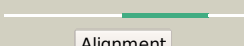
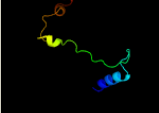
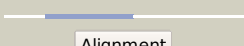
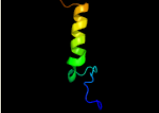

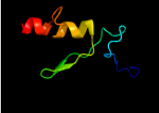










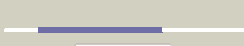

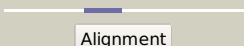
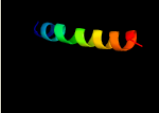
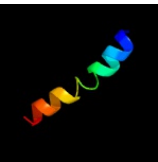
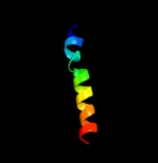
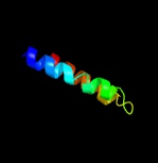
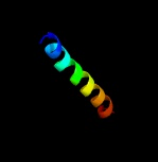
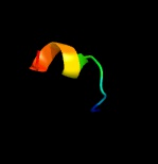

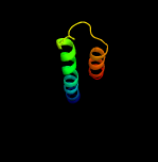
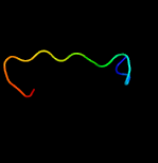
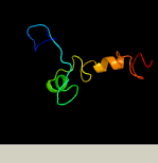


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2709_(-)_3021849_3022295
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	08a629c803044837

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4qslC_	 Alignment		42.1	17	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
2	c4qslE_	 Alignment		40.9	17	PDB header: ligase Chain: E; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
3	d1jb0f_	 Alignment		22.0	30	Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, PsaF Family: Subunit III of photosystem I reaction centre, PsaF
4	c6fosF_	 Alignment		22.0	35	PDB header: photosynthesis Chain: F; PDB Molecule: photosystem i reaction center subunit ii; PDBTitle: cyanidioschyzon merolae photosystem i
5	c3bg3A_	 Alignment		21.7	18	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
6	c3bg3B_	 Alignment		17.7	18	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
7	c3bg3C_	 Alignment		17.4	17	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
8	c4kt0F_	 Alignment		17.2	30	PDB header: electron transport Chain: F; PDB Molecule: photosystem i subunit iii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
9	c6ijjF_	 Alignment		16.3	25	PDB header: membrane protein Chain: F; PDB Molecule: psaf; PDBTitle: photosystem i of chlamydomonas reinhardtii
10	c5ir6A_	 Alignment		15.7	19	PDB header: oxidoreductase Chain: A; PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
11	c3jcue_	 Alignment		14.5	16	PDB header: membrane protein Chain: E; PDB Molecule: cytochrome b559 subunit alpha; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution

12	c2lowA_	Alignment		14.1	25	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
13	d2axte1	Alignment		14.1	20	Fold: Single transmembrane helix Superfamily: Cytochrome b559 subunits Family: Cytochrome b559 subunits
14	d2r6gf1	Alignment		13.9	15	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
15	c3kziE_	Alignment		13.7	20	PDB header: electron transport Chain: E: PDB Molecule: cytochrome b559 subunit alpha; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
16	c5f5oF_	Alignment		13.6	42	PDB header: nuclear protein/peptide Chain: F: PDB Molecule: peptide from polymerase cofactor vp35; PDBTitle: crystal structure of marburg virus nucleoprotein core domain bound to2 vp35 regulation peptide
17	c6hu9p_	Alignment		13.4	17	PDB header: oxidoreductase/electron transport Chain: P: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
18	c3rfuC_	Alignment		13.1	17	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
19	d1v54f_	Alignment		13.1	18	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Cytochrome c oxidase Subunit F
20	c6igzF_	Alignment		11.9	25	PDB header: plant protein Chain: F: PDB Molecule: psaf; PDBTitle: structure of psi-lhci
21	c4l8nA_	Alignment	not modelled	11.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pdz domain protein; PDBTitle: crystal structure of a pdz domain protein (bdi_1242) from2 parabacteroides distansonis atcc 8503 at 2.50 a resolution
22	c5mkkB_	Alignment	not modelled	11.3	15	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
23	c2y69S_	Alignment	not modelled	11.1	18	PDB header: electron transport Chain: S: PDB Molecule: cytochrome c oxidase subunit 5b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
24	c4p6vD_	Alignment	not modelled	10.5	8	PDB header: oxidoreductase Chain: D: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit d; PDBTitle: crystal structure of the na ⁺ -translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
25	c4cmxB_	Alignment	not modelled	10.4	32	PDB header: nuclear protein Chain: B: PDB Molecule: rv3378c; PDBTitle: crystal structure of rv3378c
26	c5mu5A_	Alignment	not modelled	9.7	26	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of maf glycosyltransferase from magnetospirillum magneticum2 amb-1
27	d1ehkb2	Alignment	not modelled	9.6	20	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region PDB header: replication Chain: A: PDB Molecule: dnaa-related protein;

28	c2kjqA_	Alignment	not modelled	8.3	27	PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
29	c5vz0D_	Alignment	not modelled	7.6	20	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
30	c4qvrA_	Alignment	not modelled	7.5	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized hypothetical protein ftt_1539c; PDBTitle: 2.3 angstrom crystal structure of hypothetical protein ftt1539c from2 francisella tularensis.
31	c3dinE_	Alignment	not modelled	7.3	18	PDB header: membrane protein, protein transport Chain: E: PDB Molecule: preprotein translocase subunit secg; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
32	c4aa3A_	Alignment	not modelled	7.2	13	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter,2 abcb10 (plate form)
33	c3b5wE_	Alignment	not modelled	7.0	9	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
34	c2k9pA_	Alignment	not modelled	7.0	13	PDB header: membrane protein Chain: A: PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles
35	c1z65A_	Alignment	not modelled	6.9	13	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: mouse doppel 1-30 peptide
36	c2m20B_	Alignment	not modelled	6.4	30	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
37	c2j5dA_	Alignment	not modelled	6.4	50	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnip3 transmembrane domain in lipid bicelles
38	d1f46a_	Alignment	not modelled	6.4	16	Fold: TBP-like Superfamily: Cell-division protein ZipA, C-terminal domain Family: Cell-division protein ZipA, C-terminal domain
39	c1du1A_	Alignment	not modelled	6.3	27	PDB header: signaling protein Chain: A: PDB Molecule: skeletal dihydropyridine receptor; PDBTitle: peptide fragment thr671-leu690 of the rabbit skeletal2 dihydropyridine receptor
40	c1jzpA_	Alignment	not modelled	6.3	27	PDB header: signaling protein Chain: A: PDB Molecule: skeletal dihydropyridine receptor; PDBTitle: modified peptide a (d18-a1) of the rabbit skeletal2 dihydropyridine receptor
41	c6go1A_	Alignment	not modelled	6.1	29	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase-like protein; PDBTitle: crystal structure of a bacillus anthracis peptidoglycan deacetylase
42	c2ypdB_	Alignment	not modelled	6.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: probable jmjc domain-containing histone demethylation prot PDBTitle: crystal structure of the jumonji domain of human jumonji domain2 containing 1c protein
43	c5fw5C_	Alignment	not modelled	6.1	67	PDB header: hydrolase Chain: C: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of human g3bp1 in complex with semliki forest virus2 nsp3-25 comprising two fgdf motives
44	c3g5uB_	Alignment	not modelled	6.0	19	PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
45	d2dk3a1	Alignment	not modelled	6.0	39	Fold: SH3-like barrel Superfamily: Mib/herc2 domain-like Family: Mib/herc2 domain
46	c5b2gG_	Alignment	not modelled	5.8	42	PDB header: membrane protein Chain: G: PDB Molecule: endolysin,claudin-4; PDBTitle: crystal structure of human claudin-4 in complex with c-terminal2 fragment of clostridium perfringens enterotoxin
47	c3dkmA_	Alignment	not modelled	5.8	39	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hectd1; PDBTitle: crystal structure of the hectd1 cph domain
48	c3qdrB_	Alignment	not modelled	5.5	38	PDB header: protein transport/toxin Chain: B: PDB Molecule: colicin-a; PDBTitle: structural characterization of the interaction of colicin a, colicin2 n, and tolB with the tolAiii translocon
49	c3j08A_	Alignment	not modelled	5.5	13	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
50	c2kkuA_	Alignment	not modelled	5.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein af2351 from archaeoglobus fulgidus.2 northeast structural genomics consortium target att9/ontario center3 for structural proteomics target af2351
51	c5aynA_	Alignment	not modelled	5.2	8	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state