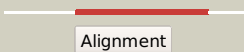

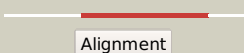

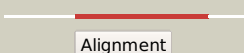

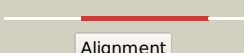





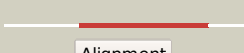

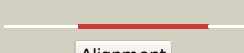














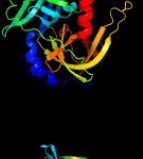



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1043c_(-)_1165785_1166810
Date	Wed Jul 31 22:05:11 BST 2019
Unique Job ID	dad62f95f23b7939

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a8aI_	 Alignment		100.0	21	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
2	c5il9A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9
3	c2r3yC_	 Alignment		100.0	25	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
4	c4flnB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2
5	d1ky9a2	 Alignment		100.0	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
6	c2z9iB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: probable serine protease pepd; PDBTitle: crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
7	c2zleB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: protease do; PDBTitle: cryo-em structure of degp12/omp
8	c1ky9A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
9	c5hmaA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like serine protease; PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
10	c3stjC_	 Alignment		100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
11	c2rceI_	 Alignment		100.0	24	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz

12	c3otpF_	Alignment		100.0	22	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
13	c3pv5B_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (n189g/p190g variant)
14	d1l1ja_	Alignment		100.0	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
15	c4ic6A_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
16	d2z9ia2	Alignment		100.0	24	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
17	c3nziA_	Alignment		100.0	24	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
18	c3gdsA_	Alignment		100.0	25	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
19	c3k6zA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
20	c5y28B_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
21	c5xdyA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis
22	d2qf3a1	Alignment	not modelled	100.0	26	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
23	c3qo6B_	Alignment	not modelled	100.0	23	PDB header: photosynthesis Chain: B: PDB Molecule: protease do-like 1, chloroplastic; PDBTitle: crystal structure analysis of the plant protease deg1
24	c4ri0A_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated
25	c4ic5B_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
26	c3stiC_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli
27	c1lcyA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2
28	c3nwuB_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
						PDB header: hydrolase

29	c5ilaA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
30	c5y2dA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra
31	c5b6IA_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803
32	d1lcyA2	Alignment	not modelled	100.0	27	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
33	c4inkA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: serine protease spld; PDBTitle: crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution
34	c3pv4A_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pd2 variant)
35	c5c2zA_	Alignment	not modelled	100.0	24	PDB header: toxin Chain: A: PDB Molecule: exfoliative toxin d2; PDBTitle: molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
36	c3mmgB_	Alignment	not modelled	100.0	20	PDB header: viral protein, hydrolase Chain: B: PDB Molecule: nuclear inclusion protein a; PDBTitle: crystal structure of tobacco vein mottling virus protease
37	c6e0uB_	Alignment	not modelled	100.0	21	PDB header: hydrolase, toxin Chain: B: PDB Molecule: serine protease; PDBTitle: staphylococcus pseudintermedius exfoliative toxin exi
38	d1qtfa_	Alignment	not modelled	100.0	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
39	d1agja_	Alignment	not modelled	99.9	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
40	c1zyoA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
41	c2w5eB_	Alignment	not modelled	99.9	20	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
42	c2w7uC_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: serine protease spla; PDBTitle: spla serine protease of staphylococcus aureus (2.4a)
43	c2vidA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: serine protease splb; PDBTitle: serine protease splb from staphylococcus aureus at 1.8a resolution
44	d1q31a_	Alignment	not modelled	99.9	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
45	d1lvmb_	Alignment	not modelled	99.9	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
46	c5jykB_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k
47	c5mm8A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: serine protease sple; PDBTitle: atomic resolution structure of sple protease from staphylococcus2 aureus
48	c6fezB_	Alignment	not modelled	99.9	19	PDB header: viral protein Chain: B: PDB Molecule: serine protease domain; PDBTitle: ryegrass mottle virus protease domain
49	c2as9B_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus
50	c1wczA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
51	c2o8IA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: v8 protease; PDBTitle: structure of v8 protease from staphylococcus aureus
52	d2o8la1	Alignment	not modelled	99.9	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
53	c1qy6A_	Alignment	not modelled	99.9	20	PDB header: protease Chain: A: PDB Molecule: serine protease; PDBTitle: structue of v8 protease from staphylococcus aureus
54	c4jcnA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: structure of esp, serine protease from staphylococcus epidermidis
55	d1cqqa_	Alignment	not modelled	99.8	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
						Fold: Trypsin-like serine proteases

56	d1p3ca_	Alignment	not modelled	99.8	20	Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
57	c5mrtA_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: lytic endopeptidase preproenzyme; PDBTitle: crystal structure of I5 protease lysobacter sp. x11
58	d1l1na_	Alignment	not modelled	99.7	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
59	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
60	d2h5ca1	Alignment	not modelled	99.7	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
61	d2qaaa1	Alignment	not modelled	99.7	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
62	d2sfaa_	Alignment	not modelled	99.7	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
63	d1arba_	Alignment	not modelled	99.7	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
64	c3wy8A_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of protease aniseq from arthrobacter nicotinovorans
65	c2ouaA_	Alignment	not modelled	99.7	14	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of nocardiosis protease (napase)
66	c3cp7B_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: alkaline serine protease al20; PDBTitle: crystal structure of a thermostable serine protease al20 from2 extremophilic microorganism
67	c2pfeA_	Alignment	not modelled	99.6	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: alkaline serine protease; PDBTitle: crystal structure of thermobifida fusca protease a (tfpa)
68	d2sgaa_	Alignment	not modelled	99.6	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
69	c2ea3A_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: chymotrypsin; PDBTitle: crystal structure of cellulomonas bogoriensis chymotrypsin
70	d1hpga_	Alignment	not modelled	99.6	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
71	c5y09B_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9 at 295 k
72	c3zv8A_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: 3c protease; PDBTitle: crystal structure of 3c protease of enterovirus 68
73	c4lk4A_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: vesb protease; PDBTitle: structure of vibrio cholerae vesb protease
74	c6esoA_	Alignment	not modelled	99.3	17	PDB header: blood clotting Chain: A: PDB Molecule: plasma kallikrein; PDBTitle: full length human plasma kallikrein with inhibitor
75	c4durA_	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: A: PDB Molecule: plasminogen; PDBTitle: the x-ray crystal structure of full-length type ii human plasminogen
76	c6bqmA_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: serine protease vesc; PDBTitle: secreted serine protease vesc from vibrio cholerae
77	c2f83A_	Alignment	not modelled	99.1	15	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
78	c2xrcD_	Alignment	not modelled	99.1	13	PDB header: immune system Chain: D: PDB Molecule: human complement factor i; PDBTitle: human complement factor i
79	c4o03A_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: prothrombin; PDBTitle: crystal structure of ca2+ bound prothrombin deletion mutant residues2 146-167
80	c2b9lA_	Alignment	not modelled	99.0	13	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
81	c3f1sB_	Alignment	not modelled	98.9	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
82	c3h7tB_	Alignment	not modelled	98.9	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)

83	d1mzaa_	Alignment	not modelled	98.9	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
84	c1zjkA_	Alignment	not modelled	98.9	16	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
85	c3h7oB_	Alignment	not modelled	98.9	16	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)
86	c5to3B_	Alignment	not modelled	98.9	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
87	c1z8gA_	Alignment	not modelled	98.9	21	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.
88	d1npma_	Alignment	not modelled	98.9	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
89	c3nxA_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: prethrombin-1; PDBTitle: crystal structure of human prethrombin-1
90	c2i6sA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
91	c2ok5A_	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
92	c3osyA_	Alignment	not modelled	98.8	15	PDB header: hydrolase Chain: A: PDB Molecule: 3c protease; PDBTitle: human enterovirus 71 3c protease
93	d1rxjb_	Alignment	not modelled	98.8	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
94	d1pytd_	Alignment	not modelled	98.8	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
95	c3h5cB_	Alignment	not modelled	98.8	11	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
96	c2ijd1_	Alignment	not modelled	98.8	19	PDB header: hydrolase, transferase Chain: 1: PDB Molecule: picornain 3c, rna-directed rna polymerase; PDBTitle: crystal structure of the poliovirus precursor protein 3cd
97	d1bioa_	Alignment	not modelled	98.8	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
98	c4kkdB_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: B: PDB Molecule: mannan-binding lectin serine protease 1; PDBTitle: the x-ray crystal structure of mannanose-binding lectin-associated2 serine proteinase-3 reveals the structural basis for enzyme3 inactivity associated with the 3mc syndrome
99	c1elvA_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: A: PDB Molecule: complement c1s component; PDBTitle: crystal structure of the catalytic domain of human complement c1s2 protease
100	d1a5ia_	Alignment	not modelled	98.7	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
101	c4m7gA_	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like protease; PDBTitle: streptomyces erythraeus trypsin
102	c1rs0A_	Alignment	not modelled	98.7	16	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)
103	d1gdna_	Alignment	not modelled	98.6	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
104	d1gvza_	Alignment	not modelled	98.6	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
105	c2asuB_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: B: PDB Molecule: hepatocyte growth factor-like protein; PDBTitle: crystal structure of the beta-chain of hgfl/msp
106	c1fizA_	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-acrosin heavy chain; PDBTitle: three dimensional structure of beta-acrosin from boar spermatozoa
107	c4jlyA_	Alignment	not modelled	98.6	19	PDB header: hydrolase Chain: A: PDB Molecule: complement c1s subcomponent; PDBTitle: the x-ray crystal structure of human complement protease c1s zymogen
108	c4iqdA_	Alignment	not modelled	98.6	14	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
						Fold: Trypsin-like serine proteases

109	d3rp2a_	Alignment	not modelled	98.6	14	Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
110	c4hzhB_	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: B: PDB Molecule: prothrombin; PDBTitle: structure of recombinant gla-domainless prothrombin mutant s525a
111	c3s9cA_	Alignment	not modelled	98.6	14	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
112	c5jxfA_	Alignment	not modelled	98.6	22	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
113	d1eufa_	Alignment	not modelled	98.5	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
114	c5jxpA_	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
115	c3woIB_	Alignment	not modelled	98.5	19	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
116	d2bhga1	Alignment	not modelled	98.5	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
117	c1z71A_	Alignment	not modelled	98.5	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: thrombin; PDBTitle: thrombin and p2 pyridine n-oxide inhibitor complex structure
118	d1a7sa_	Alignment	not modelled	98.5	10	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
119	d1z8ga1	Alignment	not modelled	98.5	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases
120	d1fi8a_	Alignment	not modelled	98.5	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Eukaryotic proteases