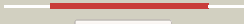

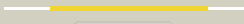







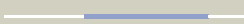

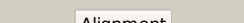


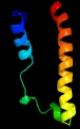





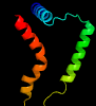
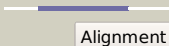

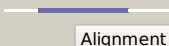
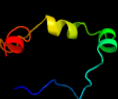



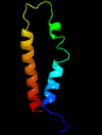
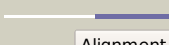





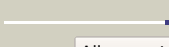


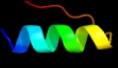
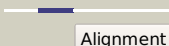
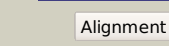
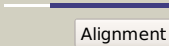
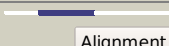

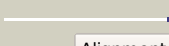

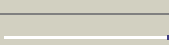


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3453 (-) _3874583_3874915
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	377b0cd89919752b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2jlnA_</a>	 Alignment		98.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
2	<a href="#">c5nvaA_</a>	 Alignment		71.3	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative sodium:solute symporter; <b>PDBTitle:</b> substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
3	<a href="#">c5edlA_</a>	 Alignment		61.3	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative hmp/thiamine permease protein ykoe; <b>PDBTitle:</b> crystal structure of an s-component of ecf transporter
4	<a href="#">c5oqtA_</a>	 Alignment		45.5	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> amino acid transporter; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
5	<a href="#">c4b03A_</a>	 Alignment		33.0	13	<b>PDB header:</b> virus <b>Chain:</b> A; <b>PDB Molecule:</b> dengue virus 1 e protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
6	<a href="#">c3giaA_</a>	 Alignment		25.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
7	<a href="#">c5ireA_</a>	 Alignment		20.0	22	<b>PDB header:</b> virus <b>Chain:</b> A; <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
8	<a href="#">c6f2wA_</a>	 Alignment		17.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative amino acid/polyamine transport protein; <b>PDBTitle:</b> bacterial asc transporter crystal structure in open to in conformation
9	<a href="#">c4ymuC_</a>	 Alignment		15.4	16	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> abc-type amino acid transport system, permease component; <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps
10	<a href="#">d1pw4a_</a>	 Alignment		14.9	12	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
11	<a href="#">c4k1cB_</a>	 Alignment		13.7	12	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> B; <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger

12	<a href="#">c5b7iC_</a>	 Alignment		13.0	16	<b>PDB header:</b> hydrolase/unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein acrf3; <b>PDBTitle:</b> cas3-acrf3 complex
13	<a href="#">c4ouaB_</a>	 Alignment		12.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> latent form of ppo4 tyrosinase; <b>PDBTitle:</b> coexistent single-crystal structure of latent and active mushroom2 tyrosinase (abppo4) mediated by a hexatungstotellurate(vi)
14	<a href="#">c3dh4A_</a>	 Alignment		12.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
15	<a href="#">c3lrcC_</a>	 Alignment		11.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
16	<a href="#">c1p58C_</a>	 Alignment		10.1	13	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> major envelope protein e; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
17	<a href="#">c4qidB_</a>	 Alignment		10.0	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacteriorhodopsin-;i; <b>PDBTitle:</b> crystal structure of haloquadratum walsbyi bacteriorhodopsin
18	<a href="#">c3f4yF_</a>	 Alignment		9.6	21	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> mutant peptide derived from hiv gp41 chr domain; <b>PDBTitle:</b> hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
19	<a href="#">d1e5xa_</a>	 Alignment		9.4	27	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
20	<a href="#">c3da1A_</a>	 Alignment		9.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
21	<a href="#">d1d4ua1</a>	 Alignment	not modelled	9.1	22	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA repair factor XPA DNA- and RPA-binding domain, C-terminal subdomain
22	<a href="#">c4k1cA_</a>	 Alignment	not modelled	9.1	16	<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
23	<a href="#">d1z9ha1</a>	 Alignment	not modelled	9.0	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
24	<a href="#">d1u7la_</a>	 Alignment	not modelled	8.9	20	<b>Fold:</b> Vacuolar ATP synthase subunit C <b>Superfamily:</b> Vacuolar ATP synthase subunit C <b>Family:</b> Vacuolar ATP synthase subunit C
25	<a href="#">c3g7aB_</a>	 Alignment	not modelled	8.9	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> chimeric alpha+alpha/beta-peptide analogue of the hiv gp41 <b>PDBTitle:</b> hiv gp41 six-helix bundle composed of a chimeric alpha+alpha/beta-2 peptide analogue of the chr domain in complex with an nhr domain3 alpha-peptide
26	<a href="#">c2rghA_</a>	 Alignment	not modelled	8.7	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
27	<a href="#">d1uaza_</a>	 Alignment	not modelled	8.4	8	<b>Fold:</b> Family A G protein-coupled receptor-like <b>Superfamily:</b> Family A G protein-coupled receptor-like <b>Family:</b> Bacteriorhodopsin-like
		 Alignment				<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase;

28	<a href="#">c2rgoA_</a>	Alignment	not modelled	8.3	38	<b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from 2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase <b>PDB header:</b> virus
29	<a href="#">c5o6vC_</a>	Alignment	not modelled	8.2	19	<b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with 2 fab fragment of neutralizing antibody 19/1786
30	<a href="#">d1xdpa4</a>	Alignment	not modelled	8.0	23	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
31	<a href="#">d2o8ra4</a>	Alignment	not modelled	7.8	38	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
32	<a href="#">d2qrra1</a>	Alignment	not modelled	7.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like
33	<a href="#">c4dl0l_</a>	Alignment	not modelled	7.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> v-type proton atpase subunit c; <b>PDBTitle:</b> crystal structure of the heterotrimeric egthead peripheral stalk2 complex of the yeast vacuolar atpase
34	<a href="#">c1ceuA_</a>	Alignment	not modelled	7.5	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hiv-1 regulatory protein n-terminal) <b>PDBTitle:</b> nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
35	<a href="#">d2yvxa3</a>	Alignment	not modelled	7.5	14	<b>Fold:</b> MgtE membrane domain-like <b>Superfamily:</b> MgtE membrane domain-like <b>Family:</b> MgtE membrane domain-like
36	<a href="#">c3wdoA_</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
37	<a href="#">c6bi6A_</a>	Alignment	not modelled	7.1	56	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yejg; <b>PDBTitle:</b> solution nmr structure of uncharacterized protein yejg
38	<a href="#">c2p3xA_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyphenol oxidase, chloroplast; <b>PDBTitle:</b> crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
39	<a href="#">c1a87A_</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
40	<a href="#">d1a87a_</a>	Alignment	not modelled	6.7	20	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
41	<a href="#">c5wsnC_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
42	<a href="#">d2c0sa1</a>	Alignment	not modelled	6.5	18	<b>Fold:</b> ROP-like <b>Superfamily:</b> BAS1536-like <b>Family:</b> BAS1536-like
43	<a href="#">c5sv1Y_</a>	Alignment	not modelled	6.4	26	<b>PDB header:</b> transport protein <b>Chain:</b> Y: <b>PDB Molecule:</b> biopolymer transport protein exbd; <b>PDBTitle:</b> structure of the exbb/exbd complex from e. coli at ph 4.5
44	<a href="#">c5yo8B_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tetraprenyl-beta-curcumin synthase; <b>PDBTitle:</b> crystal structure of beta-c25/c30/c35-prene synthase
45	<a href="#">c5oqmQ_</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> transcription initiation factor iif subunit alpha; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and 2 core mediator
46	<a href="#">c5nikK_</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump
47	<a href="#">c4fbzA_</a>	Alignment	not modelled	6.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> deltarhodopsin; <b>PDBTitle:</b> crystal structure of deltarhodopsin from haloterrigena thermotolerans
48	<a href="#">c5lno_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
49	<a href="#">c5ejoA_</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromatin assembly factor 1 subunit p90; <b>PDBTitle:</b> crystal structure of the winged helix domain in chromatin assembly2 factor 1 subunit p90
50	<a href="#">c1c0iA_</a>	Alignment	not modelled	5.9	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-amino acid oxidase; <b>PDBTitle:</b> crystal structure of d-amino acid oxidase in complex with two 2 anthranilate molecules
51	<a href="#">d2mysa2</a>	Alignment	not modelled	5.6	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
52	<a href="#">c6dg6F_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> neoleukin-2/15; <b>PDBTitle:</b> structure of a de novo designed interleukin-2/interleukin-15 mimetic
53	<a href="#">c1xioA_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> anabaena sensory rhodopsin; <b>PDBTitle:</b> anabaena sensory rhodopsin
						<b>Fold:</b> Family A G protein-coupled receptor-like

54	<a href="#">d1xioa_</a>	Alignment	not modelled	5.6	14	<b>Superfamily:</b> Family A G protein-coupled receptor-like <b>Family:</b> Bacteriorhodopsin-like
55	<a href="#">c2y9xC_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> polyphenol oxidase; <b>PDBTitle:</b> crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
56	<a href="#">c2k53A_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> a3dk08 protein; <b>PDBTitle:</b> nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
57	<a href="#">d1y7ma2</a>	Alignment	not modelled	5.3	25	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
58	<a href="#">c1oy7C_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> apoptosis/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 7; <b>PDBTitle:</b> structure and function analysis of peptide antagonists of melanoma2 inhibitor of apoptosis (ml-iap)
59	<a href="#">c2enkA_</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 30 member 9; <b>PDBTitle:</b> solution structure of a putativ dna-binding domain of the2 humansolute carrier family 30 (zinc transporter) protein
60	<a href="#">d3ceda1</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> NIL domain-like