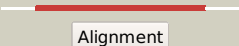



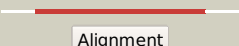





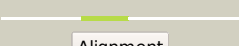
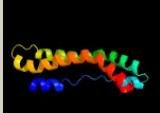
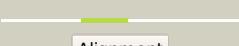


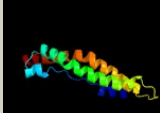




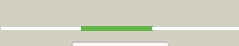



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2443_(dctA)_2740719_2742194
Date	Wed Aug 7 12:50:06 BST 2019
Unique Job ID	0bdf5fa139b2c7a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6gctA_</a>	 Alignment		100.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutral amino acid transporter b(0); <b>PDBTitle:</b> cryo-em structure of the human neutral amino acid transporter asct2
2	<a href="#">c4ky0B_</a>	 Alignment		100.0	30	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton/glutamate symporter, sdf family; <b>PDBTitle:</b> crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
3	<a href="#">d2nwwa1</a>	 Alignment		100.0	31	<b>Fold:</b> Proton glutamate symport protein <b>Superfamily:</b> Proton glutamate symport protein <b>Family:</b> Proton glutamate symport protein
4	<a href="#">c5lm4A_</a>	 Alignment		100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> excitatory amino acid transporter 1,neutral amino acid <b>PDBTitle:</b> structure of the thermostabilized eaat1 cryst-ii mutant in complex2 with l-asp and the allosteric inhibitor ucph101
5	<a href="#">c4k0eA_</a>	 Alignment		83.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
6	<a href="#">c6owsB_</a>	 Alignment		63.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> efflux pump membrane transporter; <b>PDBTitle:</b> cryo-em structure of an acinetobacter baumannii multidrug efflux pump
7	<a href="#">c4mt1A_</a>	 Alignment		63.2	8	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> drug efflux protein; <b>PDBTitle:</b> crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
8	<a href="#">c5lq3F_</a>	 Alignment		59.1	11	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> cmeb; <b>PDBTitle:</b> structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
9	<a href="#">c4czbB_</a>	 Alignment		57.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> na(+)/h(+) antiporter 1; <b>PDBTitle:</b> structure of the sodium proton antiporter mjnhap1 from2 methanocaldococcus jannaschii at ph 8.
10	<a href="#">c4r0cB_</a>	 Alignment		53.9	18	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> abgt putative transporter family; <b>PDBTitle:</b> crystal structure of the alcalivorax borkumensis ydah transporter2 reveals an unusual topology
11	<a href="#">c5a1sB_</a>	 Alignment		53.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> citrate-sodium symporter; <b>PDBTitle:</b> crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.

12	<a href="#">c4n7wA_</a>	Alignment		50.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter, sodium/bile acid symporter family; <b>PDBTitle:</b> crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
13	<a href="#">d1iwga8</a>	Alignment		48.5	15	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
14	<a href="#">c1oy8A_</a>	Alignment		47.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
15	<a href="#">c2yvxD_</a>	Alignment		47.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
16	<a href="#">c2v50A_</a>	Alignment		43.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein mexb; <b>PDBTitle:</b> the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
17	<a href="#">c4k0eC_</a>	Alignment		30.2	23	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
18	<a href="#">c6dmoA_</a>	Alignment		29.2	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein patched homolog 1; <b>PDBTitle:</b> cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
19	<a href="#">c5mg3D_</a>	Alignment		24.5	11	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocase subunit secD; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
20	<a href="#">c5i6xA_</a>	Alignment		17.6	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium-dependent serotonin transporter; <b>PDBTitle:</b> x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
21	<a href="#">c3k07A_</a>	Alignment	not modelled	17.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
22	<a href="#">d1a77a1</a>	Alignment	not modelled	16.1	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
23	<a href="#">c3ah5E_</a>	Alignment	not modelled	14.6	12	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> thymidylate synthase thyx; <b>PDBTitle:</b> crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump
24	<a href="#">c5xnmT_</a>	Alignment	not modelled	13.8	20	<b>PDB header:</b> membrane protein <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
25	<a href="#">d1iwga7</a>	Alignment	not modelled	13.7	11	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
26	<a href="#">c5mdxT_</a>	Alignment	not modelled	13.3	20	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> cryo-em structure of the psii supercomplex from arabidopsis thaliana
27	<a href="#">c5mdxt_</a>	Alignment	not modelled	13.3	20	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> cryo-em structure of the psii supercomplex from arabidopsis thaliana
28	<a href="#">c3jcuT_</a>	Alignment	not modelled	13.1	20	<b>PDB header:</b> membrane protein <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein tc; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
29	<a href="#">c3jcut</a>	Alignment	not modelled	13.1	20	<b>PDB header:</b> membrane protein <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein tc;

29	<a href="#">c3juc_</a>	Alignment	not modelled	13.1	20	<b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
30	<a href="#">d2pxrc1</a>	Alignment	not modelled	12.2	12	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
31	<a href="#">d1o26a_</a>	Alignment	not modelled	11.8	16	<b>Fold:</b> Thymidylate synthase-complementing protein Thy1 <b>Superfamily:</b> Thymidylate synthase-complementing protein Thy1 <b>Family:</b> Thymidylate synthase-complementing protein Thy1
32	<a href="#">c4i7zE_</a>	Alignment	not modelled	11.7	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of cytochrome b6f in dopg, with disordered rieske2 iron-sulfur protein soluble domain
33	<a href="#">c4pv1E_</a>	Alignment	not modelled	11.7	39	<b>PDB header:</b> electron transport/inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> cytochrome b6f structure from m. laminosus with the quinone analog2 inhibitor stigmatellin
34	<a href="#">d1m9dc_</a>	Alignment	not modelled	11.6	14	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
35	<a href="#">c4p5aB_</a>	Alignment	not modelled	11.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate synthase thyx; <b>PDBTitle:</b> crystal structure of a ump/dump methylase polb from streptomyces2 cacaoi bound with 5-br ump
36	<a href="#">c5x3xq_</a>	Alignment	not modelled	11.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> Q: <b>PDB Molecule:</b> uncharacterized protein cbiq; <b>PDBTitle:</b> 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
37	<a href="#">d1m9fd_</a>	Alignment	not modelled	10.4	12	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
38	<a href="#">c4h0IE_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> cytochrome b6f complex crystal structure from mastigocladus laminosus2 with n-side inhibitor nqno
39	<a href="#">d2e74e1</a>	Alignment	not modelled	10.1	39	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetL subunit of the cytochrome b6f complex <b>Family:</b> PetL subunit of the cytochrome b6f complex
40	<a href="#">c4h13E_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from mastigocladus2 laminosus with tds
41	<a href="#">c2e76E_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
42	<a href="#">c1vf5E_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> protein pet I; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
43	<a href="#">c2e75E_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
44	<a href="#">c2e74E_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from m.laminosus
45	<a href="#">c1vf5R_</a>	Alignment	not modelled	10.1	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> protein pet I; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
46	<a href="#">c2wlvA_</a>	Alignment	not modelled	9.8	16	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal capsid domain of hiv-2
47	<a href="#">c4r1iB_</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aminobenzoyl-glutamate transporter; <b>PDBTitle:</b> structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
48	<a href="#">c3aaqB_</a>	Alignment	not modelled	9.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
49	<a href="#">c4fc4H_</a>	Alignment	not modelled	9.1	12	<b>PDB header:</b> transport protein <b>Chain:</b> H: <b>PDB Molecule:</b> nitrite transporter nirc; <b>PDBTitle:</b> fnt family ion channel
50	<a href="#">c5gufA_</a>	Alignment	not modelled	9.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-archaeol synthase; <b>PDBTitle:</b> structural insight into an intramembrane enzyme for archaeal membrane2 lipids biosynthesis
51	<a href="#">d1mc8a1</a>	Alignment	not modelled	8.0	20	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
52	<a href="#">c3dl8C_</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> sece; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
53	<a href="#">c3dl8D_</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> sece; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
54	<a href="#">d2jeka1</a>	Alignment	not modelled	7.8	42	<b>Fold:</b> Rv1873-like <b>Superfamily:</b> Rv1873-like <b>Family:</b> Rv1873-like
55	<a href="#">c1l6nA_</a>	Alignment	not modelled	7.3	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal 283-residue fragment of the

						hiv-2 1 gag polyprotein
56	<a href="#">c4uoiB_</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> unexpected structure for the n-terminal domain of hepatitis c virus2 envelope glycoprotein e1
57	<a href="#">c5e06A_</a>	Alignment	not modelled	6.8	12	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid protein; <b>PDBTitle:</b> structure of sin nombre virus nucleoprotein in long-axis crystal form
58	<a href="#">d1rxwa1</a>	Alignment	not modelled	6.6	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
59	<a href="#">c5xamA_</a>	Alignment	not modelled	6.2	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit secdf; <b>PDBTitle:</b> crystal structure of secdf in i form at 4 a resolution
60	<a href="#">d1ul1x1</a>	Alignment	not modelled	6.0	18	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
61	<a href="#">d2yvxa3</a>	Alignment	not modelled	5.8	11	<b>Fold:</b> MgtE membrane domain-like <b>Superfamily:</b> MgtE membrane domain-like <b>Family:</b> MgtE membrane domain-like
62	<a href="#">d1b43a1</a>	Alignment	not modelled	5.1	20	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
63	<a href="#">c4k1cA_</a>	Alignment	not modelled	5.1	13	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger