


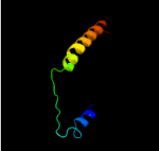
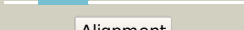
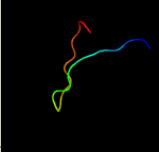
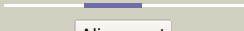




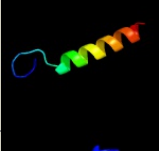
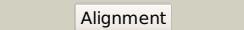

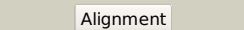
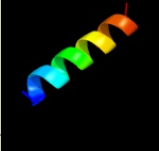
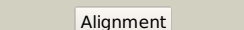
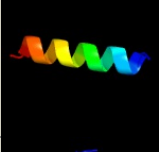
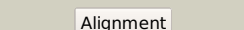

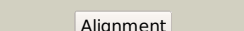



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2076c (- )_2333045_2333296
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	9abc223965213b38

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6n3qD_</a>	 Alignment		47.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocation protein sec63; <b>PDBTitle:</b> cryo-em structure of the yeast sec complex
2	<a href="#">c6nd1A_</a>	 Alignment		42.1	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein translocation protein sec63; <b>PDBTitle:</b> cryoem structure of the sec complex from yeast
3	<a href="#">c2dfxl_</a>	 Alignment		33.1	30	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> colicin-e5 immunity protein; <b>PDBTitle:</b> crystal structure of the carboxy terminal domain of colicin2 e5 complexed with its inhibitor
4	<a href="#">c6g67A_</a>	 Alignment		17.2	56	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-type2-ii; <b>PDBTitle:</b> crystal structure of a parallel eight-helix coiled coil cc-type2-ii
5	<a href="#">c6g67B_</a>	 Alignment		17.2	56	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-type2-ii; <b>PDBTitle:</b> crystal structure of a parallel eight-helix coiled coil cc-type2-ii
6	<a href="#">c3gekA_</a>	 Alignment		14.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase yhda; <b>PDBTitle:</b> crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
7	<a href="#">c6g66C_</a>	 Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv
8	<a href="#">c6g66D_</a>	 Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv
9	<a href="#">c6g66E_</a>	 Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv
10	<a href="#">c6g66B_</a>	 Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv
11	<a href="#">c6g66G_</a>	 Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv

12	<a href="#">c6g66A_</a>	Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv
13	<a href="#">c6g66F_</a>	Alignment		13.4	56	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> cc-type2-iv; <b>PDBTitle:</b> crystal structure of a parallel seven-helix coiled coil cc-type2-iv
14	<a href="#">d2f0xa1</a>	Alignment		12.8	15	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
15	<a href="#">c1zmmA_</a>	Alignment		11.6	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of human alpha-defensin-4
16	<a href="#">c1zmmC_</a>	Alignment		11.6	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of human alpha-defensin-4
17	<a href="#">c6dmqE_</a>	Alignment		11.5	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
18	<a href="#">c6dmqH_</a>	Alignment		11.5	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
19	<a href="#">c6dmqC_</a>	Alignment		11.5	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
20	<a href="#">c6dmqG_</a>	Alignment		11.5	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> G: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
21	<a href="#">c6dmqA_</a>	Alignment	not modelled	11.4	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
22	<a href="#">c1zmmB_</a>	Alignment	not modelled	11.1	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of human alpha-defensin-4
23	<a href="#">c1zmmD_</a>	Alignment	not modelled	11.1	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of human alpha-defensin-4
24	<a href="#">c6dmqB_</a>	Alignment	not modelled	11.1	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
25	<a href="#">c6dmqD_</a>	Alignment	not modelled	11.1	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
26	<a href="#">c6dmqF_</a>	Alignment	not modelled	11.1	100	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> F: <b>PDB Molecule:</b> neutrophil defensin 4; <b>PDBTitle:</b> crystal structure of the t27a mutant of human alpha defensin hnp4.
27	<a href="#">c2l35B_</a>	Alignment	not modelled	10.7	47	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12-nkg2c transmembrane heterotrimer
28	<a href="#">c4wo1A_</a>	Alignment	not modelled	10.1	47	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in

						lipidic cubic2 phase
29	<a href="#">c2l34A_</a>	Alignment	not modelled	10.1	47	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
30	<a href="#">c2l34B_</a>	Alignment	not modelled	10.1	47	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
31	<a href="#">c4wo1C_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
32	<a href="#">c4wo1B_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
33	<a href="#">c4wo1B_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
34	<a href="#">c4wo1D_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
35	<a href="#">c4wo1C_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
36	<a href="#">c4wo1A_</a>	Alignment	not modelled	9.9	47	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
37	<a href="#">d1vh5a_</a>	Alignment	not modelled	9.4	19	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
38	<a href="#">d1jlua_</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
39	<a href="#">c5nmiK_</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> membrane protein <b>Chain:</b> K: <b>PDB Molecule:</b> arg-asn-trp-val-pro-thr-ala-gln-leu-trp-gly-ala-val-gly- <b>PDBTitle:</b> cytochrome bc1 bound to the inhibitor mjm170
40	<a href="#">c5nmiX_</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> arg-asn-trp-val-pro-thr-ala-gln-leu-trp-gly-ala-val-gly- <b>PDBTitle:</b> cytochrome bc1 bound to the inhibitor mjm170
41	<a href="#">d1be3k_</a>	Alignment	not modelled	7.7	36	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
42	<a href="#">c5dm5E_</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative acyl-coa thioester hydrolase; <b>PDBTitle:</b> crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis
43	<a href="#">c2ynmD_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
44	<a href="#">c6humQ_</a>	Alignment	not modelled	6.5	47	<b>PDB header:</b> proton transport <b>Chain:</b> Q: <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit q <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
45	<a href="#">c2qwzB_</a>	Alignment	not modelled	6.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetic acid degradation-related protein; <b>PDBTitle:</b> crystal structure of a putative thioesterase (tm1040_1390) from2 silicibacter sp. tm1040 at 2.15 a resolution
46	<a href="#">c6bqzA_</a>	Alignment	not modelled	6.1	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosine-trna synthetase from acinetobacter2 baumannii with bound l-tyrosine
47	<a href="#">d2gvha2</a>	Alignment	not modelled	6.0	32	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> 4HBT-like
48	<a href="#">c2qg5D_</a>	Alignment	not modelled	5.9	40	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase; <b>PDBTitle:</b> cryptosporidium parvum calcium dependent protein kinase cgd7_1840
49	<a href="#">c2ts1A_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> ligase (synthetase) <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-tRNA synthetase; <b>PDBTitle:</b> structure of tyrosyl-tRNA synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
50	<a href="#">d2ts1a_</a>	Alignment	not modelled	5.6	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
						<b>PDB header:</b> transferase/transferase inhibitor

51	<a href="#">c5vdkA_</a>	Alignment	not modelled	5.5	50	<b>Chain:</b> A; <b>PDB Molecule:</b> wee1-like protein kinase 2; <b>PDBTitle:</b> crystal structure of human wee2 kinase domain in complex with mk1775
52	<a href="#">d1vh9a_</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Paal/Ydil-like
53	<a href="#">c3p1aA_</a>	Alignment	not modelled	5.5	55	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> membrane-associated tyrosine- and threonine-specific cdc2- <b>PDBTitle:</b> structure of human membrane-associated tyrosine- and threonine-2 specific cdc2-inhibitory kinase myt1 (pkmyt1)
54	<a href="#">c3c0hB_</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> peripheral plasma membrane protein cask; <b>PDBTitle:</b> cask cam-kinase domain- amppnp complex, p1 form
55	<a href="#">c2jq1A_</a>	Alignment	not modelled	5.2	71	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> phylloseptin-3; <b>PDBTitle:</b> phylloseptin-3