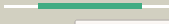
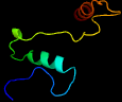
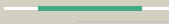
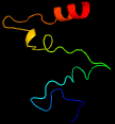

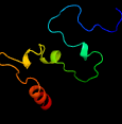



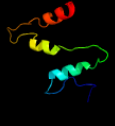
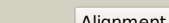

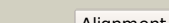

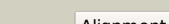
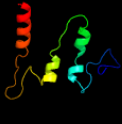






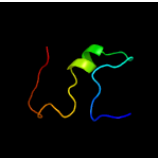
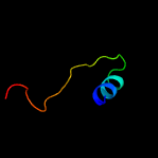
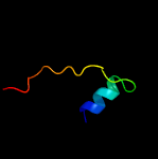
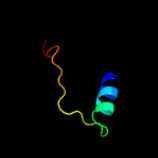

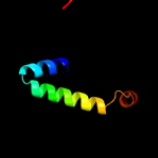
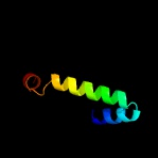
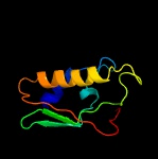
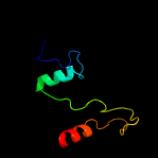


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2016 (- )_2263434_2264009
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	a572a1a45b260a3a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ntgA_</a>	 Alignment		44.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> structure of leucyl aminopeptidase from trypanosoma cruzi in complex2 with citrate
2	<a href="#">c5nthA_</a>	 Alignment		41.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminopeptidase; <b>PDBTitle:</b> structure of leucyl aminopeptidase from leishmania major in complex2 with actinonin
3	<a href="#">c4efdF_</a>	 Alignment		32.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> crystal structure of an m17 aminopeptidase from trypanosoma brucei,2 tb427tmp.02.4440
4	<a href="#">c3lnoA_</a>	 Alignment		26.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of domain of unknown function duf59 from2 bacillus anthracis
5	<a href="#">c3jruB_</a>	 Alignment		24.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable cytosol aminopeptidase; <b>PDBTitle:</b> crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
6	<a href="#">c2lqtA_</a>	 Alignment		23.7	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil-helix-coiled-coil-helix domain-containing <b>PDBTitle:</b> solution structure of chchd7
7	<a href="#">c5lhkA_</a>	 Alignment		23.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase 2, chloroplastic; <b>PDBTitle:</b> bottromycin maturation enzyme botp in complex with mn
8	<a href="#">c1gytG_</a>	 Alignment		22.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> e. coli aminopeptidase a (pepa)
9	<a href="#">d2ciwa2</a>	 Alignment		21.6	38	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> Cloroperoxidase <b>Family:</b> Cloroperoxidase
10	<a href="#">d1gyta2</a>	 Alignment		17.9	32	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Leucine aminopeptidase, C-terminal domain
11	<a href="#">c4ksiA_</a>	 Alignment		17.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase 1, chloroplastic; <b>PDBTitle:</b> crystal structure analysis of the acidic leucine aminopeptidase of2 tomato

12	<a href="#">c3kzwD</a>	Alignment		16.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
13	<a href="#">c1fcuA</a>	Alignment		15.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronoglucosaminidase; <b>PDBTitle:</b> crystal structure (trigonal) of bee venom hyaluronidase
14	<a href="#">c2atmA</a>	Alignment		14.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronoglucosaminidase; <b>PDBTitle:</b> crystal structure of the recombinant allergen ves v 2
15	<a href="#">d1fcqa</a>	Alignment		13.7	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Bee venom hyaluronidase
16	<a href="#">c4uqtB</a>	Alignment		13.5	47	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc26; <b>PDBTitle:</b> rrm-peptide structure in res complex
17	<a href="#">d2peoa1</a>	Alignment		12.5	15	<b>Fold:</b> RbcX-like <b>Superfamily:</b> RbcX-like <b>Family:</b> RbcX-like
18	<a href="#">c2peoA</a>	Alignment		12.5	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rbcx protein; <b>PDBTitle:</b> crystal structure of rbcx from anabaena ca
19	<a href="#">d1uwda</a>	Alignment		12.3	14	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
20	<a href="#">c4zi6D</a>	Alignment		11.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> crystal structure of leucine aminopeptidase from helicobacter pylori
21	<a href="#">c2pe4A</a>	Alignment	not modelled	11.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronidase-1; <b>PDBTitle:</b> structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
22	<a href="#">c3w8hB</a>	Alignment	not modelled	11.6	63	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 25; <b>PDBTitle:</b> crystal structure of ccm3 in complex with the c-terminal regulatory2 domain of stk25
23	<a href="#">d1gvia2</a>	Alignment	not modelled	11.1	27	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
24	<a href="#">c2n1dA</a>	Alignment	not modelled	11.1	50	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mrg/morf4l-binding protein; <b>PDBTitle:</b> solution structure of the mrg15-mrgbp complex
25	<a href="#">c5zwoY</a>	Alignment	not modelled	10.7	47	<b>PDB header:</b> splicing <b>Chain:</b> Y: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc26; <b>PDBTitle:</b> cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
26	<a href="#">c2mkcC</a>	Alignment	not modelled	10.6	47	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc26; <b>PDBTitle:</b> cooperative structure of the heterotrimeric pre-mrna retention and2 splicing complex
27	<a href="#">c2hc9A</a>	Alignment	not modelled	10.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine aminopeptidase 1; <b>PDBTitle:</b> structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
28	<a href="#">d1g7ya</a>	Alignment	not modelled	10.4	29	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Legume lectins
						<b>PDB header:</b> chaperone

29	<a href="#">c3ka1A</a>	Alignment	not modelled	9.4	20	<b>Chain:</b> A: <b>PDB Molecule:</b> rbcx protein; <b>PDBTitle:</b> crystal structure of rbcx from thermosynechococcus elongatus
30	<a href="#">c6cxdA</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase b; <b>PDBTitle:</b> crystal structure of peptidase b from yersinia pestis co92 at 2.75 a2 resolution
31	<a href="#">c4mjsQ</a>	Alignment	not modelled	8.2	44	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> Q: <b>PDB Molecule:</b> protein kinase c zeta type; <b>PDBTitle:</b> crystal structure of a pb1 complex
32	<a href="#">d1pwha</a>	Alignment	not modelled	8.1	26	<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
33	<a href="#">d1whja</a>	Alignment	not modelled	8.0	67	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
34	<a href="#">c2knrA</a>	Alignment	not modelled	7.7	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atc0905; <b>PDBTitle:</b> solution structure of protein atu0922 from a. tumefaciens. northeast2 structural genomics consortium target att13. ontario center for3 structural proteomics target atc0905
35	<a href="#">c3h8gC</a>	Alignment	not modelled	7.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
36	<a href="#">c4gr6B</a>	Alignment	not modelled	7.6	26	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> atrbcx2; <b>PDBTitle:</b> crystal structure of atrbcx2 from arabidopsis thaliana
37	<a href="#">c4mjbB</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4853 family protein (actodo_00621) from2 actinomyces odontolyticus atcc 17982 at 2.65 a resolution
38	<a href="#">c2yzwA</a>	Alignment	not modelled	7.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylglycohydrolase; <b>PDBTitle:</b> adp-ribosylglycohydrolase-related protein complex
39	<a href="#">c2y0nG</a>	Alignment	not modelled	7.2	58	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> male-specific lethal 1 homolog; <b>PDBTitle:</b> crystal structure of the complex between dosage2 compensation factors msl1 and msl3
40	<a href="#">c2y0nH</a>	Alignment	not modelled	7.2	58	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> male-specific lethal 1 homolog; <b>PDBTitle:</b> crystal structure of the complex between dosage2 compensation factors msl1 and msl3
41	<a href="#">c4gehB</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mst4; <b>PDBTitle:</b> crystal structure of mst4 dimerization domain complex with pdcd10
42	<a href="#">c4goqD</a>	Alignment	not modelled	7.1	45	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1491 family protein (cc_1065) from2 caulobacter crescentus cb15 at 1.87 a resolution
43	<a href="#">c5c3uA</a>	Alignment	not modelled	7.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-serine ammonia-lyase; <b>PDBTitle:</b> crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
44	<a href="#">d1whka</a>	Alignment	not modelled	6.9	44	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
45	<a href="#">c2w2hD</a>	Alignment	not modelled	6.9	63	<b>PDB header:</b> rna-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein tat; <b>PDBTitle:</b> structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from eiav
46	<a href="#">c4nvrC</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative acyltransferase; <b>PDBTitle:</b> 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
47	<a href="#">c6ff43</a>	Alignment	not modelled	6.7	58	<b>PDB header:</b> splicing <b>Chain:</b> 3: <b>PDB Molecule:</b> bud13 homolog; <b>PDBTitle:</b> human bact spliceosome core structure
48	<a href="#">c5a4hA</a>	Alignment	not modelled	6.4	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-acylglycerol-3-phosphate o-acyltransferase abhd5; <b>PDBTitle:</b> solution structure of the lipid droplet anchoring peptide2 of cgi-58 bound to dpc micelles
49	<a href="#">c6omeA</a>	Alignment	not modelled	6.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cytosol aminopeptidase; <b>PDBTitle:</b> crystal structure of a probable cytosol aminopeptidase (leucine2 aminopeptidase, lap) from chlamydia trachomatis d/uw-3/cx
50	<a href="#">c3gi7A</a>	Alignment	not modelled	5.9	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protein of unknown function duf1311; <b>PDBTitle:</b> crystal structure of a duf1311 family protein (pp0307) from2 pseudomonas putida kt2440 at 1.85 a resolution
51	<a href="#">c6c2qA</a>	Alignment	not modelled	5.8	35	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structures of cystathionine beta-synthase from saccharomyces2 cerevisiae: the structure of the plp-l-serine intermediate
52	<a href="#">d2py8a1</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> RbcX-like <b>Superfamily:</b> RbcX-like <b>Family:</b> RbcX-like
53	<a href="#">c4issA</a>	Alignment	not modelled	5.7	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> allophanate hydrolase; <b>PDBTitle:</b> semet-substituted kluyveromyces lactis allophanate

						hydrolase
54	<a href="#">c1cfgA_</a>	Alignment	not modelled	5.7	42	<b>PDB header:</b> coagulation factor <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor viii; <b>PDBTitle:</b> membrane-binding peptide from the c2 domain of factor viii2 forms an amphipathic structure as determined by nmr3 spectroscopy
55	<a href="#">c6d7yA_</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> 1.75 angstrom resolution crystal structure of the toxic c-terminal tip2 of cdia from pseudomonas aeruginosa in complex with immune protein
56	<a href="#">d1whha_</a>	Alignment	not modelled	5.6	56	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
57	<a href="#">d1tkja1</a>	Alignment	not modelled	5.6	45	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> Bacterial dinuclear zinc exopeptidases
58	<a href="#">c3ij3A_</a>	Alignment	not modelled	5.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosol aminopeptidase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
59	<a href="#">d1ut7a_</a>	Alignment	not modelled	5.5	24	<b>Fold:</b> NAC domain <b>Superfamily:</b> NAC domain <b>Family:</b> NAC domain
60	<a href="#">c3uc0B_</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
61	<a href="#">c2eecA_</a>	Alignment	not modelled	5.3	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> filamin-b; <b>PDBTitle:</b> solution structure of the 23th filamin domain from human2 filamin-b
62	<a href="#">c5ii6A_</a>	Alignment	not modelled	5.1	100	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> zona pellucida sperm-binding protein 2; <b>PDBTitle:</b> crystal structure of the zp-n1 domain of mouse sperm receptor zp2 at2 0.95 a resolution