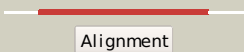

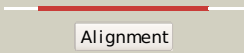







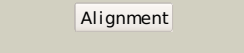

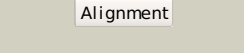

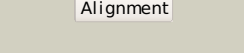



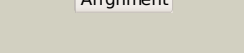

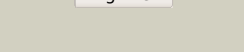


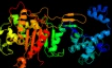






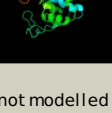


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3oc2A_</a>	 Alignment		100.0	28	<b>PDB header:</b> penicillin-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
2	<a href="#">c3pbqA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of pbp3 complexed with imipenem
3	<a href="#">c1pmdA_</a>	 Alignment		100.0	19	<b>PDB header:</b> peptidoglycan synthesis <b>Chain:</b> A; <b>PDB Molecule:</b> peptidoglycan synthesis multifunctional enzyme; <b>PDBTitle:</b> penicillin-binding protein 2x (pbp-2x)
4	<a href="#">c1mwuA_</a>	 Alignment		100.0	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein 2a; <b>PDBTitle:</b> structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain 327r at 2.60 Å resolution.
5	<a href="#">c2wadB_</a>	 Alignment		100.0	26	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> penicillin-binding protein 2b; <b>PDBTitle:</b> penicillin-binding protein 2b (pbp-2b) from streptococcus pneumoniae (strain 5204)
6	<a href="#">c3ue3A_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> septum formation, penicillin binding protein 3, <b>PDBTitle:</b> crystal structure of acinetobacter baumannii pbp3
7	<a href="#">c1qmfA_</a>	 Alignment		100.0	23	<b>PDB header:</b> peptidoglycan synthesis <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein 2x; <b>PDBTitle:</b> penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
8	<a href="#">c3equB_</a>	 Alignment		100.0	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
9	<a href="#">c3lo7A_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> penicillin-binding protein a; <b>PDBTitle:</b> crystal structure of pbpa from mycobacterium tuberculosis
10	<a href="#">d1pyya4</a>	 Alignment		100.0	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
11	<a href="#">d1rp5a4</a>	 Alignment		100.0	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase

12	<a href="#">d1vqqa3</a>	Alignment		100.0	25	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
13	<a href="#">c3dwkC</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
14	<a href="#">c3udiA</a>	Alignment		100.0	21	<b>PDB header:</b> penicillin-binding protein/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1a; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
15	<a href="#">d2c5wb1</a>	Alignment		100.0	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
16	<a href="#">c2olvA</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
17	<a href="#">c3fwlA</a>	Alignment		100.0	18	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
18	<a href="#">d1k25a4</a>	Alignment		100.0	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
19	<a href="#">c2bg1A</a>	Alignment		100.0	21	<b>PDB header:</b> peptidoglycan <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
20	<a href="#">c2jciA</a>	Alignment		100.0	21	<b>PDB header:</b> drug-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b
21	<a href="#">d2bg1a1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
22	<a href="#">d2olua2</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
23	<a href="#">c2iwdA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> methicillin resistance mecrl protein; <b>PDBTitle:</b> oxacilloyl-acylated mecrl extracellular antibiotic-sensor2 domain.
24	<a href="#">d1m6ka</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
25	<a href="#">d1k55a</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
26	<a href="#">d1k38a</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
27	<a href="#">c3hbrD</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> oxa-48; <b>PDBTitle:</b> crystal structure of oxa-48 beta-lactamase
28	<a href="#">d1nrfa</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
29	<a href="#">c3if6C</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> oxa-46 oxacillinase;

29	<a href="#">c3n0c_</a>	Alignment	not modelled	100.0	20	<b>PDBTitle:</b> crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
30	<a href="#">d1xa1a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
31	<a href="#">c2jc7A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase oxa-24; <b>PDBTitle:</b> the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
32	<a href="#">d1vqqa2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Penicillin binding protein dimerisation domain <b>Superfamily:</b> Penicillin binding protein dimerisation domain <b>Family:</b> Penicillin binding protein dimerisation domain
33	<a href="#">c2wuqB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase regulatory protein blab; <b>PDBTitle:</b> crystal structure of blab protein from streptomyces cacaoi
34	<a href="#">c2qpna_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase ges-1; <b>PDBTitle:</b> ges-1 beta-lactamase
35	<a href="#">d1g6aa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
36	<a href="#">d1iysa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
37	<a href="#">c2xftA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> orf12; <b>PDBTitle:</b> structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
38	<a href="#">d1e25a_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
39	<a href="#">d1dy6a_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
40	<a href="#">c2ov5A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbapenemase; <b>PDBTitle:</b> crystal structure of the kpc-2 carbapenemase
41	<a href="#">c2wuqA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase regulatory protein blab; <b>PDBTitle:</b> crystal structure of blab protein from streptomyces cacaoi
42	<a href="#">d1o7ea_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
43	<a href="#">d2cc1a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
44	<a href="#">d1m40a_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
45	<a href="#">c3dw0B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> class a carbapenemase kpc-2; <b>PDBTitle:</b> crystal structure of the class a carbapenemase kpc-2 at 1.62 angstrom resolution
46	<a href="#">d1bsga_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
47	<a href="#">d1buea_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
48	<a href="#">c3lezA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of a halotolerant bacterial beta-lactamase
49	<a href="#">d1djaa_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
50	<a href="#">c2j7vA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tlf2115 protein; <b>PDBTitle:</b> structure of pbp-a
51	<a href="#">d1n9ba_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
52	<a href="#">c1w7fB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
53	<a href="#">d1pyya3</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Penicillin binding protein dimerisation domain <b>Superfamily:</b> Penicillin binding protein dimerisation domain <b>Family:</b> Penicillin binding protein dimerisation domain
54	<a href="#">d1k25a3</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Penicillin binding protein dimerisation domain <b>Superfamily:</b> Penicillin binding protein dimerisation domain <b>Family:</b> Penicillin binding protein dimerisation domain
55	<a href="#">c2v20A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase tem; <b>PDBTitle:</b> structure of a tem-1 beta-lactamase insertant2 allosterically regulated by kanamycin and anions. complex3 with sulfate.

56	<a href="#">dlhzoa_</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
57	<a href="#">c3qhyA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> 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
58	<a href="#">c3cg5A_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
59	<a href="#">cli2sa_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> beta-lactamase from bacillus licheniformis bs3
60	<a href="#">dli2sa_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
61	<a href="#">c3p09B_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from francisella tularensis
62	<a href="#">dlalqa_</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
63	<a href="#">c3p09A_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of beta-lactamase from francisella tularensis
64	<a href="#">dles5a_</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
65	<a href="#">d1xp4a2</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
66	<a href="#">c3cjmA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-lactamase; <b>PDBTitle:</b> crystal structure of putative beta-lactamase (np_815223.1) from2 enterococcus faecalis v583 at 1.50 a resolution
67	<a href="#">c2bcfA_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable d-alanyl-d-alanine carboxypeptidase <b>PDBTitle:</b> crystal structure of a evolved putative penicillin-binding2 protein homolog, rv2911, from mycobacterium tuberculosis.
68	<a href="#">d3beca2</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
69	<a href="#">d1tvfa2</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
70	<a href="#">d1w79a1</a>	Alignment	not modelled	98.8	23	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
71	<a href="#">clz6fA_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 5; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 5 from e. coli in2 complex with a boronic acid inhibitor
72	<a href="#">c1xp4C_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase; <b>PDBTitle:</b> crystal structure of a peptidoglycan synthesis regulatory2 factor (pbp3) from streptococcus pneumoniae
73	<a href="#">c1tvfA_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> penicillin binding <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 4 (pbp4)2 from staphylococcus aureus
74	<a href="#">c3it9B_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dacc; <b>PDBTitle:</b> crystal structure of penicillin-binding protein 6 (pbp6)2 from e. coli in apo state
75	<a href="#">c3a3jA_</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pbp5; <b>PDBTitle:</b> crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
76	<a href="#">c2wzzA_</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
77	<a href="#">c3humB_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase/antibiotics <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin binding protein 4 from2 staphylococcus aureus col in complex with cefotaxime
78	<a href="#">c3mfdB_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dacb; <b>PDBTitle:</b> the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
79	<a href="#">d1rgya_</a>	Alignment	not modelled	98.2	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
80	<a href="#">d1onha_</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase

81	<a href="#">dlyqsa1</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
82	<a href="#">d1u60a_</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Glutaminase
83	<a href="#">c3ss4C_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glutaminase c; <b>PDBTitle:</b> crystal structure of mouse glutaminase c, phosphate-bound form
84	<a href="#">c2qmiH_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> pbp related beta-lactamase; <b>PDBTitle:</b> structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
85	<a href="#">c2dfwA_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
86	<a href="#">c3uo9B_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> glutaminase kidney isoform, mitochondrial; <b>PDBTitle:</b> crystal structure of human gac in complex with glutamate and bptes
87	<a href="#">c1zkjA_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extended-spectrum beta-lactamase; <b>PDBTitle:</b> structural basis for the extended substrate spectrum of cmv-2 10, a plasmid-encoded class c beta-lactamase
88	<a href="#">c3ih9A_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure analysis of mglu in its tris form
89	<a href="#">d1w5da1</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
90	<a href="#">d2hdsa1</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
91	<a href="#">c2pbyB_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> probable glutaminase from geobacillus kaustophilus hta426
92	<a href="#">c3czdA_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminase kidney isoform; <b>PDBTitle:</b> crystal structure of human glutaminase in complex with l-glutamate
93	<a href="#">d2olua1</a>	Alignment	not modelled	97.0	16	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PBP transglycosylase domain-like
94	<a href="#">c2qz6A_</a>	Alignment	not modelled	96.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> first crystal structure of a psychrophile class c beta-2 lactamase
95	<a href="#">c3a3eB_</a>	Alignment	not modelled	96.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
96	<a href="#">d1ci9a_</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
97	<a href="#">d2dcfa1</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
98	<a href="#">c3ozhA_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase/d-alanine carboxypeptidase; <b>PDBTitle:</b> crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
99	<a href="#">d2ex2a1</a>	Alignment	not modelled	96.2	38	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
100	<a href="#">c1ei5A_</a>	Alignment	not modelled	96.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-aminopeptidase; <b>PDBTitle:</b> crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
101	<a href="#">c3o3vB_</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of clbp peptidase domain
102	<a href="#">d1mkia_</a>	Alignment	not modelled	95.9	21	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Glutaminase
103	<a href="#">c3tg9A_</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> penicillin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein; <b>PDBTitle:</b> the crystal structure of penicillin binding protein from bacillus2 halodurans
104	<a href="#">d2drwa1</a>	Alignment	not modelled	95.6	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
105	<a href="#">d1ei5a3</a>	Alignment	not modelled	93.7	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
106	<a href="#">c3hleA_</a>	Alignment	not modelled	92.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transesterase; <b>PDBTitle:</b> simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid

107	<a href="#">d2oqoa1</a>	Alignment	not modelled	92.3	10	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PBP transglycosylase domain-like
108	<a href="#">c3i7jB_</a>	Alignment	not modelled	90.2	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase mb2281c; <b>PDBTitle:</b> crystal structure of a beta-lactamase (mb2281c) from2 mycobacterium bovis, northeast structural genomics3 consortium target mbr246
109	<a href="#">c3hzaA_</a>	Alignment	not modelled	89.3	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monofunctional glycosyltransferase; <b>PDBTitle:</b> s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
110	<a href="#">d1c8ua2</a>	Alignment	not modelled	40.3	29	<b>Fold:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Superfamily:</b> Thioesterase/thiol ester dehydrase-isomerase <b>Family:</b> Acyl-CoA thioesterase
111	<a href="#">d1zpsa1</a>	Alignment	not modelled	38.1	40	<b>Fold:</b> Hisl-like <b>Superfamily:</b> Hisl-like <b>Family:</b> Hisl-like
112	<a href="#">c3rd7A_</a>	Alignment	not modelled	34.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa thioesterase; <b>PDBTitle:</b> crystal structure of acyl-coa thioesterase from mycobacterium avium
113	<a href="#">d2v8qe2</a>	Alignment	not modelled	22.9	18	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
114	<a href="#">c2x5qa_</a>	Alignment	not modelled	22.9	34	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso1986; <b>PDBTitle:</b> crystal structure of hypothetical protein sso1986 from2 sulfolobus solfataricus p2
115	<a href="#">c3cyaA_</a>	Alignment	not modelled	22.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of putative thioesterase (yp_496845.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.70 a resolution
116	<a href="#">c3rqbB_</a>	Alignment	not modelled	22.1	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function with hot2 dog fold from alicyclobacillus acidocaldarius
117	<a href="#">c3bbjaA_</a>	Alignment	not modelled	21.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase ii; <b>PDBTitle:</b> crystal structure of a putative thioesterase ii (tfu_2367) from2 thermobifida fusca yx at 2.45 a resolution