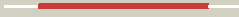


























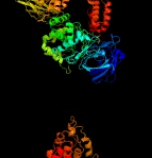


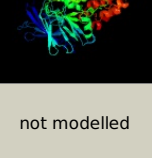


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2467_(pepN)_2768996_2771581
Date	Wed Aug 7 12:50:09 BST 2019
Unique Job ID	2b3cd5be534bc3cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fytA_	 Alignment		100.0	20	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: human aminopeptidase n (cd13) in complex with amastatin
2	c4kxdA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of human aminopeptidase a complexed with glutamate2 and calcium
3	c4f5cA_	 Alignment		100.0	21	PDB header: hydrolase/viral protein Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig aminopeptidase n3 ectodomain
4	c3se6A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 2; PDBTitle: crystal structure of the human endoplasmic reticulum aminopeptidase 2
5	c4wz9A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: agap004809-pa; PDBTitle: apn1 from anopheles gambiae
6	c1z5hB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: tricorn protease interacting factor f3; PDBTitle: crystal structures of the tricorn interacting factor f3 from2 thermoplasma acidophilum
7	c2xdtA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1
8	c4pj6B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: leucyl-cystinyl aminopeptidase; PDBTitle: crystal structure of human insulin regulated aminopeptidase with2 lysine in active site
9	c3mdjB_	 Alignment		100.0	21	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
10	c3qnfC_	 Alignment		100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
11	c5dllA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: aminopeptidase n (pepn) from francisella tularensis subsp. tularensis2 schu s4

12	c3ebhA	Alignment		100.0	16	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: m1 family aminopeptidase; PDBTitle: structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
13	c3b37A	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of e. coli aminopeptidase n in complex with tyrosine
14	c5zi7A	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of legionella pneumophila aminopeptidase a in2 complex with glutamic acid
15	c2gtqA	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
16	c3qnfA	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
17	c5furl	Alignment		100.0	13	PDB header: transcription Chain: I: PDB Molecule: transcription initiation factor tfiid subunit 2; PDBTitle: structure of human tfiid-ia bound to core promoter dna
18	c3ciaA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: cold-active aminopeptidase; PDBTitle: crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
19	c4gaaA	Alignment		100.0	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: mgc78867 protein; PDBTitle: structure of leukotriene a4 hydrolase from xenopus laevis complexed2 with inhibitor bestatin
20	c3b7uX	Alignment		100.0	18	PDB header: hydrolase Chain: X: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: leukotriene a4 hydrolase complexed with kelatorphan
21	c2xpyA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
22	c6hqaA	Alignment	not modelled	100.0	14	PDB header: transcription Chain: A: PDB Molecule: taf2; PDBTitle: molecular structure of promoter-bound yeast tfiid
23	c6a8zB	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: zinc metalloprotease, putative; PDBTitle: crystal structure of m1 zinc metallopeptidase from deinococcus2 radiodurans
24	c4fgmA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase n family protein; PDBTitle: crystal structure of the aminopeptidase n family protein q5qy1 from2 idiomarina loihiensis. northeast structural genomics consortium3 target ilr60.
25	d3b7sa3	Alignment	not modelled	100.0	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leukotriene A4 hydrolase catalytic domain
26	c3rjoA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of erap1 peptide binding domain
27	d3b7sa2	Alignment	not modelled	100.0	19	Fold: Leukotriene A4 hydrolase N-terminal domain Superfamily: Leukotriene A4 hydrolase N-terminal domain Family: Leukotriene A4 hydrolase N-terminal domain
28	c4fcaA	Alignment	not modelled	97.6	14	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.

29	c5kdjA_	Alignment	not modelled	97.2	17	PDB header: hydrolase Chain: A: PDB Molecule: f5/8 type c domain protein; PDBTitle: zmpb metallopeptidase from clostridium perfringens
30	c5kd2A_	Alignment	not modelled	97.2	13	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: bt_4244 metallopeptidase from bacteroides thetaiotaomicron
31	c2vqxA_	Alignment	not modelled	96.0	16	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
32	d1u4ga_	Alignment	not modelled	95.7	11	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
33	d1npca_	Alignment	not modelled	94.7	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
34	c3cqbB_	Alignment	not modelled	93.3	15	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
35	d1bqba_	Alignment	not modelled	93.1	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
36	c4gerB_	Alignment	not modelled	92.9	19	PDB header: hydrolase Chain: B: PDB Molecule: gentiyase metalloprotease; PDBTitle: crystal structure of gentiyase, the neutral metalloprotease of2 paenibacillus polymyxa
37	c3k7IA_	Alignment	not modelled	89.8	14	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
38	d1kjpA_	Alignment	not modelled	89.2	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
39	c6aitD_	Alignment	not modelled	89.2	18	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
40	c5mqnA_	Alignment	not modelled	89.0	11	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolases family 2, sugar binding domain; PDBTitle: glycoside hydrolase bt_0986
41	c3k7nA_	Alignment	not modelled	89.0	16	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
42	c4dd8B_	Alignment	not modelled	88.4	11	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat
43	c2dw1B_	Alignment	not modelled	88.0	10	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
44	c2erpA_	Alignment	not modelled	87.5	12	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)
45	c4jiuA_	Alignment	not modelled	87.2	15	PDB header: hydrolase Chain: A: PDB Molecule: proabylisin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
46	d4aiga_	Alignment	not modelled	87.2	12	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
47	c5ln5A_	Alignment	not modelled	86.3	26	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin and wlm domain-containing metalloprotease PDBTitle: crystal structure of the wss1 e203q mutant from s. pombe
48	d1r55a_	Alignment	not modelled	84.2	13	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
49	c6h56A_	Alignment	not modelled	83.8	21	PDB header: metal binding protein Chain: A: PDB Molecule: effector domain of pseudomonas aeruginosa vgrg2b; PDBTitle: effector domain of pseudomonas aeruginosa vgrg2b
50	c2e3xA_	Alignment	not modelled	83.6	10	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
51	c4jixB_	Alignment	not modelled	83.1	11	PDB header: hydrolase Chain: B: PDB Molecule: projannalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
52	c3g5cA_	Alignment	not modelled	82.9	14	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
53	d1nd1a_	Alignment	not modelled	82.2	14	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
54	c5xvA_	Alignment	not modelled	82.0	27	PDB header: hydrolase Chain: A: PDB Molecule: wss1p;

54	c3x0vA	Alignment	not modelled	82.0	37	PDBTitle: crystal structure of wss1 mutant from saccharomyces cerevisiae PDB header: hydrolase
55	c4ar1A	Alignment	not modelled	80.0	18	Chain: A; PDB Molecule: colh protein; PDBTitle: crystal structure of the peptidase domain of collagenase h from <i>Clostridium histolyticum</i> at 2.01 angstrom resolution.
56	c4ar9A	Alignment	not modelled	79.9	24	PDB header: hydrolase Chain: A; PDB Molecule: collagenase colt; PDBTitle: crystal structure of the peptidase domain of collagenase t2 from <i>Clostridium tetani</i> at 1.69 angstrom resolution.
57	d1kufa	Alignment	not modelled	78.7	14	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
58	c3nqzB	Alignment	not modelled	78.4	12	PDB header: hydrolase Chain: B; PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
59	c2j83B	Alignment	not modelled	78.2	23	PDB header: hydrolase Chain: B; PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
60	d1bswa	Alignment	not modelled	78.0	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
61	c3c37B	Alignment	not modelled	76.9	15	PDB header: hydrolase Chain: B; PDB Molecule: peptidase, m48 family; PDBTitle: x-ray structure of the putative zn-dependent peptidase q74d82 at the 2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
62	d1wnia	Alignment	not modelled	76.5	12	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
63	d1atla	Alignment	not modelled	75.2	9	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
64	d1quaa	Alignment	not modelled	75.1	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
65	c3dtkA	Alignment	not modelled	74.4	16	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
66	c4il3B	Alignment	not modelled	74.2	17	PDB header: hydrolase Chain: B; PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
67	c2y50A	Alignment	not modelled	72.4	20	PDB header: hydrolase Chain: A; PDB Molecule: collagenase; PDBTitle: crystal structure of collagenase g from <i>Clostridium histolyticum</i> at 2.80 angstrom resolution
68	c4k90A	Alignment	not modelled	71.0	18	PDB header: hydrolase Chain: A; PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
69	c4aw6B	Alignment	not modelled	67.7	19	PDB header: hydrolase Chain: B; PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
70	c2v4bB	Alignment	not modelled	67.6	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)
71	c2rjqA	Alignment	not modelled	66.6	19	PDB header: hydrolase Chain: A; PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound
72	c2xhqA	Alignment	not modelled	65.3	18	PDB header: hydrolase Chain: A; PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from <i>Archaeoglobus fulgidus</i> at 1.45 a resolution
73	d2ejqa1	Alignment	not modelled	63.1	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
74	c1yp1A	Alignment	not modelled	63.0	9	PDB header: hydrolase Chain: A; PDB Molecule: fii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of <i>Agkistrodon acutus</i>
75	c3o0yC	Alignment	not modelled	62.5	11	PDB header: lipid binding protein Chain: C; PDB Molecule: lipoprotein; PDBTitle: the crystal structure of the putative lipoprotein from <i>Colwellia psychrerythraea</i>
76	c3nqxA	Alignment	not modelled	61.7	13	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
77	c6be6D	Alignment	not modelled	59.5	27	PDB header: membrane protein Chain: D; PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
78	c3b8zB	Alignment	not modelled	59.5	50	PDB header: hydrolase Chain: B; PDB Molecule: protein adamts-5; PDBTitle: high resolution crystal structure of the catalytic domain of adamts-52 (aggrecanase-2)
79	c2i47A	Alignment	not modelled	56.2	21	PDB header: hydrolase Chain: A; PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
80	c2rjpC	Alignment	not modelled	55.6	33	PDB header: hydrolase Chain: C; PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound

81	d2i47a1	Alignment	not modelled	55.4	21	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
82	d1bqqm_	Alignment	not modelled	55.3	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
83	d3e11a1	Alignment	not modelled	54.1	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
84	c5kdvA_	Alignment	not modelled	53.0	20	PDB header: hydrolase Chain: A: PDB Molecule: metallopeptidase; PDBTitle: impa metallopeptidase from pseudomonas aeruginosa
85	d1jz8a3	Alignment	not modelled	52.4	15	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
86	c3deeA_	Alignment	not modelled	52.3	8	PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
87	d1k9xa_	Alignment	not modelled	51.5	11	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
88	c3lmcA_	Alignment	not modelled	50.7	20	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, zinc-dependent; PDBTitle: crystal structure of zinc-dependent peptidase from methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16
89	c3dwcA_	Alignment	not modelled	49.9	13	PDB header: hydrolase Chain: A: PDB Molecule: metallocarboxypeptidase; PDBTitle: trypanosoma cruzi metallocarboxypeptidase 1
90	c5a0sA_	Alignment	not modelled	49.1	21	PDB header: hydrolase Chain: A: PDB Molecule: zinc metalloprotease zmp1; PDBTitle: apo-structure of metalloprotease zmp1 variant e143a from clostridium2 difficile
91	c1z7hA_	Alignment	not modelled	46.1	29	PDB header: hydrolase Chain: A: PDB Molecule: tetanus toxin light chain; PDBTitle: 2.3 angstrom crystal structure of tetanus neurotoxin light chain
92	c3iukB_	Alignment	not modelled	45.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
93	d1rm8a_	Alignment	not modelled	45.3	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
94	d1j7na2	Alignment	not modelled	44.9	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains
95	c2qn0A_	Alignment	not modelled	44.6	22	PDB header: toxin Chain: A: PDB Molecule: neurotoxin; PDBTitle: structure of botulinum neurotoxin serotype c1 light chain2 protease
96	c5e3xA_	Alignment	not modelled	43.2	14	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxypeptidase 1; PDBTitle: crystal structure of thermostable carboxypeptidase (fiscp) from2 fervidobacterium islandicum aw-1
97	c2o0cB_	Alignment	not modelled	43.1	16	PDB header: signaling protein Chain: B: PDB Molecule: alr2278 protein; PDBTitle: crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
98	c2l0rA_	Alignment	not modelled	42.6	36	PDB header: hydrolase,toxin Chain: A: PDB Molecule: lethal factor; PDBTitle: conformational dynamics of the anthrax lethal factor catalytic center
99	c2x7mA_	Alignment	not modelled	42.4	18	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
100	c6fpcA_	Alignment	not modelled	42.4	16	PDB header: hydrolase Chain: A: PDB Molecule: pro-pro endopeptidase; PDBTitle: structure of the pro-pro endopeptidase (ppep-2) from paenibacillus2 alvei
101	d1f83a_	Alignment	not modelled	42.1	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Clostridium neurotoxins, catalytic domain
102	c4l7aB_	Alignment	not modelled	40.6	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative zinc-binding metallo-peptidase2 (baccac_01431) from bacteroides caccae atcc 43185 at 2.10 a3 resolution
103	c6mdxA_	Alignment	not modelled	39.9	28	PDB header: dna binding protein/dna Chain: A: PDB Molecule: spirt-like domain-containing protein spartan; PDBTitle: mechanism of protease dependent dpc repair
104	d1epwa3	Alignment	not modelled	39.4	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Clostridium neurotoxins, catalytic domain
105	c3sksA_	Alignment	not modelled	39.0	12	PDB header: hydrolase Chain: A: PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
106	c5d0bP_	Alignment	not modelled	38.8	14	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase;

106	c3u0bB	Alignment	not modelled	38.8	14	PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
107	d3btaa3	Alignment	not modelled	34.7	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Clostridium neurotoxins, catalytic domain
108	c5n0cB	Alignment	not modelled	33.2	29	PDB header: toxin Chain: B: PDB Molecule: tetanus toxin; PDBTitle: crystal structure of the tetanus neurotoxin in complex with gm1a
109	c6cz6D	Alignment	not modelled	33.2	18	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator prpr; PDBTitle: mycobacterium tuberculosis transcriptional regulator
110	c4yu5A	Alignment	not modelled	32.2	18	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
111	c3dl1A	Alignment	not modelled	32.0	50	PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent hydrolase; PDBTitle: crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution
112	c1s0bA	Alignment	not modelled	31.9	33	PDB header: toxin, hydrolase Chain: A: PDB Molecule: botulinum neurotoxin type b; PDBTitle: crystal structure of botulinum neurotoxin type b at ph 4.0
113	c6bdeA	Alignment	not modelled	31.1	15	PDB header: signaling protein Chain: A: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: crystal structure of fe(ii) unliganded h-nox protein mutant a71g from2 k. algicida
114	c3i7jB	Alignment	not modelled	30.9	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase mb2281c; PDBTitle: crystal structure of a beta-lactamase (mb2281c) from mycobacterium2 bovis, northeast structural genomics consortium target mbr246
115	d2f22a1	Alignment	not modelled	30.4	24	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
116	c3zuqA	Alignment	not modelled	30.3	35	PDB header: hydrolase Chain: A: PDB Molecule: botulinum neurotoxin type b; PDBTitle: crystal structure of an engineered botulinum neurotoxin2 type b-derivative, lc-b-gs-hn-b
117	c6nfgC	Alignment	not modelled	29.9	13	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
118	d2je8a4	Alignment	not modelled	29.7	13	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
119	c4yomA	Alignment	not modelled	29.5	19	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase brsk2; PDBTitle: structure of sad kinase
120	d1kapp2	Alignment	not modelled	28.9	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain