
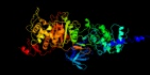





























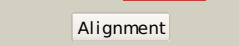



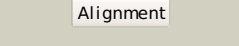
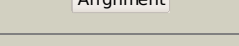




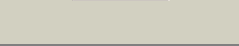
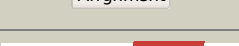



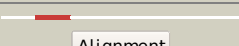
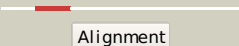
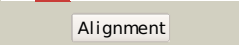
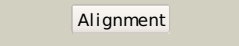

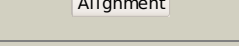
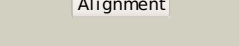
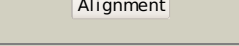











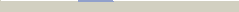
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fwlA_	 Alignment		100.0	97	PDB header: transferase, hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
2	c3dwkC_	 Alignment		100.0	27	PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
3	c2olvA_	 Alignment		100.0	26	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
4	c3udiA_	 Alignment		100.0	35	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
5	c2jciA_	 Alignment		100.0	19	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
6	c2bg1A_	 Alignment		100.0	20	PDB header: peptidoglycan Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
7	d2bg1a1	 Alignment		100.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
8	d2c5wb1	 Alignment		100.0	27	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
9	d2olua2	 Alignment		100.0	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
10	c2wadB_	 Alignment		100.0	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)
11	c1pmdA_	 Alignment		100.0	15	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)

12	c3lo7A_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
13	c1qmfA_	Alignment		100.0	15	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
14	c3pbqA_	Alignment		100.0	24	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
15	c3ue3A_	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
16	c3hzsA_	Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
17	c3oc2A_	Alignment		100.0	26	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
18	dlrp5a4	Alignment		100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
19	c3equB_	Alignment		100.0	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
20	dlpyya4	Alignment		100.0	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
21	d2oqoa1	Alignment	not modelled	100.0	44	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
22	d2olua1	Alignment	not modelled	100.0	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
23	dlvqqa3	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
24	c1mwuA_	Alignment	not modelled	100.0	20	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.
25	dlk25a4	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
26	c2iwdA_	Alignment	not modelled	100.0	18	PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mcr1 protein; PDBTitle: oxacilloyl-acylated mcr1 extracellular antibiotic-sensor2 domain.
27	dlk38a_	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
28	c3if6C_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa

29	d1m6ka_	Alignment	not modelled	100.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
30	d1k55a_	Alignment	not modelled	100.0	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
31	d1nrfa_	Alignment	not modelled	100.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
32	c2jc7A_	Alignment	not modelled	100.0	17	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
33	d1xa1a_	Alignment	not modelled	100.0	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
34	c3hbrD_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
35	c2wuqB_	Alignment	not modelled	99.9	16	PDB header: transcription Chain: B: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
36	d1dy6a_	Alignment	not modelled	99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
37	c2xftA_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
38	c2wuqA_	Alignment	not modelled	99.9	15	PDB header: transcription Chain: A: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
39	c2qpnA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
40	d1g6aa_	Alignment	not modelled	99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
41	d1iysa_	Alignment	not modelled	99.8	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
42	c2ov5A_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
43	d2cc1a1	Alignment	not modelled	99.8	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
44	d1e25a_	Alignment	not modelled	99.8	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
45	c2j7vA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: tlf12115 protein; PDBTitle: structure of pbp-a
46	c3lezA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
47	c3dw0B_	Alignment	not modelled	99.8	18	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
48	d1djaa_	Alignment	not modelled	99.8	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
49	d1buea_	Alignment	not modelled	99.8	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
50	d1bsga_	Alignment	not modelled	99.8	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
51	d1o7ea_	Alignment	not modelled	99.7	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
52	d1alqa_	Alignment	not modelled	99.7	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
53	d1m40a_	Alignment	not modelled	99.7	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
54	c1w7fB_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
55	d1n9ba_	Alignment	not modelled	99.7	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

56	c2v20A		not modelled	99.7	16	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.
57	c3qhyA		not modelled	99.7	15	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
58	c3cg5A		not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
59	d1hzoa		not modelled	99.6	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
60	d1i2sa		not modelled	99.5	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
61	c1i2sA		not modelled	99.5	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
62	c3p09B		not modelled	99.4	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
63	c3p09A		not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
64	c3cjmA		not modelled	99.2	15	PDB header: hydrolase 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
65	d3beca2		not modelled	99.0	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
66	c2bcfA		not modelled	98.9	22	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.
67	d1es5a		not modelled	98.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
68	c3a3jA		not modelled	98.8	13	PDB header: hydrolase Chain: A: PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
69	c3mfdB		not modelled	98.7	22	PDB header: hydrolase Chain: B: PDB Molecule: d-alanyl-d-alanine carboxypeptidase dacb; PDBTitle: the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
70	d1w79a1		not modelled	98.7	29	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
71	d1xp4a2		not modelled	98.6	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
72	d2b2na1		not modelled	98.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
73	c3jhjA		not modelled	98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair-coupling factor; PDBTitle: a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
74	c3fpnB		not modelled	98.4	24	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrb interaction PDBTitle: crystal structure of uvra-uvrb interaction domains
75	c2eyqA		not modelled	98.4	16	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
76	d1t5la1		not modelled	98.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
77	d2eyqa4		not modelled	98.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
78	c3it9B		not modelled	98.3	19	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
79	c1z6fA		not modelled	98.3	19	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
						PDB header: hydrolase Chain: B: PDB Molecule: penicillin-binding protein 4;

80	c3a3eB_	Alignment	not modelled	98.1	18	PDBTitle: crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
81	c1xp4C_	Alignment	not modelled	98.1	15	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
82	d1tvfa2	Alignment	not modelled	97.9	11	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
83	c1tvfA_	Alignment	not modelled	97.9	12	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
84	c3humB_	Alignment	not modelled	97.9	12	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
85	c3ih9A_	Alignment	not modelled	97.5	21	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
86	c3czdA_	Alignment	not modelled	97.4	16	PDB header: hydrolase Chain: A: PDB Molecule: glutaminase kidney isoform; PDBTitle: crystal structure of human glutaminase in complex with l-glutamate
87	c2pbyB_	Alignment	not modelled	97.4	15	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase; PDBTitle: probable glutaminase from geobacillus kaustophilus hta426
88	c2qmiH_	Alignment	not modelled	97.4	21	PDB header: hydrolase Chain: H: PDB Molecule: pbp related beta-lactamase; PDBTitle: structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
89	c3uo9B_	Alignment	not modelled	97.1	16	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
90	c2dfwA_	Alignment	not modelled	97.0	18	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
91	d1yqsa1	Alignment	not modelled	96.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
92	d2drwa1	Alignment	not modelled	96.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
93	d1onha_	Alignment	not modelled	96.8	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	d1rgya_	Alignment	not modelled	96.5	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
95	d1w5da1	Alignment	not modelled	96.4	26	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
96	c3ozhA_	Alignment	not modelled	96.3	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
97	d2hdsa1	Alignment	not modelled	96.2	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
98	c3i7jB_	Alignment	not modelled	96.0	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase mb2281c; PDBTitle: crystal structure of a beta-lactamase (mb2281c) from2 mycobacterium bovis, northeast structural genomics3 consortium target mbr246
99	d2ex2a1	Alignment	not modelled	96.0	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
100	c2qz6A_	Alignment	not modelled	95.9	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: first crystal structure of a psychrophile class c beta-2 lactamase
101	c3o3vB_	Alignment	not modelled	95.5	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of clbp peptidase domain
102	c2wzzA_	Alignment	not modelled	95.4	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
103	c1zkjA_	Alignment	not modelled	94.9	16	PDB header: hydrolase Chain: A: PDB Molecule: extended-spectrum beta-lactamase; PDBTitle: structural basis for the extended substrate spectrum of cmv-2 10, a plasmid-encoded class c beta-lactamase
104	d1mkia_	Alignment	not modelled	93.8	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
105	d1ci9a_	Alignment	not modelled	92.7	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

106	d1u60a_	 Alignment	not modelled	92.6	24	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
107	c3tg9A_	 Alignment	not modelled	86.2	20	PDB header: penicillin binding protein Chain: A: PDB Molecule: penicillin-binding protein; PDBTitle: the crystal structure of penicillin binding protein from bacillus2 halodurans
108	d2dcfa1	 Alignment	not modelled	83.4	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
109	c3hleA_	 Alignment	not modelled	83.2	16	PDB header: transferase Chain: A: PDB Molecule: transesterase; PDBTitle: simvastatin synthase (lovD), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
110	d1jz8a3	 Alignment	not modelled	50.6	22	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
111	d2ieaa3	 Alignment	not modelled	43.1	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
112	c2a6eF_	 Alignment	not modelled	40.8	20	PDB header: transferase Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme
113	d1smyf3	 Alignment	not modelled	21.5	17	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors