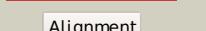
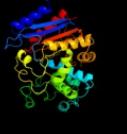
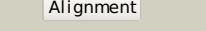
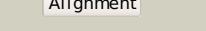
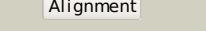
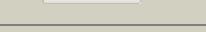
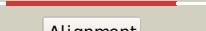
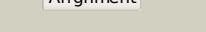
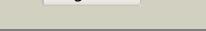


# Phyre<sup>2</sup>

Email	i.a.kelley@imperial.ac.uk
Description	P0AD70
Date	Thu Jan 5 11:20:09 GMT 2012
Unique Job ID	55651868a8e3ea35

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ozhA_</a>			100.0	61	<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
2	<a href="#">c2gmiH_</a>			100.0	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
3	<a href="#">d1rgya_</a>			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
4	<a href="#">d2hdsa1</a>			100.0	23	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
5	<a href="#">c1ei5A_</a>			100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-amino peptidase; <b>PDBTitle:</b> crystal structure of a d-amino peptidase from ochrobactrum2 anthropi
6	<a href="#">d1onha_</a>			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
7	<a href="#">c3o3vB_</a>			100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of clbp peptidase domain
8	<a href="#">c2wzzA_</a>			100.0	22	<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
9	<a href="#">c2qz6A_</a>			100.0	21	<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
10	<a href="#">c1zkjA_</a>			100.0	21	<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 cmy-2 10, a plasmid-encoded class c beta-lactamase
11	<a href="#">d2drwa1</a>			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

12	<a href="#">d1yqsa1</a>			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
13	<a href="#">c3tg9A_</a>			100.0	20	<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
14	<a href="#">d1ci9a_</a>			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
15	<a href="#">d1ei5a3</a>			100.0	18	<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="#">c3hleA_</a>			100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transesterase; <b>PDBTitle:</b> simvastatin synthase (lovad), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
17	<a href="#">d2dcfa1</a>			100.0	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
18	<a href="#">c3i7jB_</a>			100.0	25	<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) from mycobacterium bovis, northeast structural genomics3 consortium target mbr246
19	<a href="#">d1hzoa_</a>			99.5	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
20	<a href="#">d1m40a_</a>			99.4	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
21	<a href="#">c2wuqB_</a>		not modelled	99.3	15	<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
22	<a href="#">d1iysa_</a>		not modelled	99.3	17	<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="#">c2j7vA_</a>		not modelled	99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tli2115 protein; <b>PDBTitle:</b> structure of pbp-a
24	<a href="#">c3p09A_</a>		not modelled	99.3	16	<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
25	<a href="#">d1n9ba_</a>		not modelled	99.3	16	<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="#">c2ov5A_</a>		not modelled	99.3	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
27	<a href="#">c2wuqA_</a>		not modelled	99.3	15	<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
28	<a href="#">c2qpna_</a>		not modelled	99.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase ges-1; <b>PDBTitle:</b> ges-1 beta-lactamase
						<b>Fold:</b> beta-lactamase/transpeptidase-like

29	<a href="#">d1g6aa</a>	Alignment	not modelled	99.3	16	<b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
30	<a href="#">d2cc1a1</a>	Alignment	not modelled	99.2	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="#">d1tvfa2</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
32	<a href="#">c2v20A</a>	Alignment	not modelled	99.2	14	<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.
33	<a href="#">d1o7ea</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
34	<a href="#">d1buea</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
35	<a href="#">c3p09B</a>	Alignment	not modelled	99.2	16	<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
36	<a href="#">d1dy6a</a>	Alignment	not modelled	99.2	16	<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="#">d1bsga</a>	Alignment	not modelled	99.1	18	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
38	<a href="#">c1tvfA</a>	Alignment	not modelled	99.1	23	<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
39	<a href="#">c1z6fA</a>	Alignment	not modelled	99.1	22	<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
40	<a href="#">d1e25a</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
41	<a href="#">d3beca2</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
42	<a href="#">c3cjmA</a>	Alignment	not modelled	99.1	12	<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
43	<a href="#">c3a3jA</a>	Alignment	not modelled	99.1	20	<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
44	<a href="#">c3dw0B</a>	Alignment	not modelled	99.1	17	<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
45	<a href="#">c3it9B</a>	Alignment	not modelled	99.1	20	<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
46	<a href="#">d1i2sa</a>	Alignment	not modelled	99.1	17	<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="#">c1i2sA</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> beta-lactamase from bacillus licheniformis bs3
48	<a href="#">c3humB</a>	Alignment	not modelled	99.0	26	<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
49	<a href="#">c1xp4C</a>	Alignment	not modelled	99.0	14	<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
50	<a href="#">d1xp4a2</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
51	<a href="#">d1es5a</a>	Alignment	not modelled	98.9	17	<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="#">c3cg5A</a>	Alignment	not modelled	98.9	14	<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
53	<a href="#">c1w7fB</a>	Alignment	not modelled	98.8	20	<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
54	<a href="#">c3leza</a>	Alignment	not modelled	98.8	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
						<b>PDB header:</b> hydrolase

55	<a href="#">c2xftA_</a>	Alignment	not modelled	98.8	18	<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  <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
56	<a href="#">c3qhyA_</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase  <b>PDB header:</b> hydrolase
57	<a href="#">d1dja_</a>	Alignment	not modelled	98.7	12	<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.
58	<a href="#">c2bcfA_</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
59	<a href="#">d1alqa_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl-d-alanine carboxypeptidase dabc; <b>PDBTitle:</b> the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
60	<a href="#">c3mfdB_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 3; <b>PDBTitle:</b> crystal structure of ppb3 complexed with imipenem
61	<a href="#">c3pbqA_</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> hydrolase/antibiotic <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
62	<a href="#">c2jc7A_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> hydrolase <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
63	<a href="#">c3equB_</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
64	<a href="#">d1pyya4</a>	Alignment	not modelled	97.6	16	<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 (ppb-2b) from streptococcus2 pneumoniae (strain 5204)
65	<a href="#">d1rp5a4</a>	Alignment	not modelled	97.5	15	<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="#">c2wadB_</a>	Alignment	not modelled	97.4	18	<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
67	<a href="#">d1nrfa_</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> mecr1 protein; <b>PDBTitle:</b> oxacilloyl-acylated mecr1 extracellular antibiotic-sensor2 domain.
68	<a href="#">c3oc2A_</a>	Alignment	not modelled	96.8	17	<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 ppb3
69	<a href="#">c2iwdA_</a>	Alignment	not modelled	96.8	9	<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 (ppb-2x) acyl-enzyme complex
70	<a href="#">c3ue3A_</a>	Alignment	not modelled	96.7	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
71	<a href="#">d1vqqa3</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> hydrolase
72	<a href="#">d1k38a_</a>	Alignment	not modelled	96.4	18	<b>Chain:</b> A: <b>PDB Molecule:</b> oxa-46 oxacillinase; <b>PDBTitle:</b> crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
73	<a href="#">c1qmfA_</a>	Alignment	not modelled	96.3	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
74	<a href="#">c3if6C_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> penicillin-binding protein 2x; <b>PDBTitle:</b> penicillin-binding protein 2x (ppb-2x) acyl-enzyme complex
75	<a href="#">d1k25a4</a>	Alignment	not modelled	95.7	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
76	<a href="#">d1xala_</a>	Alignment	not modelled	95.7	11	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
77	<a href="#">c1pmda_</a>	Alignment	not modelled	95.6	14	<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 (ppb-2x)
78	<a href="#">d1k55a_</a>	Alignment	not modelled	94.9	15	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
79	<a href="#">c3hbrD_</a>	Alignment	not modelled	94.7	15	<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
80	<a href="#">d1w79a1</a>	Alignment	not modelled	94.6	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like

						<b>Family:</b> Dac-like
81	<a href="#">c3dwkC</a>	Alignment	not modelled	94.5	10	<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
82	<a href="#">d2c5wb1</a>	Alignment	not modelled	94.2	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
83	<a href="#">c3lo7A</a>	Alignment	not modelled	93.6	11	<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
84	<a href="#">c1mwuA</a>	Alignment	not modelled	93.5	15	<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 strain3 27r at 2.60 a resolution.
85	<a href="#">d2olu2</a>	Alignment	not modelled	92.7	10	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
86	<a href="#">c3fwIA</a>	Alignment	not modelled	91.8	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
87	<a href="#">d1m6ka</a>	Alignment	not modelled	91.6	11	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
88	<a href="#">c2jciA</a>	Alignment	not modelled	91.4	20	<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
89	<a href="#">d2bg1a1</a>	Alignment	not modelled	91.4	20	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
90	<a href="#">c2olvA</a>	Alignment	not modelled	90.9	10	<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
91	<a href="#">d1w5da1</a>	Alignment	not modelled	90.8	23	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
92	<a href="#">c2bg1A</a>	Alignment	not modelled	88.1	17	<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)
93	<a href="#">c3a3eB</a>	Alignment	not modelled	76.6	14	<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 (dabc)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
94	<a href="#">c3udiA</a>	Alignment	not modelled	75.4	14	<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
95	<a href="#">c2pbyB</a>	Alignment	not modelled	69.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> probable glutaminase from geobacillus kaustophilus hta426
96	<a href="#">c3uo9B</a>	Alignment	not modelled	67.2	23	<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
97	<a href="#">c3ss4C</a>	Alignment	not modelled	67.0	23	<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
98	<a href="#">c3czdA</a>	Alignment	not modelled	66.6	13	<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
99	<a href="#">c2dfwA</a>	Alignment	not modelled	62.1	12	<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-tolerant glutaminase from micrococcus luteus k-3
100	<a href="#">c3ih9A</a>	Alignment	not modelled	59.9	12	<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
101	<a href="#">d1u60a</a>	Alignment	not modelled	54.9	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Glutaminase
102	<a href="#">d1mkia</a>	Alignment	not modelled	50.3	9	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Glutaminase