

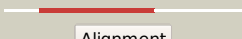
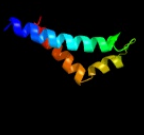




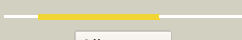
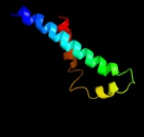
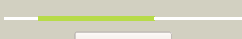

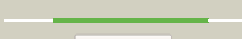



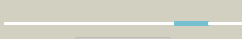







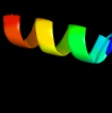

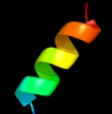






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1554_(frdC)_1760181_1760561
Date	Fri Aug 2 13:30:14 BST 2019
Unique Job ID	c7a1a7d5a735bd61

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kf6c_</a>	 Alignment		100.0	31	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
2	<a href="#">d1nekd_</a>	 Alignment		96.8	24	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
3	<a href="#">d1nekc_</a>	 Alignment		92.7	17	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
4	<a href="#">c3vr6G_</a>	 Alignment		88.4	10	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b-large subunit; <b>PDBTitle:</b> mitochondrial rhoDoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
5	<a href="#">c5xmjG_</a>	 Alignment		75.3	12	<b>PDB header:</b> electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> fumarate reductase respiratory complex; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
6	<a href="#">d2bs2c1</a>	 Alignment		68.1	14	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Fumarate reductase respiratory complex cytochrome b subunit, FrdC
7	<a href="#">d1kf6d_</a>	 Alignment		53.0	20	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
8	<a href="#">c1yq3C_</a>	 Alignment		52.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> succinate dehydrogenase cytochrome b, large subunit; <b>PDBTitle:</b> avian respiratory complex ii with oxaloacetate and ubiquinone
9	<a href="#">c2n7iA_</a>	 Alignment		32.8	13	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> prolactin receptor; <b>PDBTitle:</b> nmr structure of the prolactin receptor transmembrane domain
10	<a href="#">c2mb9A_</a>	 Alignment		26.2	5	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> b-cell lymphoma/leukemia 10; <b>PDBTitle:</b> human bcl10 card
11	<a href="#">d1lg7a_</a>	 Alignment		24.8	18	<b>Fold:</b> VSV matrix protein <b>Superfamily:</b> VSV matrix protein <b>Family:</b> VSV matrix protein

12	<a href="#">c2b1wA_</a>	Alignment		24.0	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain protein 4; <b>PDBTitle:</b> solution structure of the nod1 caspase activating and recruitment2 domain
13	<a href="#">c1p58E_</a>	Alignment		22.6	17	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2.9.5 angstrom cryo-em reconstruction
14	<a href="#">c6e28D_</a>	Alignment		21.4	27	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> caspase recruitment domain-containing protein 9; <b>PDBTitle:</b> the card9 card domain-swapped dimer
15	<a href="#">c2w2rA_</a>	Alignment		21.4	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein; <b>PDBTitle:</b> structure of the vesicular stomatitis virus matrix protein
16	<a href="#">c6j52A_</a>	Alignment		19.2	19	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-only protein; <b>PDBTitle:</b> crystal structure of card-only protein in frog virus 3
17	<a href="#">c2m5IA_</a>	Alignment		17.6	47	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> ns5a protein; <b>PDBTitle:</b> ns5a308
18	<a href="#">c6ajnF_</a>	Alignment		17.5	33	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> crystal structure of atar bound with accoa
19	<a href="#">d3ygsP_</a>	Alignment		16.9	13	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
20	<a href="#">c6n2mA_</a>	Alignment		16.5	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-containing protein 9; <b>PDBTitle:</b> nmr solution structure of the homodimeric, autoinhibited state of the card9 card and first coiled-coil
21	<a href="#">c4i16A_</a>	Alignment	not modelled	16.5	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-containing protein 11; <b>PDBTitle:</b> crystal structure of carma1 card
22	<a href="#">c2nz7A_</a>	Alignment	not modelled	15.3	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-containing protein 4; <b>PDBTitle:</b> crystal structure analysis of caspase-recruitment domain2 (card) of nod1
23	<a href="#">c6qtrD_</a>	Alignment	not modelled	14.9	36	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat y144f mutant toxin bound to the c-terminus of 2 the antitoxin atar and acetyl-coa
24	<a href="#">c3katA_</a>	Alignment	not modelled	14.3	0	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> nacht, lrr and pyd domains-containing protein 1; <b>PDBTitle:</b> crystal structure of the card domain of the human nlrp1 protein,2 northeast structural genomics consortium target hr3486e
25	<a href="#">c2n7zA_</a>	Alignment	not modelled	13.6	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-interacting serine/threonine-protein kinase 2; <b>PDBTitle:</b> solution structure of rip2 card
26	<a href="#">d3crda_</a>	Alignment	not modelled	13.5	25	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
27	<a href="#">c2m67A_</a>	Alignment	not modelled	12.4	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
						<b>PDB header:</b> calcium-binding protein/metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> sodium channel protein type 2 subunit

28	<a href="#">c2kxwB_</a>	Alignment	not modelled	12.4	44	alpha; <b>PDBTitle:</b> structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
29	<a href="#">c2m5eB_</a>	Alignment	not modelled	12.4	44	<b>PDB header:</b> calcium-binding protein/metal transport <b>Chain:</b> B; <b>PDB Molecule:</b> sodium channel protein type 2 subunit alpha; <b>PDBTitle:</b> structure of the c-domain of calcium-saturated calmodulin bound to the2 iq motif of nav1.2
30	<a href="#">c6drpB_</a>	Alignment	not modelled	12.1	27	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> cryo-em structures of asc and nlr4 card filaments reveal a unified2 mechanism of nucleation and activation of caspase-1
31	<a href="#">d1y9ba1</a>	Alignment	not modelled	11.6	13	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> VCA0319-like
32	<a href="#">c6gtsC_</a>	Alignment	not modelled	11.6	33	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat-atar complex bound dna
33	<a href="#">c5fnaD_</a>	Alignment	not modelled	11.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> caspase-1; <b>PDBTitle:</b> cryo-em reconstruction of caspase-1 card
34	<a href="#">d1dgna_</a>	Alignment	not modelled	11.3	25	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
35	<a href="#">c1p58F_</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> virus <b>Chain:</b> F; <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
36	<a href="#">c3j2pD_</a>	Alignment	not modelled	10.8	18	<b>PDB header:</b> viral protein <b>Chain:</b> D; <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> cryoem structure of dengue virus envelope protein heterotetramer
37	<a href="#">c5wsnD_</a>	Alignment	not modelled	10.2	30	<b>PDB header:</b> virus <b>Chain:</b> D; <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
38	<a href="#">c6butB_</a>	Alignment	not modelled	9.8	44	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> sodium channel protein type 2 subunit alpha; <b>PDBTitle:</b> solution structure of full-length apo mammalian calmodulin bound to2 the iq motif of the human voltage-gated sodium channel nav1.2
39	<a href="#">c2q0oC_</a>	Alignment	not modelled	9.7	28	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> probable transcriptional repressor tram; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
40	<a href="#">c4atbC_</a>	Alignment	not modelled	8.1	36	<b>PDB header:</b> immune system <b>Chain:</b> C; <b>PDB Molecule:</b> interleukin enhancer-binding factor 2; <b>PDBTitle:</b> crystal structure of the nf90-nf45 dimerisation domain2 complex with ctp
41	<a href="#">c4fm4C_</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> nitrile hydratase alpha subunit; <b>PDBTitle:</b> wild type fe-type nitrile hydratase from comamonas testosteroni ni1
42	<a href="#">d1cy5a_</a>	Alignment	not modelled	7.4	19	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
43	<a href="#">c4cbfB_</a>	Alignment	not modelled	6.9	28	<b>PDB header:</b> virus <b>Chain:</b> B; <b>PDB Molecule:</b> m protein; <b>PDBTitle:</b> near-atomic resolution cryo-em structure of dengue serotype 4 virus
44	<a href="#">c5z62N_</a>	Alignment	not modelled	6.8	25	<b>PDB header:</b> electron transport <b>Chain:</b> N; <b>PDB Molecule:</b> cytochrome c oxidase subunit ndufa4; <b>PDBTitle:</b> structure of human cytochrome c oxidase
45	<a href="#">c1wazA_</a>	Alignment	not modelled	6.7	16	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
46	<a href="#">d1ic8a2</a>	Alignment	not modelled	5.8	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
47	<a href="#">c2zidA_</a>	Alignment	not modelled	5.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dextran glucosidase; <b>PDBTitle:</b> crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
48	<a href="#">c3a0hK_</a>	Alignment	not modelled	5.5	42	<b>PDB header:</b> electron transport <b>Chain:</b> K; <b>PDB Molecule:</b> photosystem ii reaction center protein k; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
49	<a href="#">c2voyB_</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
50	<a href="#">c1uokA_</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> glucosidase <b>Chain:</b> A; <b>PDB Molecule:</b> oligo-1,6-glucosidase; <b>PDBTitle:</b> crystal structure of b. cereus oligo-1,6-glucosidase
51	<a href="#">d1uoka2</a>	Alignment	not modelled	5.2	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
52	<a href="#">d1kcf2</a>	Alignment	not modelled	5.2	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Mitochondrial resolvase ydc2 catalytic domain