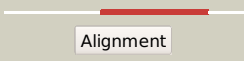

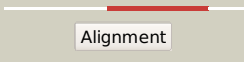

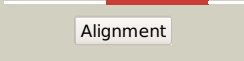

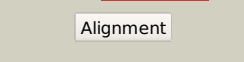

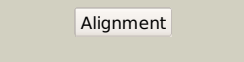

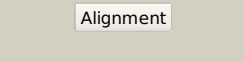

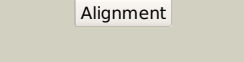

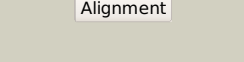

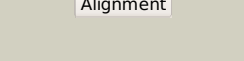

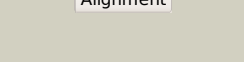

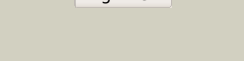



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3671c_(-)_4112500_4113693
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	a887fb1c89c06db9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k6zA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
2	c5il9A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9
3	c4flnB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2
4	c4a8aI_	 Alignment		100.0	23	PDB header: hydrolase/hydrolase Chain: I: PDB Molecule: periplasmic ph-dependent serine endoprotease degg; PDBTitle: asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
5	c2zleB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: protease do; PDBTitle: cryo-em structure of degp12/omp
6	c1ky9A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
7	c3pv5B_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (n189g/p190g variant)
8	c3otpF_	 Alignment		100.0	25	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
9	d1ky9a2	 Alignment		100.0	25	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
10	c5y28B_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
11	c2r3yC_	 Alignment		100.0	22	PDB header: hydrolase/hydrolase activator Chain: C: PDB Molecule: protease degs; PDBTitle: crystal structure of the degs protease in complex with the2 ywf activating peptide

12	c3stjC_	Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
13	c2z9iB_	Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: probable serine protease pepd; PDBTitle: crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
14	c4ic6A_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
15	c3qo6B_	Alignment		100.0	29	PDB header: photosynthesis Chain: B: PDB Molecule: protease do-like 1, chloroplastic; PDBTitle: crystal structure analysis of the plant protease deg1
16	c2rcel_	Alignment		100.0	22	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
17	c3gdsA_	Alignment		100.0	23	PDB header: hydrolase/hydrolase activator Chain: A: PDB Molecule: protease degs; PDBTitle: crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with dnrdgnvyvf peptide
18	d1l1ja_	Alignment		100.0	28	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
19	c3nziA_	Alignment		100.0	28	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
20	c5y2dA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra
21	c1lcyA_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2
22	c5xdyA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis
23	d2qf3a1	Alignment	not modelled	100.0	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
24	c5hmaA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like serine protease; PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
25	c3nwuB_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
26	d2z9ia2	Alignment	not modelled	100.0	26	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
27	c4ri0A_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated
28	c3stiC_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli
						PDB header: hydrolase

29	c5b6IA_	Alignment	not modelled	100.0	28	Chain: A: PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803
30	c3pv4A_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant)
31	d1cya2	Alignment	not modelled	100.0	29	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
32	c4ic5B_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
33	c5ilaA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
34	c3mmgB_	Alignment	not modelled	99.9	13	PDB header: viral protein, hydrolase Chain: B: PDB Molecule: nuclear inclusion protein a; PDBTitle: crystal structure of tobacco vein mottling virus protease
35	c5jykB_	Alignment	not modelled	99.9	29	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k
36	c2w5eB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: putative serine protease; PDBTitle: structural and biochemical analysis of human pathogenic2 astrovirus serine protease at 2.0 angstrom resolution
37	c1zyoA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
38	c4inkA_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: serine protease spld; PDBTitle: crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution
39	d1q31a_	Alignment	not modelled	99.9	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
40	d1qtfa_	Alignment	not modelled	99.9	22	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
41	d1lvmb_	Alignment	not modelled	99.9	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
42	d1agja_	Alignment	not modelled	99.9	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
43	c5c2zA_	Alignment	not modelled	99.9	23	PDB header: toxin Chain: A: PDB Molecule: exfoliative toxin d2; PDBTitle: molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
44	c5mm8A_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: serine protease sple; PDBTitle: atomic resolution structure of sple protease from staphylococcus2 aureus
45	c6e0uB_	Alignment	not modelled	99.9	24	PDB header: hydrolase, toxin Chain: B: PDB Molecule: serine protease; PDBTitle: staphylococcus pseudintermedius exfoliative toxin exi
46	c2vidA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: serine protease splb; PDBTitle: serine protease splb from staphylococcus aureus at 1.8a resolution
47	c2w7uC_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: C: PDB Molecule: serine protease spla; PDBTitle: spla serine protease of staphylococcus aureus (2.4a)
48	c2as9B_	Alignment	not modelled	99.8	27	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus
49	c6fezB_	Alignment	not modelled	99.8	16	PDB header: viral protein Chain: B: PDB Molecule: serine protease domain; PDBTitle: ryegrass mottle virus protease domain
50	d1cqqa_	Alignment	not modelled	99.8	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
51	c5mrtA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: lytic endopeptidase preproenzyme; PDBTitle: crystal structure of I5 protease lysobacter sp. x11
52	c4jcnA_	Alignment	not modelled	99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: structure of esp, serine protease from staphylococcus epidermidis
53	c2b0fA_	Alignment	not modelled	99.7	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: picornain 3c (protease 3c) (p3c); PDBTitle: nmr structure of the human rhinovirus 3c protease (serotype 14) with2 covalently bound ace-lealfq-ethylpropionate inhibitor
54	d1l1na_	Alignment	not modelled	99.7	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
55	c1wcza_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus

56	d2h5ca1	Alignment	not modelled	99.7	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
57	d2o8la1	Alignment	not modelled	99.7	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
58	c2o8IA	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: v8 protease; PDBTitle: structure of v8 protease from staphylococcus aureus
59	c1qy6A	Alignment	not modelled	99.7	21	PDB header: protease Chain: A: PDB Molecule: serine protease; PDBTitle: structue of v8 protease from staphylococcus aureus
60	c5y09B	Alignment	not modelled	99.7	25	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9 at 295 k
61	d2qaaa1	Alignment	not modelled	99.6	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
62	c2ouaA	Alignment	not modelled	99.6	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of nocardiosis protease (napase)
63	d2sgaa	Alignment	not modelled	99.6	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
64	d2sfaa	Alignment	not modelled	99.6	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
65	c2ea3A	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: A: PDB Molecule: chymotrypsin; PDBTitle: crystal structure of cellulomonas bogoriensis chymotrypsin
66	d1p3ca	Alignment	not modelled	99.5	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
67	c2pfeA	Alignment	not modelled	99.5	23	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: alkaline serine protease; PDBTitle: crystal structure of thermobifida fusca protease a (tfpa)
68	d1hpga	Alignment	not modelled	99.5	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
69	d1arba	Alignment	not modelled	99.5	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
70	c3zv8A	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: 3c protease; PDBTitle: crystal structure of 3c protease of enterovirus 68
71	c3wy8A	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of protease anisep from arthrobacter nicotinovorans
72	c3cp7B	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: B: PDB Molecule: alkaline serine protease al20; PDBTitle: crystal structure of a thermostable serine protease al20 from2 extremophilic microorganism
73	c4lk4A	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: A: PDB Molecule: vesb protease; PDBTitle: structure of vibrio cholerae vesb protease
74	c6bqmA	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: serine protease vesc; PDBTitle: secreted serine protease vesc from vibrio cholerae
75	c6esoA	Alignment	not modelled	98.9	18	PDB header: blood clotting Chain: A: PDB Molecule: plasma kallikrein; PDBTitle: full length human plasma kallikrein with inhibitor
76	c3osyA	Alignment	not modelled	98.7	13	PDB header: hydrolase Chain: A: PDB Molecule: 3c protease; PDBTitle: human enterovirus 71 3c protease
77	c4durA	Alignment	not modelled	98.7	24	PDB header: hydrolase Chain: A: PDB Molecule: plasminogen; PDBTitle: the x-ray crystal structure of full-length type ii human plasminogen
78	c2ijd1	Alignment	not modelled	98.7	15	PDB header: hydrolase, transferase Chain: 1: PDB Molecule: picornain 3c, rna-directed rna polymerase; PDBTitle: crystal structure of the poliovirus precursor protein 3cd
79	c3f1sB	Alignment	not modelled	98.6	15	PDB header: hydrolase inhibitor/hydrolase Chain: B: PDB Molecule: vitamin k-dependent protein z; PDBTitle: crystal structure of protein z complexed with protein z-dependent2 inhibitor
80	c2xrcD	Alignment	not modelled	98.6	22	PDB header: immune system Chain: D: PDB Molecule: human complement factor i; PDBTitle: human complement factor i
81	c2f83A	Alignment	not modelled	98.6	21	PDB header: hydrolase Chain: A: PDB Molecule: coagulation factor xi; PDBTitle: crystal structure at 2.9 angstroms resolution of human plasma2 coagulation factor xi zymogen
82	d1mzaa	Alignment	not modelled	98.5	22	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
						PDB header: hydrolase

83	c3h7tB_	Alignment	not modelled	98.5	16	Chain: B; PDB Molecule: group 3 allergen smipp-s yv004a06; PDBTitle: crystal structure of scabies mite inactivated protease paralogue s-d12 (smipp-s-d1)
84	c5to3B_	Alignment	not modelled	98.4	21	PDB header: hydrolase Chain: B; PDB Molecule: prothrombin,thrombomodulin; PDBTitle: crystal structure of thrombin mutant w215a/e217a fused to egf456 of2 thrombomodulin via a 31-residue linker and bound to ppack
85	c1zjkA_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: A; PDB Molecule: mannan-binding lectin serine protease 2; PDBTitle: crystal structure of the zymogen catalytic region of human masp-2
86	c4o03A_	Alignment	not modelled	98.4	21	PDB header: hydrolase Chain: A; PDB Molecule: prothrombin; PDBTitle: crystal structure of ca2+ bound prothrombin deletion mutant residues2 146-167
87	c4kkdB_	Alignment	not modelled	98.4	23	PDB header: hydrolase Chain: B; PDB Molecule: mannan-binding lectin serine protease 1; PDBTitle: the x-ray crystal structure of mannan-binding lectin-associated2 serine proteinase-3 reveals the structural basis for enzyme3 inactivity associated with the 3mc syndrome
88	d1npma_	Alignment	not modelled	98.3	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
89	c1elvA_	Alignment	not modelled	98.3	21	PDB header: hydrolase Chain: A; PDB Molecule: complement c1s component; PDBTitle: crystal structure of the catalytic domain of human complement c1s2 protease
90	d1mbma_	Alignment	not modelled	98.3	26	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
91	c3h5cB_	Alignment	not modelled	98.3	14	PDB header: hydrolase inhibitor/blood clotting Chain: B; PDB Molecule: vitamin k-dependent protein z; PDBTitle: x-ray structure of protein z-protein z inhibitor complex
92	c4jlyA_	Alignment	not modelled	98.2	21	PDB header: hydrolase Chain: A; PDB Molecule: complement c1s subcomponent; PDBTitle: the x-ray crystal structure of human complement protease c1s zymogen
93	d1rjxb_	Alignment	not modelled	98.2	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
94	c4iqdA_	Alignment	not modelled	98.2	20	PDB header: hydrolase Chain: A; PDB Molecule: mannan-binding lectin serine protease 1; PDBTitle: crystal structure of the zymogen catalytic region of human masp-1
95	c2b9lA_	Alignment	not modelled	98.2	18	PDB header: immune system/protein binding Chain: A; PDB Molecule: prophenoloxidase activating factor; PDBTitle: crystal structure of prophenoloxidase activating factor-ii from the2 beetle holotrichia diomphalia
96	d1pytd_	Alignment	not modelled	98.2	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
97	c2asuB_	Alignment	not modelled	98.2	13	PDB header: hydrolase Chain: B; PDB Molecule: hepatocyte growth factor-like protein; PDBTitle: crystal structure of the beta-chain of hgfl/msp
98	c3nxaA_	Alignment	not modelled	98.1	23	PDB header: hydrolase Chain: A; PDB Molecule: prethrombin-1; PDBTitle: crystal structure of human prethrombin-1
99	c2ok5A_	Alignment	not modelled	98.1	25	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: human complement factor b
100	d1gvza_	Alignment	not modelled	98.1	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
101	c3h7oB_	Alignment	not modelled	98.1	25	PDB header: hydrolase Chain: B; PDB Molecule: group 3 allergen smipp-s yv6023a04; PDBTitle: crystal structure of scabies mite inactivated protease paralogue s-i12 (smipp-s-i1)
102	c2i6sA_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A; PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
103	c1z8gA_	Alignment	not modelled	98.1	22	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: serine protease hepsin; PDBTitle: crystal structure of the extracellular region of the transmembrane2 serine protease hepsin with covalently bound preferred substrate.
104	c3faoA_	Alignment	not modelled	98.1	31	PDB header: hydrolase Chain: A; PDB Molecule: non-structural protein; PDBTitle: crystal structure of s118a mutant 3clsp of prrsv
105	d2h6ma1	Alignment	not modelled	98.1	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
106	c1rs0A_	Alignment	not modelled	98.0	22	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
107	d3rp2a_	Alignment	not modelled	97.9	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
108	d1sgfa_	Alignment	not modelled	97.9	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
						PDB header: hydrolase

109	c5jxpA_	Alignment	not modelled	97.9	18	Chain: A; PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
110	c5jxfA_	Alignment	not modelled	97.9	26	PDB header: hydrolase Chain: A; PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
111	d1bioa_	Alignment	not modelled	97.9	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
112	c3woIB_	Alignment	not modelled	97.9	36	PDB header: hydrolase Chain: B; PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
113	d1gdna_	Alignment	not modelled	97.9	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
114	c4hzhB_	Alignment	not modelled	97.9	21	PDB header: hydrolase Chain: B; PDB Molecule: prothrombin; PDBTitle: structure of recombinant gla-domainless prothrombin mutant s525a
115	d2bhga1	Alignment	not modelled	97.9	12	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
116	c1w0zU_	Alignment	not modelled	97.9	19	PDB header: hydrolase Chain: U; PDB Molecule: urokinase-type plasminogen activator; PDBTitle: urokinase type plasminogen activator
117	d1z8ga1	Alignment	not modelled	97.9	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
118	c4ashB_	Alignment	not modelled	97.9	20	PDB header: hydrolase Chain: B; PDB Molecule: ns6 protease; PDBTitle: crystal structure of the ns6 protease from murine norovirus 1
119	c1z71A_	Alignment	not modelled	97.9	18	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: thrombin; PDBTitle: thrombin and p2 pyridine n-oxide inhibitor complex structure
120	c3s9cA_	Alignment	not modelled	97.9	19	PDB header: hydrolase Chain: A; PDB Molecule: vipera russelli proteinase rvv-v gamma; PDBTitle: russell's viper venom serine proteinase, rvv-v in complex with the2 fragment (residues 1533-1546) of human factor v