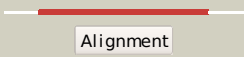

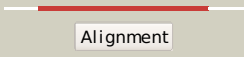

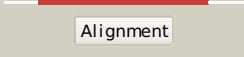

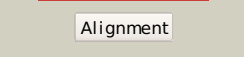

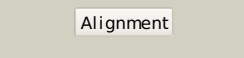

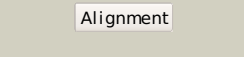

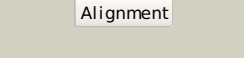

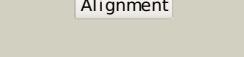

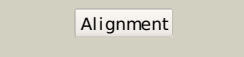
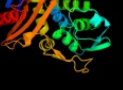
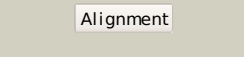

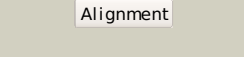












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z6fA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: penicillin-binding protein 5; PDBTitle: crystal structure of penicillin-binding protein 5 from e. coli in2 complex with a boronic acid inhibitor
2	c3it9B_	 Alignment		100.0	26	PDB header: hydrolase Chain: B; PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacc; PDBTitle: crystal structure of penicillin-binding protein 6 (pbp6)2 from e. coli in apo state
3	c3a3jA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
4	c3mfdB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacc; PDBTitle: the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
5	c1tvfA_	 Alignment		100.0	22	PDB header: penicillin binding Chain: A; PDB Molecule: penicillin binding protein 4; PDBTitle: crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus
6	c3humB_	 Alignment		100.0	22	PDB header: hydrolase/antibiotics Chain: B; PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 from2 staphylococcus aureus col in complex with cefotaxime
7	c1xp4C_	 Alignment		100.0	24	PDB header: hydrolase Chain: C; PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of a peptidoglycan synthesis regulatory2 factor (pbp3) from streptococcus pneumoniae
8	d1tvfa2	 Alignment		100.0	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
9	c2bcfA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: probable d-alanyl-d-alanine carboxypeptidase PDBTitle: crystal structure of a evolved putative penicillin-binding2 protein homolog, rv2911, from mycobacterium tuberculosis.
10	d3beca2	 Alignment		100.0	24	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
11	d1xp4a2	 Alignment		100.0	26	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

12	dles5a_	Alignment		100.0	27	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
13	c2v20A_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase tem; PDBTitle: structure of a tem-1 beta-lactamase insertant2 allosterically regulated by kanamycin and anions. complex3 with sulfate.
14	dln9ba_	Alignment		100.0	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
15	c3cg5A_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
16	c2j7vA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: tlf12115 protein; PDBTitle: structure of pbp-a
17	d1m40a_	Alignment		100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
18	c3qhyA_	Alignment		100.0	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structural, thermodynamic and kinetic analysis of the picomolar2 binding affinity interaction of the beta-lactamase inhibitor protein-3 ii (blip-ii) with class a beta-lactamases
19	d1o7ea_	Alignment		100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
20	cli2sa_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
21	dli2sa_	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
22	c3dw0B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: class a carbapenemase kpc-2; PDBTitle: crystal structure of the class a carbapenemase kpc-2 at 1.62 angstrom resolution
23	d1hzoa_	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
24	d1dy6a_	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
25	d1bsga_	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
26	d2cc1a1	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
27	dliysa_	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
28	c2ov5A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
29	c3n09B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase;

29	c3p09B	Alignment	not modelled	100.0	10	PDBTitle: crystal structure of beta-lactamase from francisella tularensis PDB header: hydrolase
30	c3cjmA	Alignment	not modelled	100.0	13	Chain: A; PDB Molecule: putative beta-lactamase; PDBTitle: crystal structure of putative beta-lactamase (np_815223.1) from2 enterococcus faecalis v583 at 1.50 a resolution
31	c2qpA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
32	c1w7fB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
33	c2wuqA	Alignment	not modelled	100.0	20	PDB header: transcription Chain: A; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
34	d1buea	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
35	c3lezA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
36	d1g6aa	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
37	d1djaa	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
38	d1alqa	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
39	c3p09A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
40	d1e25a	Alignment	not modelled	100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
41	c2wuqB	Alignment	not modelled	100.0	20	PDB header: transcription Chain: B; PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
42	c2xftA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
43	c3a3eB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: penicillin-binding protein 4; PDBTitle: crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
44	d1w79a1	Alignment	not modelled	99.9	25	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
45	d1w5da1	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
46	d2ex2a1	Alignment	not modelled	99.9	24	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
47	d1nrfa	Alignment	not modelled	99.7	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
48	d1xa1a	Alignment	not modelled	99.6	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
49	c2iwdA	Alignment	not modelled	99.6	16	PDB header: antibiotic resistance Chain: A; PDB Molecule: methicillin resistance mecrl protein; PDBTitle: oxacilloyl-acylated mecrl extracellular antibiotic-sensor2 domain.
50	c2jc7A	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase oxa-24; PDBTitle: the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
51	c3hbrD	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: D; PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
52	c3if6C	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: C; PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
53	d1k38a	Alignment	not modelled	99.4	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
54	d1k55a	Alignment	not modelled	99.4	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase mb2281c;

55	c3i7jB_	Alignment	not modelled	99.3	16	PDBTitle: crystal structure of a beta-lactamase (mb2281c) from2 mycobacterium bovis, northeast structural genomics3 consortium target mbr246
56	c2wadB_	Alignment	not modelled	99.2	17	PDB header: peptide binding protein Chain: B: PDB Molecule: penicillin-binding protein 2b; PDBTitle: penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
57	c3oc2A_	Alignment	not modelled	99.2	16	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
58	d1m6ka_	Alignment	not modelled	99.1	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
59	d1vqqa3	Alignment	not modelled	99.1	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
60	c3lo7A_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
61	c3pbqA_	Alignment	not modelled	99.0	20	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
62	c3equB_	Alignment	not modelled	99.0	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
63	c3udiA_	Alignment	not modelled	99.0	14	PDB header: penicillin-binding protein/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
64	d1pyya4	Alignment	not modelled	98.9	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
65	c1qmFA_	Alignment	not modelled	98.9	16	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
66	c3fwlA_	Alignment	not modelled	98.9	18	PDB header: transferase, hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
67	d1rp5a4	Alignment	not modelled	98.8	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
68	d1yqsa1	Alignment	not modelled	98.7	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
69	c3ue3A_	Alignment	not modelled	98.7	16	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
70	d2dcfa1	Alignment	not modelled	98.7	25	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
71	d1rgya_	Alignment	not modelled	98.6	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
72	c2qmiH_	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: H: PDB Molecule: pbp related beta-lactamase; PDBTitle: structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
73	d1ci9a_	Alignment	not modelled	98.6	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
74	c1zkjA_	Alignment	not modelled	98.5	19	PDB header: hydrolase Chain: A: PDB Molecule: extended-spectrum beta-lactamase; PDBTitle: structural basis for the extended substrate spectrum of cmy-2 10, a plasmid-encoded class c beta-lactamase
75	c3o3vB_	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of clbp peptidase domain
76	c2qz6A_	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: first crystal structure of a psychrophile class c beta-2 lactamase
77	d2hdsa1	Alignment	not modelled	98.4	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
78	d1ei5a3	Alignment	not modelled	98.3	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
79	c3hleA_	Alignment	not modelled	98.3	21	PDB header: transferase Chain: A: PDB Molecule: transesterase; PDBTitle: simvastatin synthase (lovD), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
80	c2wzzA_	Alignment	not modelled	98.3	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
81	d2c5wb1	Alignment	not modelled	98.3	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

82	d1onha_	Alignment	not modelled	98.3	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
83	c3ozhA_	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
84	c1ei5A_	Alignment	not modelled	98.2	19	PDB header: hydrolase Chain: A: PDB Molecule: d-aminopeptidase; PDBTitle: crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
85	d2drwa1	Alignment	not modelled	98.0	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
86	c3tg9A_	Alignment	not modelled	98.0	16	PDB header: penicillin binding protein Chain: A: PDB Molecule: penicillin-binding protein; PDBTitle: the crystal structure of penicillin binding protein from bacillus2 halodurans
87	c1pmdA_	Alignment	not modelled	98.0	15	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
88	c1mwuA_	Alignment	not modelled	97.9	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
89	d2bg1a1	Alignment	not modelled	97.8	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
90	c2bg1A_	Alignment	not modelled	97.7	13	PDB header: peptidoglycan Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
91	d2olua2	Alignment	not modelled	97.5	23	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
92	c2olvA_	Alignment	not modelled	97.3	19	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein 2; PDBTitle: structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
93	d1k25a4	Alignment	not modelled	97.3	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	c3dwkC_	Alignment	not modelled	97.3	22	PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
95	c2jciA_	Alignment	not modelled	96.8	15	PDB header: drug-binding protein Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b
96	c2pbyB_	Alignment	not modelled	80.7	23	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase; PDBTitle: probable glutaminase from geobacillus kaustophilus hta426
97	d1u60a_	Alignment	not modelled	75.1	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
98	c3czdA_	Alignment	not modelled	73.9	13	PDB header: hydrolase Chain: A: PDB Molecule: glutaminase kidney isoform; PDBTitle: crystal structure of human glutaminase in complex with l-glutamate
99	c3uo9B_	Alignment	not modelled	67.8	13	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
100	c2dfwA_	Alignment	not modelled	46.0	22	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
101	c3ih9A_	Alignment	not modelled	42.4	22	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
102	c1tcmB_	Alignment	not modelled	38.3	19	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
103	c3nqyA_	Alignment	not modelled	38.2	40	PDB header: hydrolase Chain: A: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a