



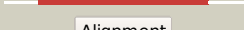

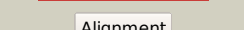

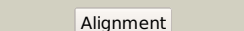





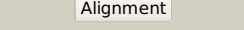

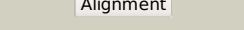

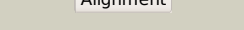

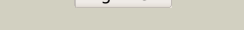









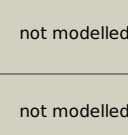


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0291_(mycP3)_354498_355883
Date	Tue Jul 23 14:50:35 BST 2019
Unique Job ID	815838cd9ed4fce5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j94A_	 Alignment		100.0	45	PDB header: hydrolase Chain: A: PDB Molecule: membrane-anchored mycosin mycp1; PDBTitle: crystal structure of mycp1 from the esx-1 type vii secretion system
2	d1r6va_	 Alignment		100.0	24	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
3	c4kg7A_	 Alignment		100.0	65	PDB header: hydrolase Chain: A: PDB Molecule: peptidase s8 and s53, subtilisin, kexin, sedolisin; PDBTitle: structure of mycp3 protease from the type vii (esx-3) secretion2 system.
4	c4tr2A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like 1 serine protease; PDBTitle: crystal structure of pvsb1
5	c2oxaA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: extracellular serine protease; PDBTitle: crystal structure of serine protease of aeromonas sobria
6	c3vtaB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l
7	c1r64A_	 Alignment		100.0	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kexin; PDBTitle: the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor
8	c3i74B_	 Alignment		100.0	32	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: subtilisin-like protease; PDBTitle: crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
9	c1p8jB_	 Alignment		100.0	22	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: furin precursor; PDBTitle: crystal structure of the proprotein convertase furin
10	c1xf1A_	 Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: c5a peptidase; PDBTitle: structure of c5a peptidase- a key virulence factor from2 streptococcus
11	c5xyrA_	 Alignment		100.0	29	PDB header: lyase Chain: A: PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species

12	c5xxzB_	Alignment		100.0	26	PDB header: lyase Chain: B: PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species
13	c3qfhE_	Alignment		100.0	28	PDB header: hydrolase Chain: E: PDB Molecule: epidermin leader peptide processing serine protease epip; PDBTitle: 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
14	c3t41B_	Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: epidermin leader peptide processing serine protease epip; PDBTitle: 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus
15	c6mw4A_	Alignment		100.0	24	PDB header: signaling protein Chain: A: PDB Molecule: putative germination-specific protease; PDBTitle: structure of pseudoprotease cspc from clostridioides difficile
16	c3bpsA_	Alignment		100.0	25	PDB header: hydrolase/lipid transport Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9:egf-a complex
17	c4mzdA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: nisin leader peptide-processing serine protease nisp; PDBTitle: high resolution crystal structure of the nisin leader peptidase nisp2 from lactococcus lactis
18	c1wmeA_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protease; PDBTitle: crystal structure of alkaline serine protease kp-43 from bacillus sp.2 ksm-kp43 (1.50 angstrom, 293 k)
19	c5vlpA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9 complex with ldlr antagonist peptide and fab7g7
20	d1p8ja2	Alignment		100.0	21	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
21	c4lvnA_	Alignment	not modelled	100.0	22	PDB header: hydrolase/inhibitor/immune system Chain: A: PDB Molecule: subtilisin-like serine protease; PDBTitle: crystal structure of pfsb1-prodomain-nimp.m7 fab complex
22	c4i0wB_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: protease cspb; PDBTitle: structure of the clostridium perfringens cspb protease
23	c4aktB_	Alignment	not modelled	100.0	28	PDB header: hydrolase/peptide Chain: B: PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocyclase in complex with peptide
24	c2iy9A_	Alignment	not modelled	100.0	28	PDB header: toxin Chain: A: PDB Molecule: suba; PDBTitle: crystal structure of the a-subunit of the ab5 toxin from e.2 coli
25	c2pmwB_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
26	d1v6ca_	Alignment	not modelled	100.0	35	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
27	c3whiA_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin e; PDBTitle: crystal structure of unautoprocessed form of is1-inserted pro-2 subtilisin e
28	d2id4a2	Alignment	not modelled	100.0	22	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases

29	d1bh6a_	Alignment	not modelled	100.0	34	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
30	c3afgA_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like serine protease; PDBTitle: crystal structure of pron-tk-sp from thermococcus kodakaraensis
31	d1meeA_	Alignment	not modelled	100.0	31	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
32	d1to2e_	Alignment	not modelled	100.0	33	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
33	c4zoqM_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: M: PDB Molecule: intracellular serine protease; PDBTitle: crystal structure of a lanthipeptide protease
34	c5vllA_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: short pcsk9 delta-p' complex with peptide pep3
35	d1gcia_	Alignment	not modelled	100.0	31	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
36	d1r0re_	Alignment	not modelled	100.0	31	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
37	d1dbia_	Alignment	not modelled	100.0	34	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
38	d1wmda2	Alignment	not modelled	100.0	23	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
39	c3vv3B_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: deseasin mcp-01; PDBTitle: crystal structure of deseasin mcp-01 from pseudoalteromonas sp. sm9913
40	c2z2zA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: tk-subtilisin precursor; PDBTitle: crystal structure of unautoprocessed form of tk-subtilisin soaked by2 10mm cacl2
41	d1thma_	Alignment	not modelled	100.0	34	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
42	d1gnsa_	Alignment	not modelled	100.0	29	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
43	c5yl7A_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: pseudoalteromonas arctica pamc 21717; PDBTitle: proteases from pseudoalteromonas arctica pamc 21717 (pro21717)
44	c2z2yC_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: tk-subtilisin; PDBTitle: crystal structure of autoprocessed form of tk-subtilisin
45	c2w2qA_	Alignment	not modelled	100.0	25	PDB header: hydrolase/receptor Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9-deltac d374h mutant bound to wt egf-a of ldlr
46	c3lpcA_	Alignment	not modelled	100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: aprb2; PDBTitle: crystal structure of a subtilisin-like protease
47	c5z6oA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: protease; PDBTitle: crystal structure of penicillium cyclopium protease
48	c3f7oB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646)
49	c3lxuX_	Alignment	not modelled	100.0	34	PDB header: hydrolase Chain: X: PDB Molecule: tripeptidyl-peptidase 2; PDBTitle: crystal structure of tripeptidyl peptidase 2 (tpp ii)
50	c1s2nB_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: extracellular subtilisin-like serine proteinase; PDBTitle: crystal structure of a cold adapted subtilisin-like serine proteinase
51	d1sioa_	Alignment	not modelled	100.0	18	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Serine-carboxyl proteinase, SCP
52	d2pwaa1	Alignment	not modelled	100.0	23	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
53	d2ixta1	Alignment	not modelled	100.0	26	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
54	c4h6wB_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: n-terminal cyanobactin protease; PDBTitle: structure of prenylagaramide maturation protease paga
55	c4aksA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocyclase domain

56	c4dztA	Alignment	not modelled	100.0	25	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: aqualysin-1; PDBTitle: aqualysin i: the crystal structure of a serine protease from an2 extreme thermophile, thermus aquaticus yt-1
57	c2x8jB	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: intracellular subtilisin protease; PDBTitle: intracellular subtilisin precursor from b. clausii
58	c2b6nA	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: proteinase k; PDBTitle: the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
59	d1t1ga	Alignment	not modelled	100.0	19	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Serine-carboxyl proteinase, SCP
60	c6f9mA	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: the lippy/f-motif in an intracellular subtilisin protease is involved2 in inhibition
61	c3zxxA	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of self-cleaved protease domain of pata
62	d1ga6a	Alignment	not modelled	100.0	18	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Serine-carboxyl proteinase, SCP
63	c3zxyA	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of s218a mutant of the protease domain of pata
64	ct1eA	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: kumamolisin; PDBTitle: high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
65	c3edyA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure of the precursor form of human tripeptidyl-peptidase2 1
66	c3ee6A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i
67	d1k78a2	Alignment	not modelled	75.1	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
68	d1mzga	Alignment	not modelled	74.9	32	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
69	d6paxa2	Alignment	not modelled	69.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
70	d1ni7a	Alignment	not modelled	63.6	24	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
71	c1wloA	Alignment	not modelled	46.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sufe protein; PDBTitle: solution structure of the hypothetical protein from thermus2 thermophilus hb8
72	c2k27A	Alignment	not modelled	32.9	26	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
73	d2ga1a1	Alignment	not modelled	18.7	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
74	c1b74A	Alignment	not modelled	13.8	40	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
75	d1b74a1	Alignment	not modelled	13.5	40	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
76	c3uhfB	Alignment	not modelled	13.1	30	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
77	d1pdnc	Alignment	not modelled	11.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
78	c2k9yA	Alignment	not modelled	10.3	22	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
79	c2k9yB	Alignment	not modelled	10.3	22	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
80	c5a49l	Alignment	not modelled	9.5	39	PDB header: protein binding Chain: l: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-222) of2 drosophila oskar in c222
81	d1ixsa	Alignment	not modelled	9.1	12	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
82	c2jfzB	Alignment	not modelled	9.1	30	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate

					racemase2 in complex with d-glutamate and an inhibitor
83	c6h3aB_	Alignment	not modelled	8.4	9 PDB header: ligase Chain: B: PDB Molecule: swi/snf-related matrix-associated actin-dependent regulator PDBTitle: crystal structure of the kap1 rbcc domain in complex with the smarcad12 cue1 domain.
84	c4plaA_	Alignment	not modelled	8.3	35 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
85	d1s6la1	Alignment	not modelled	7.9	23 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
86	c3j21O_	Alignment	not modelled	7.1	27 PDB header: ribosome Chain: O: PDB Molecule: 50s ribosomal protein l18p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
87	d1k47a1	Alignment	not modelled	6.7	17 Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
88	c2zbvC_	Alignment	not modelled	5.8	19 PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from thermotoga2 maritima
89	c6paxA_	Alignment	not modelled	5.7	24 PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
90	c2q6oB_	Alignment	not modelled	5.5	16 PDB header: biosynthetic protein Chain: B: PDB Molecule: hypothetical protein; PDBTitle: sall-y70t with sam and cl
91	c3ut2B_	Alignment	not modelled	5.4	13 PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase 2; PDBTitle: crystal structure of fungal magkatg2
92	d2pmra1	Alignment	not modelled	5.3	25 Fold: immunoglobulin/albumin-binding domain-like Superfamily: AF1782-like Family: AF1782-like
93	c3sjrB_	Alignment	not modelled	5.1	21 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unkwon function protein cv_1783 from2 chromobacterium violaceum atcc 12472