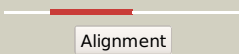

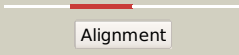

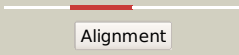

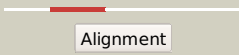

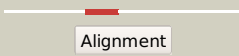

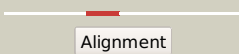

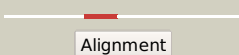

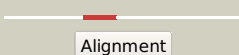

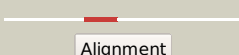

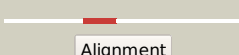

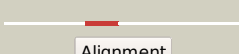
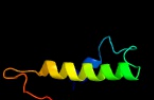


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0419_(lpqM)_505089_506585
 Date Tue Jul 23 14:50:49 BST 2019
 Unique Job ID 141893a7baf2e934

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c37B_	 Alignment		98.2	25	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m48 family; PDBTitle: x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
2	c4aw6B_	 Alignment		97.6	25	PDB header: hydrolase Chain: B: PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
3	c4il3B_	 Alignment		97.5	26	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
4	c6aitD_	 Alignment		97.0	22	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
5	c3dtkA_	 Alignment		96.4	28	PDB header: gene regulation Chain: A: PDB Molecule: irre protein; PDBTitle: crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
6	c2vqxA_	 Alignment		96.0	18	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
7	d1kjpA_	 Alignment		95.3	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
8	d1bqba_	 Alignment		94.9	35	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
9	d1npca_	 Alignment		94.9	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
10	c4gerB_	 Alignment		94.4	18	PDB header: hydrolase Chain: B: PDB Molecule: gentlyase metalloprotease; PDBTitle: crystal structure of gentlyase, the neutral metalloprotease of2 paenibacillus polymyxa
11	c4k90A_	 Alignment		94.2	21	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus

12	c3cqbB_	Alignment		93.6	29	PDB header: hydrolase Chain: B; PDB Molecule: probable protease htpx homolog; PDBTitle: crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
13	c3nqzB_	Alignment		93.5	13	PDB header: hydrolase Chain: B; PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
14	c3nqxA_	Alignment		92.9	15	PDB header: hydrolase Chain: A; PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of vibriolysin mcp-02 mature enzyme, a zinc2 metalloprotease from m4 family
15	c3sksA_	Alignment		92.9	48	PDB header: hydrolase Chain: A; PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
16	c5l43B_	Alignment		91.6	27	PDB header: hydrolase Chain: B; PDB Molecule: k-26 dipeptidyl carboxypeptidase; PDBTitle: structure of k26-dcp
17	c3ce2A_	Alignment		91.4	33	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomophila abortus
18	c1y791_	Alignment		91.1	23	PDB header: hydrolase Chain: 1; PDB Molecule: peptidyl-dipeptidase dcp; PDBTitle: crystal structure of the e.coli dipeptidyl carboxypeptidase2 dcp in complex with a peptidic inhibitor
19	c2h1jA_	Alignment		91.1	48	PDB header: hydrolase Chain: A; PDB Molecule: oligoendopeptidase f; PDBTitle: 3.1 a x-ray structure of putative oligoendopeptidase f: crystals grown2 by microfluidic seeding
20	d1s4bp_	Alignment		91.0	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
21	c4ka8A_	Alignment	not modelled	90.6	30	PDB header: hydrolase Chain: A; PDB Molecule: oligopeptidase a; PDBTitle: structure of organellar oligopeptidase
22	d1u4ga_	Alignment	not modelled	90.5	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
23	d1l1ip_	Alignment	not modelled	89.7	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
24	c6cz6D_	Alignment	not modelled	88.9	22	PDB header: transcription Chain: D; PDB Molecule: hth-type transcriptional regulator pprp; PDBTitle: mycobacterium tuberculosis transcriptional regulator
25	c3zukB_	Alignment	not modelled	88.3	14	PDB header: hydrolase/inhibitor Chain: B; PDB Molecule: endopeptidase, peptidase family m13; PDBTitle: crystal structure of mycobacterium tuberculosis zinc metalloprotease2 zmp1 in complex with inhibitor
26	c4iuwA_	Alignment	not modelled	88.1	18	PDB header: hydrolase Chain: A; PDB Molecule: neutral endopeptidase; PDBTitle: crystal structure of pepo from lactobacillus rhamnosis hn001 (dr20)
27	c1slmA_	Alignment	not modelled	87.6	14	PDB header: hydrolase Chain: A; PDB Molecule: stromelysin-1; PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
28	c2mzeA_	Alignment	not modelled	87.0	9	PDB header: hydrolase Chain: A; PDB Molecule: matrilysin; PDBTitle: nmr solution structure of the pro form of human matrilysin (prommp-7)
						Fold: Zincin-like

29	d1dmta_	Alignment	not modelled	87.0	23	Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neutral endopeptidase (neprilysin)
30	c3k7lA_	Alignment	not modelled	86.4	40	PDB header: hydrolase Chain: A: PDB Molecule: atragin; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
31	d1mmqa_	Alignment	not modelled	86.2	10	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
32	c3dwbA_	Alignment	not modelled	86.0	18	PDB header: hydrolase Chain: A: PDB Molecule: endothelin-converting enzyme 1; PDBTitle: structure of human ece-1 complexed with phosphoramidon
33	d2ejqa1	Alignment	not modelled	85.2	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
34	c2qr4B_	Alignment	not modelled	85.2	26	PDB header: hydrolase Chain: B: PDB Molecule: peptidase m3b, oligoendopeptidase f; PDBTitle: crystal structure of oligoendopeptidase-f from enterococcus faecium
35	d1hovA_	Alignment	not modelled	85.1	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
36	d2ajfa1	Alignment	not modelled	84.9	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
37	d1r55A_	Alignment	not modelled	84.6	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
38	c2e3xA_	Alignment	not modelled	84.5	31	PDB header: hydrolase, blood clotting, toxin Chain: A: PDB Molecule: coagulation factor x-activating enzyme heavy chain; PDBTitle: crystal structure of russell's viper venom metalloproteinase
39	d2i47a1	Alignment	not modelled	84.5	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
40	c2dw1B_	Alignment	not modelled	84.4	43	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
41	c6be6D_	Alignment	not modelled	84.4	38	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
42	c3k7nA_	Alignment	not modelled	84.3	31	PDB header: hydrolase Chain: A: PDB Molecule: k-like; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
43	c2erpA_	Alignment	not modelled	83.9	46	PDB header: toxin Chain: A: PDB Molecule: vascular apoptosis-inducing protein 1; PDBTitle: crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
44	c2i47A_	Alignment	not modelled	83.3	38	PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
45	d1nd1a_	Alignment	not modelled	83.0	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
46	d1atla_	Alignment	not modelled	82.7	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
47	d4aiga_	Alignment	not modelled	82.3	43	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
48	d1wnia_	Alignment	not modelled	82.2	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
49	d1uzea_	Alignment	not modelled	82.1	27	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
50	c2c6nA_	Alignment	not modelled	81.9	24	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: angiotensin-converting enzyme, somatic isoform; PDBTitle: structure of human somatic angiotensin-i converting enzyme n domain2 with lisinopril
51	d1quaa_	Alignment	not modelled	81.8	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
52	c3g5cA_	Alignment	not modelled	81.7	18	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
53	d1j36a_	Alignment	not modelled	81.3	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
54	c2v4bB_	Alignment	not modelled	81.3	38	PDB header: hydrolase Chain: B: PDB Molecule: adamts-1; PDBTitle: crystal structure of human adamts-1 catalytic domain and cysteine-2 rich domain (apo-form)
						Fold: Zincin-like

55	d1kufa_	Alignment	not modelled	81.2	38	Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
56	c2rjpC_	Alignment	not modelled	80.8	31	PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound
57	c5th6D_	Alignment	not modelled	80.5	16	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: matrix metalloproteinase-9,matrix metalloproteinase-9; PDBTitle: structure determination of a potent, selective antibody inhibitor of 2 human mmp9 (apo mmp9)
58	c4dd8B_	Alignment	not modelled	80.5	46	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat
59	c2rjqA_	Alignment	not modelled	79.8	38	PDB header: hydrolase Chain: A: PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound
60	d1bswa_	Alignment	not modelled	79.2	46	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
61	c2xs4A_	Alignment	not modelled	78.7	54	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium
62	d1y93a1	Alignment	not modelled	78.3	10	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
63	d1xuca1	Alignment	not modelled	77.8	62	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
64	c5kdjA_	Alignment	not modelled	77.7	50	PDB header: hydrolase Chain: A: PDB Molecule: f5/8 type c domain protein; PDBTitle: zmpb metallopeptidase from clostridium perfringens
65	d1g9ka2	Alignment	not modelled	77.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
66	d1sata2	Alignment	not modelled	77.5	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
67	d1bqqm_	Alignment	not modelled	77.4	13	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
68	d1cxva_	Alignment	not modelled	76.8	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
69	c3b8zB_	Alignment	not modelled	76.8	36	PDB header: hydrolase Chain: B: PDB Molecule: protein adamts-5; PDBTitle: high resolution crystal structure of the catalytic domain of adamts-52 (aggrecanase-2)
70	c1yp1A_	Alignment	not modelled	76.5	43	PDB header: hydrolase Chain: A: PDB Molecule: fii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
71	d1k7ia2	Alignment	not modelled	75.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
72	d1hv5a_	Alignment	not modelled	75.6	14	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
73	c1su3A_	Alignment	not modelled	75.6	17	PDB header: hydrolase Chain: A: PDB Molecule: interstitial collagenase; PDBTitle: x-ray structure of human prommp-1: new insights into2 collagenase action
74	d1rm8a_	Alignment	not modelled	75.4	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
75	d1q3aa_	Alignment	not modelled	75.4	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
76	c4fcaA_	Alignment	not modelled	74.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a functionally unknown conserved protein from2 bacillus anthracis str. ames.
77	d1i76a_	Alignment	not modelled	74.4	62	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
78	c2jsdA_	Alignment	not modelled	74.1	16	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngH
79	c5kd2A_	Alignment	not modelled	74.0	50	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: bt_4244 metallopeptidase from bacteroides thetaiotaomicron
80	c2cltB_	Alignment	not modelled	73.9	46	PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase.
81	d1qiba_	Alignment	not modelled	72.9	62	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain

82	d1kapp2	Alignment	not modelled	72.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralyisin-like metalloprotease, catalytic (N-terminal) domain
83	c3ba0A	Alignment	not modelled	72.1	50	PDB header: hydrolase Chain: A: PDB Molecule: macrophage metalloelastase; PDBTitle: crystal structure of full-length human mmp-12
84	d2ovxa1	Alignment	not modelled	72.1	62	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
85	d1hy7a_	Alignment	not modelled	70.8	13	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
86	c4yu5A	Alignment	not modelled	70.8	75	PDB header: hydrolase Chain: A: PDB Molecule: immune inhibitor a, metalloprotease; PDBTitle: crystal structure of selenomethionine variant of bacillus anthracis2 immune inhibitor a2 peptidase zymogen
87	d1cglA	Alignment	not modelled	70.1	54	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
88	c1jiwP	Alignment	not modelled	69.7	50	PDB header: hydrolase/hydrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
89	c5czwA	Alignment	not modelled	68.6	70	PDB header: hydrolase Chain: A: PDB Molecule: myrolysin; PDBTitle: crystal structure of myrolysin
90	c3o0yC	Alignment	not modelled	68.5	8	PDB header: lipid binding protein Chain: C: PDB Molecule: lipoprotein; PDBTitle: the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
91	c1eakA	Alignment	not modelled	68.5	58	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant
92	d1hfca	Alignment	not modelled	68.3	13	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
93	c2l0rA	Alignment	not modelled	64.0	47	PDB header: hydrolase, toxin Chain: A: PDB Molecule: lethal factor; PDBTitle: conformational dynamics of the anthrax lethal factor catalytic center
94	c4g0dD	Alignment	not modelled	63.9	13	PDB header: hydrolase Chain: D: PDB Molecule: collagenase 3; PDBTitle: human collagenase 3 (mmp-13) full form with peptides from pro-domain
95	c1wgzC	Alignment	not modelled	63.1	40	PDB header: hydrolase Chain: C: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of carboxypeptidase 1 from thermus thermophilus
96	d1eaka2	Alignment	not modelled	62.7	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
97	c5kdvA	Alignment	not modelled	62.5	60	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: impa metallopeptidase from pseudomonas aeruginosa
98	c2j83B	Alignment	not modelled	61.8	44	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
99	c3p24C	Alignment	not modelled	60.5	78	PDB header: hydrolase Chain: C: PDB Molecule: bft-3; PDBTitle: structure of profragilysin-3 from bacteroides fragilis
100	c1l6jA	Alignment	not modelled	60.2	67	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-9; PDBTitle: crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
101	c1om8A	Alignment	not modelled	58.4	50	PDB header: hydrolase Chain: A: PDB Molecule: serralyisin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
102	d1k9xa	Alignment	not modelled	58.1	47	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
103	c4on1B	Alignment	not modelled	57.3	67	PDB header: hydrolase Chain: B: PDB Molecule: putative metalloprotease ii; PDBTitle: crystal structure of metalloproteinase-ii from bacteroides fragilis
104	c4jiuA	Alignment	not modelled	55.3	21	PDB header: hydrolase Chain: A: PDB Molecule: proabylysin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
105	d1asta	Alignment	not modelled	53.3	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Astacin
106	c3lqbA	Alignment	not modelled	52.7	50	PDB header: hydrolase Chain: A: PDB Molecule: loc792177 protein; PDBTitle: crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
107	d1fbla2	Alignment	not modelled	51.7	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
108	d1c7ka	Alignment	not modelled	51.0	75	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease

109	d1j7na2	Alignment	not modelled	50.9	47	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains
110	c3edhA	Alignment	not modelled	50.9	40	PDB header: hydrolase Chain: A; PDB Molecule: bone morphogenetic protein 1; PDBTitle: crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
111	c5givD	Alignment	not modelled	47.7	38	PDB header: hydrolase Chain: D; PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of m32 carboxypeptidase from deinococcus radiodurans2 r1
112	c3vtgA	Alignment	not modelled	47.6	50	PDB header: hydrolase Chain: A; PDB Molecule: high choriolytic enzyme 1; PDBTitle: high choriolytic enzyme 1 (hce-1), a hatching enzyme zinc-protease2 from oryzias latipes (medaka fish)
113	c5e3xA	Alignment	not modelled	45.9	47	PDB header: hydrolase Chain: A; PDB Molecule: thermostable carboxypeptidase 1; PDBTitle: crystal structure of thermostable carboxypeptidase (fiscp) from2 fervidobacterium islandicum aw-1
114	c5xbvA	Alignment	not modelled	45.6	18	PDB header: hydrolase Chain: A; PDB Molecule: wss1p; PDBTitle: crystal structure of wss1 mutant from saccharomyces cerevisiae
115	c3p1vB	Alignment	not modelled	45.3	21	PDB header: hydrolase Chain: B; PDB Molecule: metallo-endopeptidase; PDBTitle: crystal structure of a metallo-endopeptidases (bacova_00663) from2 bacteroides ovatus at 1.93 a resolution
116	c6fpcA	Alignment	not modelled	45.3	25	PDB header: hydrolase Chain: A; PDB Molecule: pro-pro endopeptidase; PDBTitle: structure of the pro-pro endopeptidase (ppep-2) from paenibacillus2 alvei
117	c1satA	Alignment	not modelled	45.1	50	PDB header: hydrolase (serine protease) Chain: A; PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
118	c5a0sA	Alignment	not modelled	44.4	20	PDB header: hydrolase Chain: A; PDB Molecule: zinc metalloprotease zmp1; PDBTitle: apo-structure of metalloprotease zmp1 variant e143a from clostridium2 difficile
119	c3dwcA	Alignment	not modelled	43.8	33	PDB header: hydrolase Chain: A; PDB Molecule: metallocarboxypeptidase; PDBTitle: trypanosoma cruzi metallocarboxypeptidase 1
120	c4jixB	Alignment	not modelled	42.3	11	PDB header: hydrolase Chain: B; PDB Molecule: projannalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin