






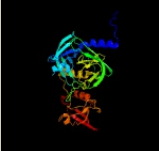
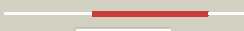















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1223_(htrA)_1365881_1367467
Date	Wed Jul 31 22:05:31 BST 2019
Unique Job ID	28bb591af2146172

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xdyA_	 Alignment		100.0	97	PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis
2	c3stjC_	 Alignment		100.0	39	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
3	c2zleB_	 Alignment		100.0	38	PDB header: hydrolase Chain: B: PDB Molecule: protease do; PDBTitle: cryo-em structure of degp12/omp
4	c4ic6A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
5	c1ky9A_	 Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
6	c3otpF_	 Alignment		100.0	37	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
7	c4a8aI_	 Alignment		100.0	37	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
8	c3pv5B_	 Alignment		100.0	40	PDB header: hydrolase Chain: B: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (n189g/p190g variant)
9	c3qo6B_	 Alignment		100.0	35	PDB header: photosynthesis Chain: B: PDB Molecule: protease do-like 1, chloroplastic; PDBTitle: crystal structure analysis of the plant protease deg1
10	c5il9A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9
11	c2z9iB_	 Alignment		100.0	49	PDB header: hydrolase Chain: B: PDB Molecule: probable serine protease pepd; PDBTitle: crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form

12	c4flnB_	Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2
13	c3gdsA_	Alignment		100.0	35	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
14	c1lcyA_	Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2
15	c4ri0A_	Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated
16	c5b6lA_	Alignment		100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803
17	c3pv4A_	Alignment		100.0	39	PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant)
18	c2r3yC_	Alignment		100.0	39	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
19	c5y2dA_	Alignment		100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra
20	c5jykB_	Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k
21	d1ky9a2	Alignment	not modelled	100.0	44	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
22	c2rceI_	Alignment	not modelled	100.0	40	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
23	c5y09B_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9 at 295 k
24	d1l1ja_	Alignment	not modelled	100.0	42	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
25	d2z9ia2	Alignment	not modelled	100.0	55	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
26	d2qf3a1	Alignment	not modelled	100.0	43	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
27	c5y28B_	Alignment	not modelled	100.0	46	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
28	c3nziA_	Alignment	not modelled	100.0	38	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
29	c3etiC_	Alignment	not modelled	100.0	48	PDB header: hydrolase Chain: C: PDB Molecule: protease degq;

29	c3suc_	Alignment	not modelled	100.0	40	PDBTitle: crystal structure of the protease domain of degq from escherichia coli PDB header: hydrolase
30	c5hmaA_	Alignment	not modelled	100.0	27	Chain: A: PDB Molecule: trypsin-like serine protease; PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
31	c4ic5B_	Alignment	not modelled	100.0	41	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
32	c3nwuB_	Alignment	not modelled	100.0	43	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
33	d1lcyA2	Alignment	not modelled	100.0	36	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
34	c3k6zA_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
35	c5ilaA_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
36	c3mmgB_	Alignment	not modelled	100.0	17	PDB header: viral protein, hydrolase Chain: B: PDB Molecule: nuclear inclusion protein a; PDBTitle: crystal structure of tobacco vein mottling virus protease
37	d1q31a_	Alignment	not modelled	100.0	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
38	c1zyoA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
39	d1lvmb_	Alignment	not modelled	99.9	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
40	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
41	d1qtfa_	Alignment	not modelled	99.9	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
42	c4inkA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: serine protease spld; PDBTitle: crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution
43	c2l97A_	Alignment	not modelled	99.9	37	PDB header: protein binding Chain: A: PDB Molecule: putative serine protease; PDBTitle: solution structure of htra pdz domain from streptococcus pneumoniae
44	d1agja_	Alignment	not modelled	99.9	22	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
45	c5c2zA_	Alignment	not modelled	99.9	25	PDB header: toxin Chain: A: PDB Molecule: exfoliative toxin d2; PDBTitle: molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
46	c6e0uB_	Alignment	not modelled	99.9	21	PDB header: hydrolase, toxin Chain: B: PDB Molecule: serine protease; PDBTitle: staphylococcus pseudintermedius exfoliative toxin exi
47	c5mm8A_	Alignment	not modelled	99.9	23	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	17	PDB header: viral protein Chain: B: PDB Molecule: serine protease domain; PDBTitle: ryegrass mottle virus protease domain
49	c2vidA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: serine protease splb; PDBTitle: serine protease splb from staphylococcus aureus at 1.8a resolution
50	c2w7uC_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: C: PDB Molecule: serine protease spla; PDBTitle: spla serine protease of staphylococcus aureus (2.4a)
51	d1cqqa_	Alignment	not modelled	99.8	17	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
52	c2b0fA_	Alignment	not modelled	99.8	21	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
53	c2as9B_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus
54	c4jcnA_	Alignment	not modelled	99.8	28	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: structure of esp, serine protease from staphylococcus epidermidis
55	c2o8lA_	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: v8 protease; PDBTitle: structure of v8 protease from staphylococcus aureus

56	d2o8la1	Alignment	not modelled	99.8	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
57	c1qv6A	Alignment	not modelled	99.8	22	PDB header: protease Chain: A: PDB Molecule: serine protease; PDBTitle: structue of v8 protease from staphylococcus aureus
58	d2qaaa1	Alignment	not modelled	99.7	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
59	c2p3wB	Alignment	not modelled	99.7	33	PDB header: protein binding Chain: B: PDB Molecule: probable serine protease htra3; PDBTitle: crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
60	c5mrtA	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: lytic endopeptidase preproenzyme; PDBTitle: crystal structure of I5 protease lysobacter sp. x11
61	d1l1na	Alignment	not modelled	99.7	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
62	d2z9ia1	Alignment	not modelled	99.7	30	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Htra-like serine proteases
63	c2joaA	Alignment	not modelled	99.7	26	PDB header: protein binding Chain: A: PDB Molecule: serine protease htra1; PDBTitle: htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
64	d1lcya1	Alignment	not modelled	99.7	25	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Htra-like serine proteases
65	c4jj0B	Alignment	not modelled	99.7	22	PDB header: electron transport Chain: B: PDB Molecule: mamp; PDBTitle: crystal structure of mamp
66	d2h5ca1	Alignment	not modelled	99.7	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
67	c1wczA	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
68	c2ouaA	Alignment	not modelled	99.7	25	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of nocardioptis protease (napase)
69	c2n7pA	Alignment	not modelled	99.7	18	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of pdz domain
70	d2sfaa	Alignment	not modelled	99.7	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
71	c2pfeA	Alignment	not modelled	99.6	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: alkaline serine protease; PDBTitle: crystal structure of thermobifida fusca protease a (tfpa)
72	d1ky9a1	Alignment	not modelled	99.6	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Htra-like serine proteases
73	d2i4sa1	Alignment	not modelled	99.6	11	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
74	c5hj1A	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase c protein; PDBTitle: crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
75	d2sgaa	Alignment	not modelled	99.6	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
76	c2kl1A	Alignment	not modelled	99.6	21	PDB header: protein binding Chain: A: PDB Molecule: ylbl protein; PDBTitle: solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
77	c3i18A	Alignment	not modelled	99.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2051 protein; PDBTitle: crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
78	d1p3ca	Alignment	not modelled	99.6	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
79	d1hpga	Alignment	not modelled	99.5	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
80	d1arba	Alignment	not modelled	99.5	13	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
81	c2ea3A	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: A: PDB Molecule: chymotrypsin; PDBTitle: crystal structure of cellulomonas bogoriensis chymotrypsin
82	c3zv8A	Alianment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: 3c protease;

					PDBTitle: crystal structure of 3c protease of enterovirus 68
83	d2i6va1	Alignment	not modelled	99.5	13 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
84	c2kjpA	Alignment	not modelled	99.5	18 PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ylbl; PDBTitle: solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
85	d2hgaa1	Alignment	not modelled	99.5	20 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: MTH1368 C-terminal domain-like
86	d1sota1	Alignment	not modelled	99.4	30 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
87	d1fc6a3	Alignment	not modelled	99.4	21 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Tail specific protease PDZ domain
88	c3wkIA	Alignment	not modelled	99.4	30 PDB header: hydrolase Chain: A; PDB Molecule: putative zinc metalloprotease aq_1964; PDBTitle: the periplasmic pdz tandem fragment of the rsep homologue from aquifex2 aeolicus
89	c4o06A	Alignment	not modelled	99.3	24 PDB header: chaperone Chain: A; PDB Molecule: probable 26s proteasome regulatory subunit p27; PDBTitle: 1.15a resolution structure of the proteasome assembly chaperone nas22 pdz domain
90	c2zplA	Alignment	not modelled	99.3	20 PDB header: hydrolase Chain: A; PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain a
91	c3cp7B	Alignment	not modelled	99.3	15 PDB header: hydrolase Chain: B; PDB Molecule: alkaline serine protease al20; PDBTitle: crystal structure of a thermostable serine protease al20 from2 extremophilic microorganism
92	c3rleA	Alignment	not modelled	99.3	13 PDB header: membrane protein Chain: A; PDB Molecule: golgi reassembly-stacking protein 2; PDBTitle: crystal structure of grasp55 grasp domain (residues 7-208)
93	c4lk4A	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: A; PDB Molecule: vesb protease; PDBTitle: structure of vibrio cholerae vesb protease
94	d1ky9b2	Alignment	not modelled	99.3	26 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
95	c3wy8A	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: A; PDB Molecule: serine protease; PDBTitle: crystal structure of protease anisep from arthrobacter nicotinovorans
96	c2zpmA	Alignment	not modelled	99.3	28 PDB header: hydrolase Chain: A; PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
97	c4revA	Alignment	not modelled	99.3	21 PDB header: membrane protein Chain: A; PDB Molecule: golgi reassembly-stacking protein 1; PDBTitle: crystal structure of the grasp65-gm130 c-terminal peptide complex
98	c6bqmA	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: A; PDB Molecule: serine protease vesc; PDBTitle: secreted serine protease vesc from vibrio cholerae
99	c2krqA	Alignment	not modelled	99.2	28 PDB header: signaling protein Chain: A; PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf1; PDBTitle: solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
100	c6esoA	Alignment	not modelled	99.2	15 PDB header: blood clotting Chain: A; PDB Molecule: plasma kallikrein; PDBTitle: full length human plasma kallikrein with inhibitor
101	c2yuyA	Alignment	not modelled	99.2	17 PDB header: signaling protein Chain: A; PDB Molecule: rho gtpase activating protein 21; PDBTitle: solution structure of pdz domain of rho gtpase activating2 protein 21
102	c3shuB	Alignment	not modelled	99.1	28 PDB header: cell adhesion Chain: B; PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3
103	c5oakA	Alignment	not modelled	99.1	20 PDB header: protein binding Chain: A; PDB Molecule: bazooka, isoform c_ld29223p; PDBTitle: structure of the dmpar3 pdz1 domain in complex with the dmpar6 pbm
104	d1x5qa1	Alignment	not modelled	99.1	22 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
105	d1wfga	Alignment	not modelled	99.1	21 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
106	d1ueqa	Alignment	not modelled	99.1	24 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
107	c2eaqA	Alignment	not modelled	99.1	29 PDB header: metal binding protein Chain: A; PDB Molecule: lim domain only protein 7; PDBTitle: crystal structure of pdz domain of kiaa0858 (lim), ms07932 from homo sapiens
108	c2kjdA	Alignment	not modelled	99.1	30 PDB header: signaling protein Chain: A; PDB Molecule: sodium/hydrogen exchange regulatory cofactor nhe-

						PDBTitle: solution structure of extended pdz2 domain from nherf1 (150-2 270)
109	c3l4fD_	Alignment	not modelled	99.1	24	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein 1; PDBTitle: crystal structure of betapix coiled-coil domain and shank pdz complex
110	c2komA_	Alignment	not modelled	99.1	22	PDB header: signaling protein Chain: A: PDB Molecule: partitioning defective 3 homolog; PDBTitle: solution structure of humar par-3b pdz2 (residues 451-549)
111	d1rgwa_	Alignment	not modelled	99.1	10	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
112	c5wouA_	Alignment	not modelled	99.1	26	PDB header: cell adhesion Chain: A: PDB Molecule: protein lap4; PDBTitle: crystal structure of drosophila melanogaster scribble pdz1 domain in2 complex with guk-holder
113	c2egkC_	Alignment	not modelled	99.1	25	PDB header: protein binding Chain: C: PDB Molecule: general receptor for phosphoinositides 1-associated PDBTitle: crystal structure of tamalin pdz-intrinsic ligand fusion protein
114	d1uf1a_	Alignment	not modelled	99.1	28	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
115	d1m5za_	Alignment	not modelled	99.0	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
116	c3diwB_	Alignment	not modelled	99.0	23	PDB header: signaling protein/cell adhesion Chain: B: PDB Molecule: tax1-binding protein 3; PDBTitle: c-terminal beta-catenin bound tip-1 structure
117	c4durA_	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: plasminogen; PDBTitle: the x-ray crystal structure of full-length type ii human plasminogen
118	c6bxgA_	Alignment	not modelled	99.0	20	PDB header: hydrolase/peptide Chain: A: PDB Molecule: tail-specific protease; PDBTitle: 1.45 angstrom resolution crystal structure of pdz domain of carboxy-2 terminal protease from vibrio cholerae in complex with peptide.
119	c4c2dC_	Alignment	not modelled	99.0	20	PDB header: hydrolase/peptide Chain: C: PDB Molecule: carboxy-terminal processing protease ctpb; PDBTitle: crystal structure of the protease ctpb in an active state
120	c2v90E_	Alignment	not modelled	99.0	23	PDB header: protein binding Chain: E: PDB Molecule: pdz domain-containing protein 3; PDBTitle: crystal structure of the 3rd pdz domain of intestine- and kidney-2 enriched pdz domain ikepp (pdzd3)