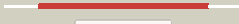



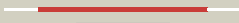




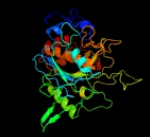














# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3449_(mycP4)_3869931_3871298
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	527fe4ca6de84530

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4j94A_</a>	 Alignment		100.0	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-anchored mycosin mycp1; <b>PDBTitle:</b> crystal structure of mycp1 from the esx-1 type vii secretion system
2	<a href="#">d1r6va_</a>	 Alignment		100.0	25	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
3	<a href="#">c4tr2A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like 1 serine protease; <b>PDBTitle:</b> crystal structure of pvsb1
4	<a href="#">c4kg7A_</a>	 Alignment		100.0	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase s8 and s53, subtilisin, kexin, sedolisin; <b>PDBTitle:</b> structure of mycp3 protease from the type vii (esx-3) secretion2 system.
5	<a href="#">c2oxaA_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular serine protease; <b>PDBTitle:</b> crystal structure of serine protease of aeromonas sobria
6	<a href="#">c3vtaB_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cucumisin; <b>PDBTitle:</b> crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l
7	<a href="#">c1r64A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kexin; <b>PDBTitle:</b> the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor
8	<a href="#">c1p8jB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> furin precursor; <b>PDBTitle:</b> crystal structure of the proprotein convertase furin
9	<a href="#">c1xf1A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> c5a peptidase; <b>PDBTitle:</b> structure of c5a peptidase- a key virulence factor from2 streptococcus
10	<a href="#">c3i74B_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> subtilisin-like protease; <b>PDBTitle:</b> crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
11	<a href="#">c5xyrA_</a>	 Alignment		100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> chemokine protease c; <b>PDBTitle:</b> crystal structure of a serine protease from streptococcus species

12	<a href="#">c5xxzB_</a>	Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> chemokine protease c; <b>PDBTitle:</b> crystal structure of a serine protease from streptococcus species
13	<a href="#">c3qfhE_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> epidermin leader peptide processing serine protease epip; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
14	<a href="#">c3t41B_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> epidermin leader peptide processing serine protease epip; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus
15	<a href="#">c3bpsA_</a>	Alignment		100.0	25	<b>PDB header:</b> hydrolase/lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> pcsk9:egf-a complex
16	<a href="#">c6mw4A_</a>	Alignment		100.0	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative germination-specific protease; <b>PDBTitle:</b> structure of pseudoprotease cspc from clostridioides difficile
17	<a href="#">c2iy9A_</a>	Alignment		100.0	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> suba; <b>PDBTitle:</b> crystal structure of the a-subunit of the ab5 toxin from e.2 coli
18	<a href="#">c4mzdA_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nisin leader peptide-processing serine protease nisp; <b>PDBTitle:</b> high resolution crystal structure of the nisin leader peptidase nisp2 from lactococcus lactis
19	<a href="#">c5vlpA_</a>	Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> pcsk9 complex with ldlr antagonist peptide and fab7g7
20	<a href="#">d1p8ja2</a>	Alignment		100.0	19	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
21	<a href="#">c1wmeA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease; <b>PDBTitle:</b> crystal structure of alkaline serine protease kp-43 from bacillus sp.2 ksm-kp43 (1.50 angstrom, 293 k)
22	<a href="#">c3afgA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like serine protease; <b>PDBTitle:</b> crystal structure of pron-tk-sp from thermococcus kodakaraensis
23	<a href="#">c2pmwB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
24	<a href="#">c4aktB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> thiazoline oxidase/subtilisin-like protease; <b>PDBTitle:</b> patg macrocyclase in complex with peptide
25	<a href="#">c4lvnA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase/inhibitor/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like serine protease; <b>PDBTitle:</b> crystal structure of psub1-prodomain-nimp.m7 fab complex
26	<a href="#">d2id4a2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
27	<a href="#">c3whiA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin e; <b>PDBTitle:</b> crystal structure of unautoprocessed form of is1-inserted pro-2 subtilisin e
28	<a href="#">c4i0wB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease cspb; <b>PDBTitle:</b> structure of the clostridium perfringens cspb protease

29	<a href="#">d1v6ca_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
30	<a href="#">c4zoqM_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> intracellular serine protease; <b>PDBTitle:</b> crystal structure of a lanthipeptide protease
31	<a href="#">d1bh6a_</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
32	<a href="#">d1meeaa_</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
33	<a href="#">c5vllA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> short pcsk9 delta-p' complex with peptide pep3
34	<a href="#">d1to2e_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
35	<a href="#">d1qcia_</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
36	<a href="#">d1dbia_</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
37	<a href="#">d1r0re_</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
38	<a href="#">d1thma_</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
39	<a href="#">c3vv3B_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> deseasin mcp-01; <b>PDBTitle:</b> crystal structure of deseasin mcp-01 from pseudoalteromonas sp. sm9913
40	<a href="#">d1wmdda2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
41	<a href="#">c5yl7A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pseudoalteromonas arctica pamc 21717; <b>PDBTitle:</b> proteases from pseudoalteromonas arctica pamc 21717 (pro21717)
42	<a href="#">d1gnsa_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
43	<a href="#">c2w2qA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> pcsk9-deltac d374h mutant bound to wt egf-a of ldlr
44	<a href="#">c2z2zA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tk-subtilisin precursor; <b>PDBTitle:</b> crystal structure of unautoprocessed form of tk-subtilisin soaked by2 10mm cacl2
45	<a href="#">c3f7oB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646)
46	<a href="#">c5z6oA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease; <b>PDBTitle:</b> crystal structure of penicillium cyclopium protease
47	<a href="#">c3lpcA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aprb2; <b>PDBTitle:</b> crystal structure of a subtilisin-like protease
48	<a href="#">c2z2yC_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> tk-subtilisin; <b>PDBTitle:</b> crystal structure of autoprocessed form of tk-subtilisin
49	<a href="#">c2b6nA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proteinase k; <b>PDBTitle:</b> the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
50	<a href="#">c4dztA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> aqualysin-1; <b>PDBTitle:</b> aqualysin i: the crystal structure of a serine protease from an2 extreme thermophile, thermus aquaticus yt-1
51	<a href="#">c1s2nB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular subtilisin-like serine proteinase; <b>PDBTitle:</b> crystal structure of a cold adapted subtilisin-like serine proteinase
52	<a href="#">d2ixta1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
53	<a href="#">c3lxuX_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> tripeptidyl-peptidase 2; <b>PDBTitle:</b> crystal structure of tripeptidyl peptidase 2 (tpp ii)
54	<a href="#">c4aksA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thiazoline oxidase/subtilisin-like protease; <b>PDBTitle:</b> patg macrocyclase domain
55	<a href="#">d2pwaa1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases

56	<a href="#">c4h6wB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-terminal cyanobactin protease; <b>PDBTitle:</b> structure of prenylagaramide maturation protease paga
57	<a href="#">d1sioa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Serine-carboxyl proteinase, SCP
58	<a href="#">c2x8jB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> intracellular subtilisin protease; <b>PDBTitle:</b> intracellular subtilisin precursor from b. clausii
59	<a href="#">c3zxxA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like protein; <b>PDBTitle:</b> structure of self-cleaved protease domain of pata
60	<a href="#">c6f9mA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> the lipyf-motif in an intracellular subtilisin protease is involved2 in inhibition
61	<a href="#">d1t1ga_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Serine-carboxyl proteinase, SCP
62	<a href="#">d1ga6a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Serine-carboxyl proteinase, SCP
63	<a href="#">c3zxyA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like protein; <b>PDBTitle:</b> structure of s218a mutant of the protease domain of pata
64	<a href="#">c1tleA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kumamolisin; <b>PDBTitle:</b> high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
65	<a href="#">c3ee6A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tripeptidyl-peptidase 1; <b>PDBTitle:</b> crystal structure analysis of tripeptidyl peptidase -i
66	<a href="#">c3edyA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tripeptidyl-peptidase 1; <b>PDBTitle:</b> crystal structure of the precursor form of human tripeptidyl-peptidase2 1
67	<a href="#">d1mzga_</a>	Alignment	not modelled	49.4	29	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
68	<a href="#">d1k78a2</a>	Alignment	not modelled	47.3	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
69	<a href="#">d1ni7a_</a>	Alignment	not modelled	36.7	24	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
70	<a href="#">d6paxa2</a>	Alignment	not modelled	36.5	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
71	<a href="#">c1wloA_</a>	Alignment	not modelled	25.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sufe protein; <b>PDBTitle:</b> solution structure of the hypothetical protein from thermus2 thermophilus hb8
72	<a href="#">d1b74a1</a>	Alignment	not modelled	13.4	30	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
73	<a href="#">c1b74A_</a>	Alignment	not modelled	13.2	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase from aquifex pyrophilus
74	<a href="#">c3uhfB_</a>	Alignment	not modelled	13.1	40	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
75	<a href="#">c2k27A_</a>	Alignment	not modelled	12.7	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
76	<a href="#">c3j21O_</a>	Alignment	not modelled	10.2	24	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 50s ribosomal protein l18p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
77	<a href="#">c3iz5O_</a>	Alignment	not modelled	9.5	25	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l5 (l18p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
78	<a href="#">c2jfzB_</a>	Alignment	not modelled	8.8	40	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
79	<a href="#">c2q6oB_</a>	Alignment	not modelled	8.1	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> sall-y70t with sam and cl
80	<a href="#">d2ga1a1</a>	Alignment	not modelled	7.9	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Alr1493-like
81	<a href="#">c2zbc_</a>	Alignment	not modelled	7.4	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from thermotoga2 maritima
82	<a href="#">d1ixsa_</a>	Alianment	not modelled	6.8	11	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> DNA helicase RuvA subunit, C-terminal domain

					<b>Family:</b> DNA helicase RuvA subunit, C-terminal domain
83	<a href="#">c4plaA_</a>	Alignment	not modelled	6.7	35
84	<a href="#">c2ph5A_</a>	Alignment	not modelled	5.7	16

**PDB header:**transferase,hydrolase  
**Chain:** A: **PDB Molecule:**chimera protein of phosphatidylinositol 4-kinase type 2-  
**PDBTitle:** crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp  
**PDB header:**transferase  
**Chain:** A: **PDB Molecule:**homospermidine synthase;  
**PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54