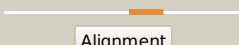

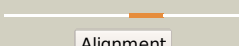
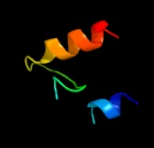
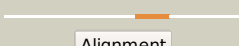

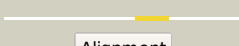

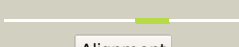




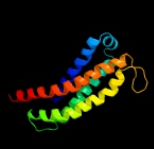

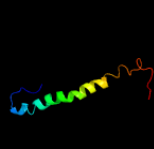







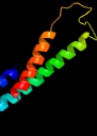




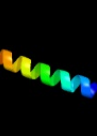
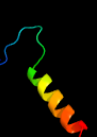



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2856_nicT_3166694_3167812
 Date Wed Aug 7 12:50:52 BST 2019
 Unique Job ID 4fc477315f5282dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ui9A_	 Alignment		83.8	38	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: atomic structure of the human anaphase-promoting complex
2	c5a31A_	 Alignment		83.0	38	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: structure of the human apc-cdh1-hsl1-ubch10 complex.
3	c5l9uA_	 Alignment		82.0	29	PDB header: signaling protein Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: model of human anaphase-promoting complex/cyclosome (apc/c-cdh1) with2 a cross linked ubiquitin variant-substrate-ube2c (ubch10) complex3 representing key features of multiubiquitination
4	c5khrA_	 Alignment		79.4	29	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: model of human anaphase-promoting complex/cyclosome complex (apc152 deletion mutant) in complex with the e2 ube2c/ubch10 poised for3 ubiquitin ligation to substrate (apc/c-cdc20-substrate-ube2c)
5	c5khuA_	 Alignment		62.0	29	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 1; PDBTitle: model of human anaphase-promoting complex/cyclosome (apc15 deletion2 mutant), in complex with the mitotic checkpoint complex (apc/c-cdc20-3 mcc) based on cryo em data at 4.8 angstrom resolution
6	c5vkvA_	 Alignment		53.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccda; PDBTitle: solution nmr structure of the membrane electron transporter ccda
7	c5xamA_	 Alignment		50.2	15	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secd; PDBTitle: crystal structure of secdf in i form at 4 a resolution
8	d1fftb2	 Alignment		41.6	15	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
9	c3kb4D_	 Alignment		37.9	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
10	d1nvpd1	 Alignment		36.9	27	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
11	c5gasN_	 Alignment		34.2	26	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2

12	d1nh2d1	Alignment		33.4	36	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
13	c6hwhw	Alignment		27.4	18	PDB header: electron transport Chain: W: PDB Molecule: cytochrome c oxidase subunit 3; PDBTitle: structure of a functional obligate respiratory supercomplex from <i>Mycobacterium smegmatis</i>
14	c1rr2A	Alignment		25.8	14	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
15	d1h2sa	Alignment		24.0	15	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
16	c6cfwE	Alignment		22.7	35	PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
17	c1nvpD	Alignment		22.3	21	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia gamma chain; PDBTitle: human tfiia/tbp/dna complex
18	c5xvjB	Alignment		20.3	38	PDB header: gene regulation Chain: B: PDB Molecule: phd finger protein alfin-like 7; PDBTitle: crystal structure of al7 pal domain
19	c1qgeE	Alignment		17.9	32	PDB header: hydrolase Chain: E: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
20	c6csmC	Alignment		17.4	17	PDB header: membrane protein Chain: C: PDB Molecule: gtacr1; PDBTitle: crystal structure of the natural light-gated anion channel gtacr1
21	c4hhsA	Alignment	not modelled	16.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-dioxygenase; PDBTitle: crystal structure of fatty acid alpha-dioxygenase (<i>Arabidopsis thaliana</i>)
22	d2h8pc1	Alignment	not modelled	15.0	17	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
23	c2zyfA	Alignment	not modelled	14.9	11	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from <i>Thermophilus</i> 2 complexed with magnesium ion and alpha-ketoglutarate
24	c1nh2D	Alignment	not modelled	14.5	29	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia small chain; PDBTitle: crystal structure of a yeast tfiia/tbp/dna complex
25	d1fftC	Alignment	not modelled	14.3	18	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
26	c2jo1A	Alignment	not modelled	14.2	29	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the Na,K-ATPase regulatory protein fxyd1 in 2 micelles
27	c6gyhA	Alignment	not modelled	14.0	20	PDB header: proton transport Chain: A: PDB Molecule: family a g protein-coupled receptor-like protein; PDBTitle: crystal structure of the light-driven proton pump <i>Coccomyxa2 subellipsoidea</i> rhodopsin csr
28	c6o7ua	Alignment	not modelled	13.5	17	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: <i>Saccharomyces cerevisiae</i> v-ATPase stv1-vo

29	c5zktB	Alignment	not modelled	12.1	38	PDB header: transcription Chain: B: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
30	c6o7xa	Alignment	not modelled	11.9	17	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
31	d2fyma2	Alignment	not modelled	11.3	23	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
32	c3jcuw	Alignment	not modelled	11.2	26	PDB header: membrane protein Chain: W: PDB Molecule: photosystem ii reaction center w protein, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
33	c5azdA	Alignment	not modelled	11.1	23	PDB header: transport protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of thermophilic rhodopsin.
34	c4mndA	Alignment	not modelled	11.1	23	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
35	c1skhA	Alignment	not modelled	10.9	19	PDB header: unknown function Chain: A: PDB Molecule: major prion protein 2; PDBTitle: n-terminal (1-30) of bovine prion protein
36	c6agfB	Alignment	not modelled	10.9	14	PDB header: membrane protein Chain: B: PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
37	c5zktA	Alignment	not modelled	10.6	33	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
38	c5xsyB	Alignment	not modelled	10.3	20	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated sodium channel beta subunit 1; PDBTitle: structure of the nav1.4-beta1 complex from electric eel
39	d1j2za	Alignment	not modelled	10.0	15	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
40	c2nx9B	Alignment	not modelled	10.0	18	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
41	c3kcvG	Alignment	not modelled	9.6	13	PDB header: transport protein Chain: G: PDB Molecule: probable formate transporter 1; PDBTitle: structure of formate channel
42	c4lhfA	Alignment	not modelled	9.4	23	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
43	c6owsB	Alignment	not modelled	9.4	14	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
44	c3wt9A	Alignment	not modelled	8.8	14	PDB header: proton transport Chain: A: PDB Molecule: rhodopsin i; PDBTitle: crystal structure of the cell-free synthesized membrane protein,2 acetabularia rhodopsin i, at 1.48 angstrom
45	c5doqC	Alignment	not modelled	8.7	37	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
46	c5ir6C	Alignment	not modelled	8.7	37	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
47	d2i9fa1	Alignment	not modelled	8.4	33	Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Arterivirus nucleocapsid protein
48	d1jcb6	Alignment	not modelled	8.2	50	Fold: PheT/TiS domain Superfamily: PheT/TiS domain Family: B3/B4 domain of PheRS, PheT
49	d1x9ia	Alignment	not modelled	7.9	24	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
50	d1l7va	Alignment	not modelled	7.4	14	Fold: ABC transporter involved in vitamin B12 uptake, BtuC Superfamily: ABC transporter involved in vitamin B12 uptake, BtuC Family: ABC transporter involved in vitamin B12 uptake, BtuC
51	c4b4tT	Alignment	not modelled	7.3	18	PDB header: hydrolase Chain: T: PDB Molecule: 26s proteasome regulatory subunit rpn12; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
52	c6e1jB	Alignment	not modelled	7.3	17	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
53	c2i9fB	Alignment	not modelled	6.8	33	PDB header: viral protein Chain: B: PDB Molecule: nucleocapsid; PDBTitle: structure of the equine arterivirus nucleocapsid protein
54	c3msqC	Alignment	not modelled	6.6	12	PDB header: biosynthetic protein Chain: C: PDB Molecule: putative ubiquinone biosynthesis protein; PDBTitle: crystal structure of a putative ubiquinone biosynthesis

						protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
55	c3t57A_	Alignment	not modelled	6.4	15	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine o-acyltransferase domain-containing PDBTitle: activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
56	c5ks8D_	Alignment	not modelled	6.4	11	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
57	c5m4sA_	Alignment	not modelled	6.2	21	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor iia subunit 2,transcription PDBTitle: transcription factor tfiia as a single chain protein
58	d1ex9a_	Alignment	not modelled	6.1	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
59	d1f4nb_	Alignment	not modelled	6.0	60	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
60	c6agbj_	Alignment	not modelled	6.0	13	PDB header: hydrolase/rna Chain: J: PDB Molecule: ribonuclease p/mrp protein subunit rpp1; PDBTitle: cryo-em structure of yeast ribonuclease p
61	c2bbjB_	Alignment	not modelled	5.9	17	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
62	c3cyvA_	Alignment	not modelled	5.9	23	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
63	c4jr8A_	Alignment	not modelled	5.7	14	PDB header: proton transport Chain: A: PDB Molecule: cruxrhodopsin-3; PDBTitle: crystal structure of cruxrhodopsin-3 from haloarcula vallismortis at2 2.3 angstrom resolution
64	c6mzdA_	Alignment	not modelled	5.7	83	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 1; PDBTitle: human tfiid lobe a canonical
65	c6elhA_	Alignment	not modelled	5.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
66	c3ewbX_	Alignment	not modelled	5.6	15	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
67	c4qidB_	Alignment	not modelled	5.6	18	PDB header: membrane protein Chain: B: PDB Molecule: bacteriorhodopsin-i; PDBTitle: crystal structure of haloquadratum walsbyi bacteriorhodopsin
68	c4mt1A_	Alignment	not modelled	5.6	15	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
69	c4hu8A_	Alignment	not modelled	5.5	40	PDB header: hydrolase Chain: A: PDB Molecule: gh10 xylanase; PDBTitle: crystal structure of a bacterial ig-like domain containing gh102 xylanase from termite gut
70	c1n0wB_	Alignment	not modelled	5.5	71	PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer type 2 susceptibility protein; PDBTitle: crystal structure of a rad51-brca2 brc repeat complex
71	c2v50A_	Alignment	not modelled	5.5	15	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
72	c6eyuA_	Alignment	not modelled	5.5	21	PDB header: membrane protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of the inward h(+) pump xenorhodopsin
73	c1bctA_	Alignment	not modelled	5.4	20	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
74	d1gmua2	Alignment	not modelled	5.3	42	Fold: Ferredoxin-like Superfamily: Urease metallochaperone UreE, C-terminal domain Family: Urease metallochaperone UreE, C-terminal domain
75	c5ch6B_	Alignment	not modelled	5.3	12	PDB header: transcription Chain: B: PDB Molecule: frigida; PDBTitle: crystal structure of frigida flowering-time regulator
76	c6n1fD_	Alignment	not modelled	5.2	64	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, 2og-fe(ii) oxygenase family; PDBTitle: crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
77	d1kw3b2	Alignment	not modelled	5.2	19	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradial dioxygenases
78	c1zxxA_	Alignment	not modelled	5.1	29	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
79	c6e3yE_	Alignment	not modelled	5.1	36	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

80	d1f4na_	Alignment	not modelled	5.1	60	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
81	c3n00B_	Alignment	not modelled	5.0	71	PDB header: transcription regulator Chain: B: PDB Molecule: nuclear receptor corepressor 1; PDBTitle: crystal structure of a deletion mutant of human reverba ligand binding2 domain bound with an ncor id1 peptide determined to 2.60a