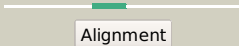


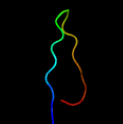


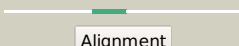

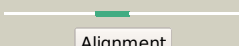

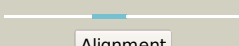

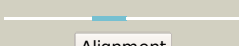




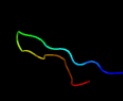

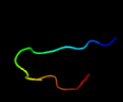

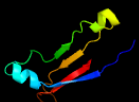

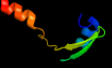





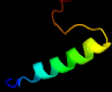



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2680 (-) _2996115_2996747
Date	Wed Aug 7 12:50:33 BST 2019
Unique Job ID	d4a3236a4522749d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zivA_</a>	 Alignment		45.9	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> calpain 9; <b>PDBTitle:</b> catalytic domain of human calpain-9
2	<a href="#">d1ziva1</a>	 Alignment		45.9	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Calpain large subunit, catalytic domain (domain II)
3	<a href="#">c6bdtC_</a>	 Alignment		44.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> calpain-3; <b>PDBTitle:</b> crystal structure of human calpain-3 protease core mutant-c129s
4	<a href="#">d1kful3</a>	 Alignment		43.4	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Calpain large subunit, catalytic domain (domain II)
5	<a href="#">c3hlzA_</a>	 Alignment		43.3	41	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein bt_1490; <b>PDBTitle:</b> crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
6	<a href="#">d1mdwa_</a>	 Alignment		38.3	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Calpain large subunit, catalytic domain (domain II)
7	<a href="#">d2r9fa1</a>	 Alignment		37.7	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Calpain large subunit, catalytic domain (domain II)
8	<a href="#">d1zcmal</a>	 Alignment		36.2	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Calpain large subunit, catalytic domain (domain II)
9	<a href="#">d1qxp4</a>	 Alignment		33.1	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Calpain large subunit, catalytic domain (domain II)
10	<a href="#">c1qxpB_</a>	 Alignment		30.0	33	<b>PDB header:</b> hydrolase chimera <b>Chain:</b> B; <b>PDB Molecule:</b> mu-like calpain; <b>PDBTitle:</b> crystal structure of a mu-like calpain
11	<a href="#">d1w96a1</a>	 Alignment		24.9	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like

12	<a href="#">d1ulza1</a>	Alignment		18.9	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
13	<a href="#">d2p3pa1</a>	Alignment		18.1	21	<b>Fold:</b> PG1388-like <b>Superfamily:</b> PG1388-like <b>Family:</b> PG1388-like
14	<a href="#">c4a4kl</a>	Alignment		17.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> antiviral helicase ski2; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski2 insertion domain
15	<a href="#">d2j9ga1</a>	Alignment		15.7	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
16	<a href="#">c4rcnA</a>	Alignment		14.7	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain acyl-coa carboxylase; <b>PDBTitle:</b> structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
17	<a href="#">c1vkoA</a>	Alignment		13.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
18	<a href="#">d2ipqx1</a>	Alignment		13.5	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> STY4665 C-terminal domain-like
19	<a href="#">d1p1ja1</a>	Alignment		12.6	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
20	<a href="#">c5civA</a>	Alignment		11.7	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sibling bacteriocin; <b>PDBTitle:</b> sibling lethal factor precursor - dfsb
21	<a href="#">c1p1hD</a>	Alignment	not modelled	11.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of the 1l-myo-inositol/nad+ complex
22	<a href="#">c1kfxL</a>	Alignment	not modelled	9.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> m-calpain large subunit; <b>PDBTitle:</b> crystal structure of human m-calpain form i
23	<a href="#">d1snna</a>	Alignment	not modelled	9.3	33	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
24	<a href="#">d1xd5a</a>	Alignment	not modelled	9.2	18	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins
25	<a href="#">d1vkoal</a>	Alignment	not modelled	9.0	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
26	<a href="#">c4lqbA</a>	Alignment	not modelled	8.7	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein kfla3161
27	<a href="#">d1z1za1</a>	Alignment	not modelled	8.6	18	<b>Fold:</b> Phage tail protein-like <b>Superfamily:</b> Phage tail protein-like <b>Family:</b> Lambda phage gpU-like
28	<a href="#">c4p6dA</a>	Alignment	not modelled	8.4	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> structure of ribb complexed with po4 ion
29	<a href="#">c2t7kP</a>	Alignment	not modelled	8.4	40	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of ty1 transposition protein 107;

29	<a href="#">c3v7B_</a>	Alignment	not modelled	8.4	40	<b>PDBTitle:</b> complex structure of rtt107p and phosphorylated histone h2a <b>PDB header:</b> hydrolase
30	<a href="#">c2advB_</a>	Alignment	not modelled	8.3	30	<b>Chain:</b> B; <b>PDB Molecule:</b> glutaryl 7- aminocephalosporanic acid acylase; <b>PDBTitle:</b> crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
31	<a href="#">d1jcb1</a>	Alignment	not modelled	8.2	36	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
32	<a href="#">c3u9sl_</a>	Alignment	not modelled	7.7	22	<b>PDB header:</b> ligase <b>Chain:</b> I; <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
33	<a href="#">c3mioA_</a>	Alignment	not modelled	7.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
34	<a href="#">d1tksa_</a>	Alignment	not modelled	7.3	17	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
35	<a href="#">d1k4ia_</a>	Alignment	not modelled	7.2	11	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
36	<a href="#">c5ks8B_</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> pyruvate carboxylase subunit alpha; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
37	<a href="#">c3mz2A_</a>	Alignment	not modelled	7.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdj_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution
38	<a href="#">c3l2uA_</a>	Alignment	not modelled	7.2	12	<b>PDB header:</b> recombination/dna <b>Chain:</b> A; <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
39	<a href="#">c5mlkB_</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
40	<a href="#">c3v4dC_</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> aminoacrylate peracid reductase ruc; <b>PDBTitle:</b> crystal structure of ruc protein a member of the yjgf family from2 e.coli
41	<a href="#">c5zt3A_</a>	Alignment	not modelled	6.9	26	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> wa352; <b>PDBTitle:</b> crystal structure of wa352 from oryza sativa
42	<a href="#">c1ll4A_</a>	Alignment	not modelled	6.8	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> chitinase 1; <b>PDBTitle:</b> structure of c. immitis chitinase 1 complexed with2 allosamidin
43	<a href="#">c2mulA_</a>	Alignment	not modelled	6.8	28	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase huwe1; <b>PDBTitle:</b> solution structure of the ubm1 domain of human huwe1/arf-bp1
44	<a href="#">c5m32p_</a>	Alignment	not modelled	6.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> P; <b>PDB Molecule:</b> proteasome subunit alpha type-4; <b>PDBTitle:</b> human 26s proteasome in complex with oprozomib
45	<a href="#">d1w96c1</a>	Alignment	not modelled	6.6	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
46	<a href="#">c4qslC_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase
47	<a href="#">d2v4jc1</a>	Alignment	not modelled	6.4	43	<b>Fold:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Superfamily:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Family:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase
48	<a href="#">c3va7A_</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> klla0e08119p; <b>PDBTitle:</b> crystal structure of the kluyveromyces lactis urea carboxylase
49	<a href="#">c4pdtA_</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> mannose recognizing lectin; <b>PDBTitle:</b> japanese marasmius oreades lectin
50	<a href="#">c3brtC_</a>	Alignment	not modelled	6.2	80	<b>PDB header:</b> transferase/transcription <b>Chain:</b> C; <b>PDB Molecule:</b> inhibitor of nuclear factor kappa-b kinase subunit beta, <b>PDBTitle:</b> nemo/ikk association domain structure
51	<a href="#">d2g4ca1</a>	Alignment	not modelled	6.0	45	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
52	<a href="#">c3n6rK_</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> ligase <b>Chain:</b> K; <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
53	<a href="#">c4js0B_</a>	Alignment	not modelled	5.7	45	<b>PDB header:</b> signaling protein/signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> brain-specific angiogenesis inhibitor 1-associated protein <b>PDBTitle:</b> complex of cdc42 with the crib-pr domain of irsp53 <b>PDB header:</b> unknown function

54	<a href="#">c2kq5A_</a>	Alignment	not modelled	5.6	37	<b>Chain:</b> A: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
55	<a href="#">c2l5bA_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> activator of apoptosis harakiri; <b>PDBTitle:</b> solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
56	<a href="#">c2vxcA_</a>	Alignment	not modelled	5.5	23	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rhp9; <b>PDBTitle:</b> structure of the crb2-brct2 domain complex with phosphopeptide.
57	<a href="#">c1yx3A_</a>	Alignment	not modelled	5.4	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dsrc; <b>PDBTitle:</b> nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
58	<a href="#">c2dhyA_</a>	Alignment	not modelled	5.4	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
59	<a href="#">c1r7gA_</a>	Alignment	not modelled	5.1	30	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
60	<a href="#">c1r7cA_</a>	Alignment	not modelled	5.1	30	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 50% tfe)