
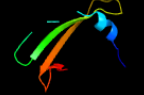


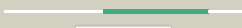






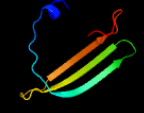



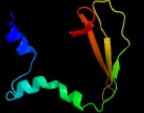

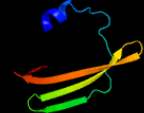

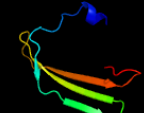





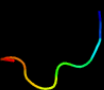







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2376c_cfp2_2655619_2656125
Date	Mon Aug 5 13:25:53 BST 2019
Unique Job ID	c042518f2de9896a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rsxA_</a>	 Alignment		59.0	19	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yoeb; <b>PDBTitle:</b> solution structure of iesa, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis
2	<a href="#">c3k7cC_</a>	 Alignment		49.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> putative ntf2-like transpeptidase; <b>PDBTitle:</b> crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
3	<a href="#">c3robC_</a>	 Alignment		45.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
4	<a href="#">c4iffC_</a>	 Alignment		45.6	19	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> fusion of phage phi29 gp7 protein and cell division protein <b>PDBTitle:</b> structural organization of ftsb, a transmembrane protein of the2 bacterial divisome
5	<a href="#">c1nohB_</a>	 Alignment		44.0	19	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> head morphogenesis protein; <b>PDBTitle:</b> the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
6	<a href="#">c6bjuD_</a>	 Alignment		41.2	12	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> atzh; <b>PDBTitle:</b> the structure of atzh: a little known member of the atrazine breakdown2 pathway
7	<a href="#">c3fkaD_</a>	 Alignment		38.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized ntf-2 like protein; <b>PDBTitle:</b> crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
8	<a href="#">c4fczB_</a>	 Alignment		37.3	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> toluene-tolerance protein; <b>PDBTitle:</b> crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
9	<a href="#">d2rcda1</a>	 Alignment		36.3	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
10	<a href="#">d2owpa1</a>	 Alignment		35.9	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
11	<a href="#">c4hzbE_</a>	 Alignment		35.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii

12	<a href="#">c5lfiA</a>	Alignment		28.6	20	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> lactococcin-a immunity protein; <b>PDBTitle:</b> lactococcin a immunity protein
13	<a href="#">d2o8ra1</a>	Alignment		28.5	16	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PPK N-terminal domain-like <b>Family:</b> PPK N-terminal domain-like
14	<a href="#">d1xdpa1</a>	Alignment		28.2	16	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> PPK N-terminal domain-like <b>Family:</b> PPK N-terminal domain-like
15	<a href="#">c4c1oA</a>	Alignment		24.9	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> geobacillus thermoglucosidasius gh family 52 xylosidase
16	<a href="#">d3b7ca1</a>	Alignment		22.2	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
17	<a href="#">d3b8la1</a>	Alignment		22.1	25	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
18	<a href="#">c3mtuE</a>	Alignment		21.2	22	<b>PDB header:</b> contractile protein <b>Chain:</b> E: <b>PDB Molecule:</b> capsid assembly scaffolding protein,tropomyosin alpha-1 <b>PDBTitle:</b> structure of the tropomyosin overlap complex from chicken smooth2 muscle
19	<a href="#">c2iabB</a>	Alignment		20.0	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
20	<a href="#">c4gb5A</a>	Alignment		19.6	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of kfla4162 protein from kribbella flavida
21	<a href="#">c5d9rA</a>	Alignment	not modelled	16.8	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein accumulation and replication of chloroplasts 6, <b>PDBTitle:</b> crystal structure of a conserved domain in the intermembrane space2 region of the plastid division protein arc6
22	<a href="#">d2a90a1</a>	Alignment	not modelled	16.4	22	<b>Fold:</b> WWE domain <b>Superfamily:</b> WWE domain <b>Family:</b> WWE domain
23	<a href="#">c3bb9D</a>	Alignment	not modelled	15.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative orphan protein; <b>PDBTitle:</b> crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
24	<a href="#">c5n02B</a>	Alignment	not modelled	15.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaconate coa-transferase family, subunit b; <b>PDBTitle:</b> crystal structure of the decarboxylase aiba/aibb c56s variant
25	<a href="#">d3ef8a1</a>	Alignment	not modelled	14.3	42	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
26	<a href="#">d2chca1</a>	Alignment	not modelled	14.2	25	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
27	<a href="#">d2rfra1</a>	Alignment	not modelled	13.9	38	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
28	<a href="#">d2fp7b1</a>	Alignment	not modelled	13.5	27	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases

						<b>Family:</b> Viral proteases
29	<a href="#">c3a76B_</a>	Alignment	not modelled	13.4	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina
30	<a href="#">d3ebya1</a>	Alignment	not modelled	11.1	33	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
31	<a href="#">c5wlgA_</a>	Alignment	not modelled	10.9	19	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7,microtubule- <b>PDBTitle:</b> crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1
32	<a href="#">d1befa_</a>	Alignment	not modelled	10.1	36	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
33	<a href="#">c3e90B_</a>	Alignment	not modelled	10.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ns3 protease; <b>PDBTitle:</b> west Nile virus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
34	<a href="#">c3lkwA_</a>	Alignment	not modelled	9.8	27	<b>PDB header:</b> viral protein,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of nonstructural protein 2b and <b>PDBTitle:</b> crystal structure of dengue virus 1 ns2b/ns3 protease active site2 mutant
35	<a href="#">c4m9mA_</a>	Alignment	not modelled	9.8	36	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> ns2b-ns3 protease; <b>PDBTitle:</b> ns2b-ns3 protease from dengue virus at ph 8.5
36	<a href="#">d2ljob1</a>	Alignment	not modelled	9.7	27	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
37	<a href="#">c2lmzA_</a>	Alignment	not modelled	9.7	18	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin im17a; <b>PDBTitle:</b> solution nmr structure of the novel conotoxin im23a from conus2 imperialis
38	<a href="#">c5lc0B_</a>	Alignment	not modelled	9.6	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ns2b-ns3 protease,ns2b-ns3 protease; <b>PDBTitle:</b> crystal structure of zika virus ns2b-ns3 protease in complex with a2 boronate inhibitor
39	<a href="#">c2yolA_</a>	Alignment	not modelled	9.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease subunit ns2b, serine protease ns3; <b>PDBTitle:</b> west Nile virus ns2b-ns3 protease in complex with 3,4-2 dichlorophenylacetyl-lys-lys-gcma
40	<a href="#">d3blza1</a>	Alignment	not modelled	8.5	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sba10622-like
41	<a href="#">c4z9nB_</a>	Alignment	not modelled	8.2	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
42	<a href="#">c4lehA_</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> bile acid 7-alpha dehydratase, baie; <b>PDBTitle:</b> crystal structure of a bile-acid 7-alpha dehydratase (closi_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution
43	<a href="#">c5ldrA_</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-d-galactosidase; <b>PDBTitle:</b> crystal structure of a cold-adapted dimeric beta-d-galactosidase from2 paracoccus sp. 32d strain in complex with galactose
44	<a href="#">c5dudB_</a>	Alignment	not modelled	8.1	33	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ybgj; <b>PDBTitle:</b> crystal structure of e. coli ybgjk
45	<a href="#">d2fomb1</a>	Alignment	not modelled	8.1	36	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
46	<a href="#">d2ba0g2</a>	Alignment	not modelled	8.0	23	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
47	<a href="#">d3stda_</a>	Alignment	not modelled	7.9	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
48	<a href="#">d1v74a_</a>	Alignment	not modelled	7.4	38	<b>Fold:</b> Colicin D/E5 nuclease domain <b>Superfamily:</b> Colicin D/E5 nuclease domain <b>Family:</b> Colicin D nuclease domain
49	<a href="#">c4dnyA_</a>	Alignment	not modelled	7.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metalloprotease stce; <b>PDBTitle:</b> crystal structure of enterohemorrhagic e. coli stce(132-251)
50	<a href="#">d1ldpa_</a>	Alignment	not modelled	7.2	17	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
51	<a href="#">c5u9oD_</a>	Alignment	not modelled	7.1	23	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> plastid division protein cdp1, chloroplastic,plastid <b>PDBTitle:</b> cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1
52	<a href="#">d2k0bx1</a>	Alignment	not modelled	7.1	57	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
53	<a href="#">c2iv8A_</a>	Alignment	not modelled	6.6	57	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-binding protein p62;

53	<a href="#">c2jy0A_</a>	Alignment	not modelled	6.8	37	<b>PDBTitle:</b> nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
54	<a href="#">d3e99a1</a>	Alignment	not modelled	6.6	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
55	<a href="#">c2jh9A_</a>	Alignment	not modelled	6.5	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vp4 core protein; <b>PDBTitle:</b> the structure of bluetongue virus vp4 reveals a2 multifunctional rna-capping production-line
56	<a href="#">d3d9ra1</a>	Alignment	not modelled	6.4	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
57	<a href="#">c3f7eB_</a>	Alignment	not modelled	5.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn- <b>PDBTitle:</b> msmeg_3380 f420 reductase
58	<a href="#">c6co6B_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable coa-transferase beta subunit; <b>PDBTitle:</b> crystal structure of rhodococcus jostii rha1 ipdab
59	<a href="#">c2phcB_</a>	Alignment	not modelled	5.3	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ph0987; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
60	<a href="#">d3eipa_</a>	Alignment	not modelled	5.3	40	<b>Fold:</b> FKBP-like <b>Superfamily:</b> Colicin E3 immunity protein <b>Family:</b> Colicin E3 immunity protein
61	<a href="#">d1poib_</a>	Alignment	not modelled	5.3	28	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase beta subunit-like
62	<a href="#">c4y4vB_</a>	Alignment	not modelled	5.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical secreted protein; <b>PDBTitle:</b> structure of helicobacter pylori csd6 in the d-ala-bound state
63	<a href="#">c5fv6B_</a>	Alignment	not modelled	5.1	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> kpflo11a1; <b>PDBTitle:</b> kpflo11 presents a novel member of the flo11 family with a2 unique recognition pattern for homophilic interactions
64	<a href="#">d2cu6a1</a>	Alignment	not modelled	5.1	37	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
65	<a href="#">c3dukD_</a>	Alignment	not modelled	5.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution