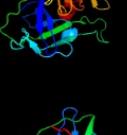
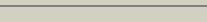
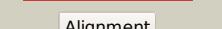
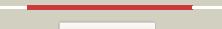
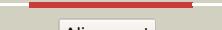
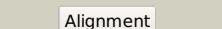
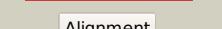
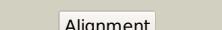
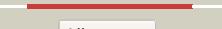
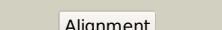
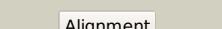
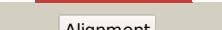
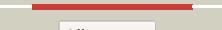


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1815 (-) _2057535_2058200
Date	Fri Aug 2 13:30:42 BST 2019
Unique Job ID	03946589de05d7a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mrtA</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lytic endopeptidase preproenzyme; <b>PDBTitle:</b> crystal structure of l5 protease lysobacter sp. xl1
2	<a href="#">d2h5ca1</a>	 Alignment		100.0	24	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
3	<a href="#">c2pfeA</a>	 Alignment		99.9	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline serine protease; <b>PDBTitle:</b> crystal structure of thermobifida fusca protease a (tfpa)
4	<a href="#">d2sgaa</a>	 Alignment		99.9	26	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
5	<a href="#">d2qaaa1</a>	 Alignment		99.9	23	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
6	<a href="#">c2ouaA</a>	 Alignment		99.9	22	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of nocardiosis protease (napase)
7	<a href="#">d1hpga</a>	 Alignment		99.9	27	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
8	<a href="#">c2ea3A</a>	 Alignment		99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chymotrypsin; <b>PDBTitle:</b> crystal structure of cellulomonas bogoriensis chymotrypsin
9	<a href="#">d2sfaa</a>	 Alignment		99.9	24	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
10	<a href="#">d1agja</a>	 Alignment		99.3	13	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
11	<a href="#">c4inkA</a>	 Alignment		99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease spld; <b>PDBTitle:</b> crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution

12	<a href="#">c6e0uB</a>			99.1	12	<b>PDB header:</b> hydrolase, toxin <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> staphylococcus pseudintermedius exfoliative toxin exi
13	<a href="#">c5c2zA</a>			99.1	17	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> exfoliative toxin d2; <b>PDBTitle:</b> molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
14	<a href="#">c2w7uC</a>			99.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> serine protease spla; <b>PDBTitle:</b> spla serine protease of staphylococcus aureus (2.4a)
15	<a href="#">c3cp7B</a>			99.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline serine protease al20; <b>PDBTitle:</b> crystal structure of a thermostable serine protease al20 from2 extremophilic microorganism
16	<a href="#">c1zyoA</a>			98.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
17	<a href="#">d1qtfA</a>			98.9	13	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
18	<a href="#">d2o8la1</a>			98.8	12	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
19	<a href="#">c2o8IA</a>			98.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v8 protease; <b>PDBTitle:</b> structure of v8 protease from staphylococcus aureus
20	<a href="#">c1qy6A</a>			98.8	12	<b>PDB header:</b> protease <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> strucute of v8 protease from staphylococcus aureus
21	<a href="#">c5hmaA</a>		not modelled	98.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trypsin-like serine protease; <b>PDBTitle:</b> crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
22	<a href="#">d1lvmb</a>		not modelled	98.8	14	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
23	<a href="#">c4jcnA</a>		not modelled	98.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl endopeptidase; <b>PDBTitle:</b> structure of esp, serine protease from staphylococcus epidermidis
24	<a href="#">d1arba</a>		not modelled	98.7	22	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
25	<a href="#">d1p3ca</a>		not modelled	98.7	17	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
26	<a href="#">d2z9ia2</a>		not modelled	98.7	18	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
27	<a href="#">c4ic5B</a>		not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 5, chloroplastic; <b>PDBTitle:</b> crystal structure of deg5
28	<a href="#">c2vidA</a>		not modelled	98.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease splb; <b>PDBTitle:</b> serine protease splb from staphylococcus aureus at 1.8a resolution
29	<a href="#">c3wv8A</a>		not modelled	98.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease;

29	<a href="#">c5wyom</a>	Alignment	not modelled	98.0	10	<b>PDBTitle:</b> crystal structure of protease anisep from arthrobacter nicotinovorans
30	<a href="#">c5ilaA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> deg9 protease domain
31	<a href="#">c3mmgB</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> viral protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear inclusion protein a; <b>PDBTitle:</b> crystal structure of tobacco vein mottling virus protease
32	<a href="#">c2z9iB</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease pepd; <b>PDBTitle:</b> crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
33	<a href="#">c1wczA</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl endopeptidase; <b>PDBTitle:</b> crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
34	<a href="#">d1g31a</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
35	<a href="#">c4ic6A</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 8, chloroplastic; <b>PDBTitle:</b> crystal structure of deg8
36	<a href="#">c3nziA</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> substrate induced remodeling of the active site regulates htra12 activity
37	<a href="#">c5mm8A</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease sple; <b>PDBTitle:</b> atomic resolution structure of sple protease from staphylococcus2 aureus
38	<a href="#">c3k6zA</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible membrane-associated serine protease; <b>PDBTitle:</b> crystal structure of rv3671c protease, inactive form
39	<a href="#">c5y28B</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic serine endoprotease degp-like; <b>PDBTitle:</b> crystal structure of h. pylori htra with pdz2 deletion
40	<a href="#">d2qf3a1</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
41	<a href="#">c2rcel</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> dfp modified degs delta pdz
42	<a href="#">c2w5eB</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative serine protease; <b>PDBTitle:</b> structural and biochemical analysis of human pathogenic2 astrovirus serine protease at 2.0 angstrom resolution
43	<a href="#">c3nwuB</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> substrate induced remodeling of the active site regulates htra12 activity
44	<a href="#">d1ky9a2</a>	Alignment	not modelled	98.3	15	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
45	<a href="#">c6fezB</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease domain; <b>PDBTitle:</b> ryegrass mottle virus protease domain
46	<a href="#">c4flnB</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 2, chloroplastic; <b>PDBTitle:</b> crystal structure of plant protease deg2
47	<a href="#">c4a8al</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase/hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> periplasmic ph-dependent serine endoprotease degq; <b>PDBTitle:</b> asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
48	<a href="#">c2as9B</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> functional and structural characterization of spl proteases from2 staphylococcus aureus
49	<a href="#">c2f83A</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor xi; <b>PDBTitle:</b> crystal structure at 2.9 angstroms resolution of human plasma2 coagulation factor xi zymogen
50	<a href="#">d1lcya2</a>	Alignment	not modelled	98.2	16	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
51	<a href="#">c3f1sB</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> hydrolase inhibitor/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> vitamin k-dependent protein z; <b>PDBTitle:</b> crystal structure of protein z complexed with protein z-dependent2 inhibitor
52	<a href="#">c2zleB</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> cryo-em structure of degp12/omp
53	<a href="#">d1cqqa</a>	Alignment	not modelled	98.2	14	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
54	<a href="#">c2r3yC</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> C: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of the degs protease in complex with the2 ywf activating peptide
55	<a href="#">d1l1ja</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases

56	<a href="#">c3qo6B</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 1, chloroplastic; <b>PDBTitle:</b> crystal structure analysis of the plant protease deg1
57	<a href="#">c5b6IA</a>	Alignment	not modelled	98.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine protease hhoa; <b>PDBTitle:</b> structure of deg protease hhoa from <i>synechocystis sp. pcc 6803</i>
58	<a href="#">c4bx5A</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> factor x-like protease; <b>PDBTitle:</b> crystal structure of the prothrombinase complex from the2 venom of <i>pseudonaja textilis</i>
59	<a href="#">c3stiC</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease degq; <b>PDBTitle:</b> crystal structure of the protease + pdz1 domain of degq from2 <i>escherichia coli</i>
60	<a href="#">c6esoA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> plasma kallikrein; <b>PDBTitle:</b> full length human plasma kallikrein with inhibitor
61	<a href="#">c5y2dA</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic serine endopeptidase degp-like; <b>PDBTitle:</b> crystal structure of <i>h. pylori</i> htra
62	<a href="#">c2xrcD</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> human complement factor i; <b>PDBTitle:</b> human complement factor i
63	<a href="#">c5xdyA</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein htra; <b>PDBTitle:</b> crystal structure of htral from <i>mycobacterium tuberculosis</i>
64	<a href="#">c1ky9A</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> crystal structure of degp (htra)
65	<a href="#">c4o03A</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prothrombin; <b>PDBTitle:</b> crystal structure of ca2+ bound prothrombin deletion mutant residues2 146-167
66	<a href="#">c4durA</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> plasminogen; <b>PDBTitle:</b> the x-ray crystal structure of full-length type ii human plasminogen
67	<a href="#">c1lcyA</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> htral serine protease; <b>PDBTitle:</b> crystal structure of the mitochondrial serine protease htral
68	<a href="#">c2i6sA</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement c2a fragment; <b>PDBTitle:</b> complement component c2a
69	<a href="#">c1elvA</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement c1s component; <b>PDBTitle:</b> crystal structure of the catalytic domain of human complement c1s2 protease
70	<a href="#">c4ri0A</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htral3; <b>PDBTitle:</b> serine protease htral3, mutationally inactivated
71	<a href="#">c2ok5A</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement factor b; <b>PDBTitle:</b> human complement factor b
72	<a href="#">c5il9A</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> crystal structure of deg9
73	<a href="#">c4lk4A</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vesb protease; <b>PDBTitle:</b> structure of <i>vibrio cholerae</i> vesb protease
74	<a href="#">c3otpF</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> crystal structure of the degp dodecamer with a model substrate
75	<a href="#">c3h5cB</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> hydrolase inhibitor/blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> vitamin k-dependent protein z; <b>PDBTitle:</b> x-ray structure of protein z-protein z inhibitor complex
76	<a href="#">c3pv4A</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> degq; <b>PDBTitle:</b> structure of <i>legionella fallonii</i> degq (delta-pdz2 variant)
77	<a href="#">c3pv5B</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> degq; <b>PDBTitle:</b> structure of <i>legionella fallonii</i> degq (n189g/p190g variant)
78	<a href="#">c1rs0A</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement factor b; <b>PDBTitle:</b> crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
79	<a href="#">c6bqmA</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease vesc; <b>PDBTitle:</b> secreted serine protease vesc from <i>vibrio cholerae</i>
80	<a href="#">c3stiC</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease degq; <b>PDBTitle:</b> crystal structure of the protease domain of degq from <i>escherichia coli</i>
81	<a href="#">c1zjkA</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan-binding lectin serine protease 2; <b>PDBTitle:</b> crystal structure of the zymogen catalytic region of human masp-2
82	<a href="#">c2b9IA</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> immune system/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> prophenoloxidase activating factor; <b>PDBTitle:</b> crystal structure of prophenoloxidase activating factor-ii

						from the2 beetle holotrichia diomphalia
83	<a href="#">c4kkdB_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mannan-binding lectin serine protease 1; <b>PDBTitle:</b> the x-ray crystal structure of mannose-binding lectin-associated2 serine proteinase-3 reveals the structural basis for enzyme3 inactivity associated with the 3mc syndrome
84	<a href="#">c1gpzB_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> complement c1r component; <b>PDBTitle:</b> the crystal structure of the zymogen catalytic domain of complement2 protease c1r
85	<a href="#">d1mbma_</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
86	<a href="#">d1ptyd_</a>	Alignment	not modelled	97.5	23	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
87	<a href="#">c4j1yA_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> complement c1s subcomponent; <b>PDBTitle:</b> the x-ray crystal structure of human complement protease c1s zymogen
88	<a href="#">c2asub_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hepatocyte growth factor-like protein; <b>PDBTitle:</b> crystal structure of the beta-chain of hgfl/msp
89	<a href="#">c1md7A_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> c1r complement serine protease; <b>PDBTitle:</b> monomeric structure of the zymogen of complement protease2 c1r
90	<a href="#">c1ybwa_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor activator precursor; <b>PDBTitle:</b> protease domain of hgfa with no inhibitor
91	<a href="#">c1z8gA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease hepsin; <b>PDBTitle:</b> crystal structure of the extracellular region of the transmembrane2 serine protease hepsin with covalently bound preferred substrate.
92	<a href="#">c4f4oC_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> oxygen transport/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> haptoglobin; <b>PDBTitle:</b> structure of the haptoglobin-haemoglobin complex
93	<a href="#">d1mzaa_</a>	Alignment	not modelled	97.4	20	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
94	<a href="#">c3gdsA_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with drndgnvyyf peptide
95	<a href="#">c1q3xA_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan-binding lectin serine protease 2; <b>PDBTitle:</b> crystal structure of the catalytic region of human masp-2
96	<a href="#">d1eaxa_</a>	Alignment	not modelled	97.3	15	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
97	<a href="#">c1z71A_</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> thrombin; <b>PDBTitle:</b> thrombin and p2 pyridine n-oxide inhibitor complex structure
98	<a href="#">d1l1na_</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
99	<a href="#">c1w0zU_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> U: <b>PDB Molecule:</b> urokinase-type plasminogen activator; <b>PDBTitle:</b> urokinase type plasminogen activator
100	<a href="#">c2vntE_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> urokinase-type plasminogen activator; <b>PDBTitle:</b> urokinase-type plasminogen activator inhibitor complex with2 a 1-(7-sulphoamidoisoquinoliny)guanidine
101	<a href="#">d1biao_</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
102	<a href="#">c3faoA_</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein; <b>PDBTitle:</b> crystal structure of s118a mutant 3clsp of prrv
103	<a href="#">c3e16B_</a>	Alignment	not modelled	96.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prostasin; <b>PDBTitle:</b> x-ray structure of human prostasin in complex with benzoxazole warhead2 peptidomimic, lysine in p3
104	<a href="#">d3rp2a_</a>	Alignment	not modelled	96.7	15	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
105	<a href="#">d1a5ia_</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
106	<a href="#">d1rfna_</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
107	<a href="#">c4igdA_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan-binding lectin serine protease 1; <b>PDBTitle:</b> crystal structure of the zymogen catalytic region of human masp-1
108	<a href="#">c1fizA_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-acrosin heavy chain; <b>PDBTitle:</b> three dimensional structure of beta-acrosin from boar spermatozoa

109	<a href="#">c3h7oB</a>		Alignment	not modelled	96.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> group 3 allergen smipp-s yv6023a04; <b>PDBTitle:</b> crystal structure of scabies mite inactivated protease parologue s-i12 (smipp-s-i1)
110	<a href="#">c3h7tB</a>		Alignment	not modelled	96.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> group 3 allergen smipp-s yvt004a06; <b>PDBTitle:</b> crystal structure of scabies mite inactivated protease parologue s-d12 (smipp-s-d1)
111	<a href="#">c3fzzB</a>		Alignment	not modelled	96.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> granzyme c; <b>PDBTitle:</b> structure of grc
112	<a href="#">c1ghwH</a>		Alignment	not modelled	96.1	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> thrombin; <b>PDBTitle:</b> a novel serine protease inhibition motif involving a multi-centered2 short hydrogen bonding network at the active site
113	<a href="#">d1gdna</a>		Alignment	not modelled	96.1	19	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
114	<a href="#">d1fi8a</a>		Alignment	not modelled	96.0	17	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
115	<a href="#">c4xe4A</a>		Alignment	not modelled	96.0	17	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> coagulation factor xii; <b>PDBTitle:</b> coagulation factor xii protease domain crystal structure
116	<a href="#">c3s9cA</a>		Alignment	not modelled	96.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vipera russelli proteinase rvv-v gamma; <b>PDBTitle:</b> russell's viper venom serine proteinase, rvv-v in complex with the2 fragment (residues 1533-1546) of human factor v
117	<a href="#">d1gvkb</a>		Alignment	not modelled	95.9	16	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
118	<a href="#">c5xrfA</a>		Alignment	not modelled	95.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> snake venom serine protease da-36; <b>PDBTitle:</b> crystal structure of da-36, a thrombin-like enzyme from2 deinagkistrodon acutus
119	<a href="#">d1si5h</a>		Alignment	not modelled	95.8	16	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Eukaryotic proteases
120	<a href="#">d1os8a</a>		Alignment	not modelled	95.8	16	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases