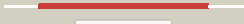



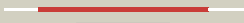



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3668c_(-)_4109961_4110659
Date	Fri Aug 9 18:20:35 BST 2019
Unique Job ID	f57683428c12e95b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h5ca1	 Alignment		100.0	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
2	d2qaaa1	 Alignment		100.0	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
3	c2ouaA_	 Alignment		100.0	25	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of nocardioptis protease (napase)
4	c5mrta_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: lytic endopeptidase preproenzyme; PDBTitle: crystal structure of I5 protease lysobacter sp. xl1
5	c2pfeA_	 Alignment		100.0	24	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: alkaline serine protease; PDBTitle: crystal structure of thermobifida fusca protease a (tfpa)
6	d2sfaa_	 Alignment		100.0	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
7	d2sgaa_	 Alignment		99.9	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
8	c2ea3A_	 Alignment		99.9	28	PDB header: hydrolase Chain: A: PDB Molecule: chymotrypsin; PDBTitle: crystal structure of cellulomonas bogoriensis chymotrypsin
9	d1hpga_	 Alignment		99.9	22	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
10	c2zleB_	 Alignment		99.6	16	PDB header: hydrolase Chain: B: PDB Molecule: protease do; PDBTitle: cryo-em structure of degp12/omp
11	c4a8a1_	 Alignment		99.6	14	PDB header: hydrolase/hydrolase Chain: I: PDB Molecule: periplasmic ph-dependent serine endoprotease degq; PDBTitle: asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme

12	c3pv5B_	Alignment		99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (n189g/p190g variant)
13	c5il9A_	Alignment		99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9
14	c4flnB_	Alignment		99.5	21	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2
15	c1ky9A_	Alignment		99.5	11	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
16	d1ky9a2	Alignment		99.5	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
17	c2z9iB_	Alignment		99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: probable serine protease pepd; PDBTitle: crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
18	c3otpF_	Alignment		99.5	15	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
19	c6e0uB_	Alignment		99.5	17	PDB header: hydrolase, toxin Chain: B: PDB Molecule: serine protease; PDBTitle: staphylococcus pseudintermedius exfoliative toxin exi
20	c2r3yC_	Alignment		99.5	18	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
21	d1lvmb_	Alignment	not modelled	99.5	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
22	c3stjC_	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
23	d1q31a_	Alignment	not modelled	99.5	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
24	c4inkA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: serine protease spld; PDBTitle: crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution
25	c5ilaA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
26	c3pv4A_	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant)
27	d1agja_	Alignment	not modelled	99.4	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
28	d2qf3a1	Alignment	not modelled	99.4	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
29	c5hmaA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like serine protease;

29	c3mmgA_	Alignment	not modelled	99.4	17	PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
30	c3qo6B_	Alignment	not modelled	99.4	19	PDB header: photosynthesis Chain: B: PDB Molecule: protease do-like 1, chloroplastic; PDBTitle: crystal structure analysis of the plant protease deg1
31	d1l1ja_	Alignment	not modelled	99.4	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
32	c3mmgB_	Alignment	not modelled	99.4	11	PDB header: viral protein, hydrolase Chain: B: PDB Molecule: nuclear inclusion protein a; PDBTitle: crystal structure of tobacco vein mottling virus protease
33	c3nziA_	Alignment	not modelled	99.4	20	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
34	c5y28B_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
35	c5c2zA_	Alignment	not modelled	99.4	20	PDB header: toxin Chain: A: PDB Molecule: exfoliative toxin d2; PDBTitle: molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
36	d2z9ia2	Alignment	not modelled	99.3	10	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
37	c3gdsA_	Alignment	not modelled	99.3	17	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
38	c5y2dA_	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra
39	c4ic5B_	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
40	c3k6zA_	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
41	c2rcel_	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
42	c4ic6A_	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
43	c3nwuB_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
44	c2w7uC_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: C: PDB Molecule: serine protease spla; PDBTitle: spla serine protease of staphylococcus aureus (2.4a)
45	c5xdyA_	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis
46	c2vidA_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: A: PDB Molecule: serine protease splb; PDBTitle: serine protease splb from staphylococcus aureus at 1.8a resolution
47	c1zyoA_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
48	c1lcyA_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2
49	d1arba_	Alignment	not modelled	99.1	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
50	d1lcyA2	Alignment	not modelled	99.1	13	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
51	c4jcnA_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: structure of esp, serine protease from staphylococcus epidermidis
52	d1qtfa_	Alignment	not modelled	99.1	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
53	c4ri0A_	Alignment	not modelled	99.1	19	PDB header: hydrolase Chain: A: PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated
54	c2w5eB_	Alignment	not modelled	99.1	16	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
55	d1cqqa_	Alignment	not modelled	99.0	13	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
						PDB header: viral protein

56	c6fezB_	Alignment	not modelled	99.0	11	Chain: B: PDB Molecule: serine protease domain; PDBTitle: ryegrass mottle virus protease domain
57	c3stiC_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli
58	c5mm8A_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: serine protease sple; PDBTitle: atomic resolution structure of sple protease from staphylococcus2 aureus
59	c2o8la_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: v8 protease; PDBTitle: structure of v8 protease from staphylococcus aureus
60	d2o8la1	Alignment	not modelled	99.0	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
61	c1qy6A_	Alignment	not modelled	98.9	17	PDB header: protease Chain: A: PDB Molecule: serine protease; PDBTitle: structue of v8 protease from staphylococcus aureus
62	c5b6lA_	Alignment	not modelled	98.9	23	PDB header: hydrolase Chain: A: PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803
63	c5jykB_	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k
64	c1wczA_	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
65	d1p3ca_	Alignment	not modelled	98.8	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
66	c3wy8A_	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of protease aniseq from arthrobacter nicotinovorans
67	d1l1na_	Alignment	not modelled	98.7	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
68	c2as9B_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus
69	c3cp7B_	Alignment	not modelled	98.6	20	PDB header: hydrolase Chain: B: PDB Molecule: alkaline serine protease al20; PDBTitle: crystal structure of a thermostable serine protease al20 from2 extremophilic microorganism
70	c2b0fA_	Alignment	not modelled	98.5	15	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
71	c4lk4A_	Alignment	not modelled	98.4	18	PDB header: hydrolase Chain: A: PDB Molecule: vesb protease; PDBTitle: structure of vibrio cholerae vesb protease
72	c2xrcD_	Alignment	not modelled	98.3	16	PDB header: immune system Chain: D: PDB Molecule: human complement factor i; PDBTitle: human complement factor i
73	d1mzaa_	Alignment	not modelled	98.2	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
74	c2f83A_	Alignment	not modelled	98.2	22	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
75	c6bqmA_	Alignment	not modelled	98.2	20	PDB header: hydrolase Chain: A: PDB Molecule: serine protease vesc; PDBTitle: secreted serine protease vesc from vibrio cholerae
76	c6esoA_	Alignment	not modelled	98.1	21	PDB header: blood clotting Chain: A: PDB Molecule: plasma kallikrein; PDBTitle: full length human plasma kallikrein with inhibitor
77	c4durA_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: plasminogen; PDBTitle: the x-ray crystal structure of full-length type ii human plasminogen
78	c3h7tB_	Alignment	not modelled	98.1	17	PDB header: hydrolase Chain: B: PDB Molecule: group 3 allergen smipp-s yvt004a06; PDBTitle: crystal structure of scabies mite inactivated protease paralogue s-d12 (smipp-s-d1)
79	d1gvza_	Alignment	not modelled	98.0	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
80	c2ok5A_	Alignment	not modelled	98.0	21	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
81	c4o03A_	Alignment	not modelled	98.0	19	PDB header: hydrolase Chain: A: PDB Molecule: prothrombin; PDBTitle: crystal structure of ca2+ bound prothrombin deletion mutant residues2 146-167
82	d1sgfa_	Alignment	not modelled	97.9	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases

83	c2i6sA_	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: A; PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
84	c3f1sB_	Alignment	not modelled	97.9	14	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
85	c3zv8A_	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: A; PDB Molecule: 3c protease; PDBTitle: crystal structure of 3c protease of enterovirus 68
86	c1rs0A_	Alignment	not modelled	97.8	21	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)
87	c3h7oB_	Alignment	not modelled	97.8	17	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)
88	d3rp2a_	Alignment	not modelled	97.7	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
89	c5to3B_	Alignment	not modelled	97.7	17	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
90	c4hzhB_	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: B; PDB Molecule: prothrombin; PDBTitle: structure of recombinant gla-domainless prothrombin mutant s525a
91	c1zjkA_	Alignment	not modelled	97.7	15	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
92	c3nxA_	Alignment	not modelled	97.6	16	PDB header: hydrolase Chain: A; PDB Molecule: prethrombin-1; PDBTitle: crystal structure of human prethrombin-1
93	c1elvA_	Alignment	not modelled	97.6	12	PDB header: hydrolase Chain: A; PDB Molecule: complement c1s component; PDBTitle: crystal structure of the catalytic domain of human complement c1s2 protease
94	d1npma_	Alignment	not modelled	97.6	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
95	c4bxsA_	Alignment	not modelled	97.6	17	PDB header: blood clotting Chain: A; PDB Molecule: factor x-like protease; PDBTitle: crystal structure of the prothrombinase complex from the2 venom of pseudonaja textilis
96	c1z8gA_	Alignment	not modelled	97.6	20	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.
97	d1bioa_	Alignment	not modelled	97.6	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
98	c2b9lA_	Alignment	not modelled	97.6	22	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
99	c1z7lA_	Alignment	not modelled	97.5	16	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: thrombin; PDBTitle: thrombin and p2 pyridine n-oxide inhibitor complex structure
100	c3e16B_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: B; PDB Molecule: prostasin; PDBTitle: x-ray structure of human prostasin in complex with benzoxazole warhead2 peptidomimic, lysine in p3
101	d1rrka1	Alignment	not modelled	97.5	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
102	c3s9cA_	Alignment	not modelled	97.4	17	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
103	c2asuB_	Alignment	not modelled	97.4	19	PDB header: hydrolase Chain: B; PDB Molecule: hepatocyte growth factor-like protein; PDBTitle: crystal structure of the beta-chain of hgfl/msp
104	c2qxhA_	Alignment	not modelled	97.4	15	PDB header: hydrolase Chain: A; PDB Molecule: kallikrein-7; PDBTitle: crystal structure of human kallikrein 7 in complex with suc-2 ala-ala-pro-phe-chloromethylketone
105	d1ao5a_	Alignment	not modelled	97.4	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
106	d1pytd_	Alignment	not modelled	97.4	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
107	c4kkdB_	Alignment	not modelled	97.4	16	PDB header: hydrolase Chain: B; PDB Molecule: mannan-binding lectin serine protease 1; PDBTitle: 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
108	c4f4oC_	Alignment	not modelled	97.3	16	PDB header: oxygen transport/transport protein Chain: C; PDB Molecule: haptoglobin; PDBTitle: structure of the haptoglobin-haemoglobin complex

109	c3h5cB_	Alignment	not modelled	97.3	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
110	d1ezxc_	Alignment	not modelled	97.3	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
111	d1lo6a_	Alignment	not modelled	97.3	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
112	c2zchP_	Alignment	not modelled	97.2	17	PDB header: immune system Chain: P: PDB Molecule: prostate-specific antigen; PDBTitle: crystal structure of human prostate specific antigen2 complexed with an activating antibody
113	c3faoA_	Alignment	not modelled	97.2	19	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein; PDBTitle: crystal structure of s118a mutant 3clsp of prrsv
114	d1sgfg_	Alignment	not modelled	97.1	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
115	c1md7A_	Alignment	not modelled	97.1	13	PDB header: hydrolase Chain: A: PDB Molecule: c1r complement serine protease; PDBTitle: monomeric structure of the zymogen of complement protease2 c1r
116	d1op0a_	Alignment	not modelled	97.1	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
117	c2bdiO_	Alignment	not modelled	97.1	14	PDB header: hydrolase Chain: O: PDB Molecule: kallikrein-4; PDBTitle: human kallikrein 4 complex with cobalt and p-2 aminobenzamidine
118	c1ybwA_	Alignment	not modelled	97.1	22	PDB header: hydrolase Chain: A: PDB Molecule: hepatocyte growth factor activator precursor; PDBTitle: protease domain of hgfa with no inhibitor
119	d1rjxb_	Alignment	not modelled	97.0	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
120	c5xrfA_	Alignment	not modelled	97.0	12	PDB header: hydrolase Chain: A: PDB Molecule: snake venom serine protease da-36; PDBTitle: crystal structure of da-36, a thrombin-like enzyme from2 deinagkistrodon acutus