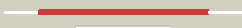



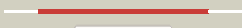







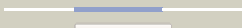


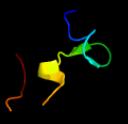



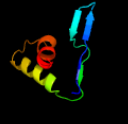




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2468c (- )_2771654_2772157
Date	Wed Aug 7 12:50:09 BST 2019
Unique Job ID	c55f016ca0d2437e

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6hwhT_</a>	 Alignment		100.0	72	<b>PDB header:</b> electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> uncharacterized protein msmeg_4692/msmei_4575; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
2	<a href="#">c2lt2A_</a>	 Alignment		99.9	16	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr structure of ba42 protein from the psychrophilic bacteria bizionia2 argentinensis sp. nov.
3	<a href="#">c5anpB_</a>	 Alignment		99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> ba41; <b>PDBTitle:</b> crystal structure of the ba41 protein from bizionia argentinensis
4	<a href="#">c2kw7A_</a>	 Alignment		99.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
5	<a href="#">c3ptjA_</a>	 Alignment		99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> upf0603 protein at1g54780, chloroplastic; <b>PDBTitle:</b> structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein atpl18.3
6	<a href="#">c2kptA_</a>	 Alignment		99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative secreted protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a
7	<a href="#">c5t3uA_</a>	 Alignment		27.4	8	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
8	<a href="#">d1v6ga2</a>	 Alignment		24.3	28	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
9	<a href="#">c3sqgF_</a>	 Alignment		19.6	24	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> methyl-coenzyme m reductase, gamma subunit; <b>PDBTitle:</b> crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
10	<a href="#">c5h63C_</a>	 Alignment		18.9	18	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> transferase; <b>PDBTitle:</b> structure of transferase mutant-c23s,c199s
11	<a href="#">c5h60A_</a>	 Alignment		15.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> transferase; <b>PDBTitle:</b> structure of transferase mutant-c23s,c199s

12	<a href="#">c3lfhF_</a>	Alignment		15.3	15	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> phosphotransferase system, mannose/fructose-specific <b>PDBTitle:</b> crystal structure of manxa from thermoanaerobacter tengcongensis
13	<a href="#">c6aciA_</a>	Alignment		14.5	21	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> t3ss secreted effector nleb homolog; <b>PDBTitle:</b> crystal structure of epec effector nleb in complex with fadd death2 domain
14	<a href="#">d1q44a_</a>	Alignment		14.0	8	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
15	<a href="#">c4p6iB_</a>	Alignment		13.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> crispr-associated endoribonuclease cas2; <b>PDBTitle:</b> crystal structure of the cas1-cas2 complex from escherichia coli
16	<a href="#">d1efpb_</a>	Alignment		12.8	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
17	<a href="#">c5a8wl_</a>	Alignment		12.5	22	<b>PDB header:</b> transferase <b>Chain:</b> I; <b>PDB Molecule:</b> methyl-coenzyme m reductase ii; <b>PDBTitle:</b> methyl-coenzyme m reductase ii from methanothermobacter wolfeii at 1.2 8 a resolution
18	<a href="#">c5h5yB_</a>	Alignment		12.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> non-lee encoded effector protein nleb; <b>PDBTitle:</b> structure of transferase mutant-c23s,c199s
19	<a href="#">d1hbnc_</a>	Alignment		12.2	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Methyl-coenzyme M reductase subunits <b>Family:</b> Methyl-coenzyme M reductase gamma chain
20	<a href="#">d1w26a2</a>	Alignment		11.8	8	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
21	<a href="#">d1o94c_</a>	Alignment	not modelled	11.5	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
22	<a href="#">c2wkdA_</a>	Alignment	not modelled	11.2	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> orf34p2; <b>PDBTitle:</b> crystal structure of a double ile-to-met mutant of protein orf34 from2 lactococcus phage p2
23	<a href="#">d2a8na1</a>	Alignment	not modelled	10.2	18	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
24	<a href="#">d1j3wa_</a>	Alignment	not modelled	9.7	22	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
25	<a href="#">c1om8A_</a>	Alignment	not modelled	9.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serralysin; <b>PDBTitle:</b> crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
26	<a href="#">c5cajB_</a>	Alignment	not modelled	8.6	21	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> upf0246 protein yaaa; <b>PDBTitle:</b> crystal structure of e. coli yaaa, a member of the duf328/upf02462 family
27	<a href="#">c6fahB_</a>	Alignment	not modelled	8.6	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit card; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
28	<a href="#">c3lmaC_</a>	Alignment	not modelled	8.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> stage v sporulation protein ad (spovad); <b>PDBTitle:</b> crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6. <b>PDB header:</b> hydrolase

29	<a href="#">c4makA_</a>	Alignment	not modelled	8.1	16	<b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endoribonuclease cas2; <b>PDBTitle:</b> crystal structure of a putative ssrna endonuclease cas2, crispr2 adaptation protein from e.coli
30	<a href="#">c3d3jA_</a>	Alignment	not modelled	7.6	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
31	<a href="#">c3bs9A_</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleolysin tia-1 isoform p40; <b>PDBTitle:</b> x-ray structure of human tia-1 rrm2
32	<a href="#">d1efvb_</a>	Alignment	not modelled	7.3	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
33	<a href="#">d2d9ia1</a>	Alignment	not modelled	7.2	13	<b>Fold:</b> IF3-like <b>Superfamily:</b> SMR domain-like <b>Family:</b> Smr domain
34	<a href="#">c3ncpD_</a>	Alignment	not modelled	7.0	12	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii (glnb-2); <b>PDBTitle:</b> glnk2 from archaeoglobus fulgidus
35	<a href="#">c2j83B_</a>	Alignment	not modelled	6.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ulilysin; <b>PDBTitle:</b> ulilysin metalloprotease in complex with batimastat.
36	<a href="#">c3adyA_</a>	Alignment	not modelled	6.7	15	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> dotd; <b>PDBTitle:</b> crystal structure of dotd from legionella
37	<a href="#">d1nxua_</a>	Alignment	not modelled	6.6	16	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
38	<a href="#">c3g98B_</a>	Alignment	not modelled	6.5	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
39	<a href="#">d1wkqa_</a>	Alignment	not modelled	6.4	17	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
40	<a href="#">c5nsjB_</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> pre-glycoprotein polyprotein gp complex; <b>PDBTitle:</b> gp1 receptor-binding domain from whitewater arroyo mammarenavirus
41	<a href="#">c3excX_</a>	Alignment	not modelled	6.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the rna'se sso8090 from sulfolobus solfataricus
42	<a href="#">c2kp6A_</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein cv0237 from chromobacterium2 violaceum. northeast structural genomics consortium (nesg) target3 cvt1
43	<a href="#">c5opth_</a>	Alignment	not modelled	5.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of ksrp in context of trypanosoma cruzi 40s
44	<a href="#">d2i0xa1</a>	Alignment	not modelled	5.6	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> TTP0101/SSO1404-like <b>Family:</b> TTP0101/SSO1404-like
45	<a href="#">d2f3ga_</a>	Alignment	not modelled	5.6	13	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
46	<a href="#">c2hjjA_</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ykff; <b>PDBTitle:</b> solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
47	<a href="#">d2hja1</a>	Alignment	not modelled	5.5	14	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> YcfA/nrd intein domain <b>Family:</b> Ykff-like
48	<a href="#">c4xcwF_</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> molybdopter adenyl/transferase; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
49	<a href="#">c1v1hB_</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> adenovirus <b>Chain:</b> B: <b>PDB Molecule:</b> fibrin, fiber protein; <b>PDBTitle:</b> adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibrin foldon trimerisation motif with a short3 linker
50	<a href="#">d2a3ra1</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
51	<a href="#">d1p9ya_</a>	Alignment	not modelled	5.3	5	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
52	<a href="#">c4es2A_</a>	Alignment	not modelled	5.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bh0342 protein; <b>PDBTitle:</b> double-stranded endonuclease activity in b. halodurans clustered2 regularly interspaced short palindromic repeats (crispr)-associated3 cas2 protein