Phyre^{2}

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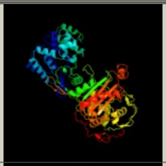
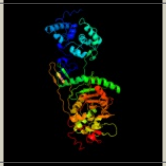
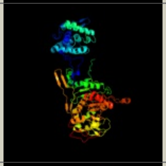
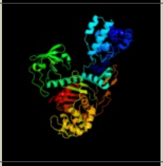
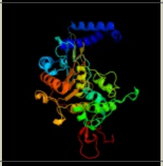
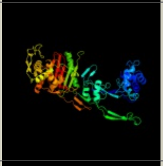
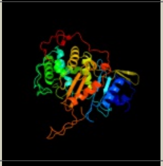
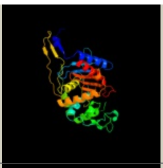
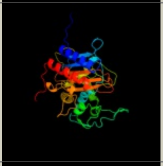
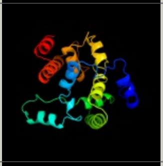
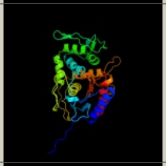
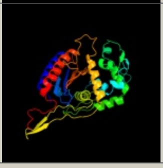
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dwkC_	Alignment		100.0	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
2	c3fwlA_	Alignment		100.0	32	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
3	c2olvA_	Alignment		100.0	29	**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	44	**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	26	**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	26	**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	27	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
8	d2c5wb1	Alignment		100.0	28	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
9	c2wadB_	Alignment		100.0	18	**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)
10	d2olua2	Alignment		100.0	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
11	c1pmdA_	Alignment		100.0	19	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**peptidoglycan synthesis multifunctional enzyme; **PDBTitle:** penicillin-binding protein 2x (pbp-2x)

12	c3lo7A_	Alignment		100.0	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein a; **PDBTitle:** crystal structure of pbpa from mycobacterium tuberculosis
13	c1qmfA_	Alignment		100.0	24	**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	29	**PDB header:**hydrolase/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of pbp3 complexed with imipenem
15	d2olua1	Alignment		100.0	38	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
16	c3hzsA_	Alignment		100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monofunctional glycosyltransferase; **PDBTitle:** s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
17	c3equB_	Alignment		100.0	26	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
18	c3oc2A_	Alignment		100.0	29	**PDB header:**penicillin-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
19	c3ue3A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
20	d1rp5a4	Alignment		100.0	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
21	d2oqoa1	Alignment	not modelled	100.0	57	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
22	d1pyya4	Alignment	not modelled	100.0	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
23	d1vqqa3	Alignment	not modelled	100.0	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
24	c1mwuA_	Alignment	not modelled	100.0	19	**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	d1k25a4	Alignment	not modelled	100.0	24	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
26	c2iwdA_	Alignment	not modelled	100.0	19	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**methicillin resistance mecr1 protein; **PDBTitle:** oxacilloyl-acylated mecr1 extracellular antibiotic-sensor2 domain.
27	d1k38a_	Alignment	not modelled	100.0	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
28	d1m6ka_	Alignment	not modelled	100.0	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
						Fold:beta-lactamase/transpeptidase-like

29	d1nrfa_	Alignment	not modelled	100.0	22	**Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
30	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
31	d1k55a_	Alignment	not modelled	100.0	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
32	c2jc7A_	Alignment	not modelled	100.0	24	**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	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
34	c3hbrD_	Alignment	not modelled	100.0	20	**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	d1g6aa_	Alignment	not modelled	99.8	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
37	c2qpnA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ges-1; **PDBTitle:** ges-1 beta-lactamase
38	d1dy6a_	Alignment	not modelled	99.8	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
39	c2xftA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**orf12; **PDBTitle:** structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
40	d1iysa_	Alignment	not modelled	99.8	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
41	c2wuqA_	Alignment	not modelled	99.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**beta-lactamase regulatory protein blab; **PDBTitle:** crystal structure of blab protein from streptomyces cacaoi
42	c2ov5A_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbapenemase; **PDBTitle:** crystal structure of the kpc-2 carbapenemase
43	d2cc1a1	Alignment	not modelled	99.8	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
44	c3dw0B_	Alignment	not modelled	99.8	16	**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
45	c3lezA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of a halotolerant bacterial beta-lactamase
46	c2j7vA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tll2115 protein; **PDBTitle:** structure of pbp-a
47	d1djaa_	Alignment	not modelled	99.7	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
48	d1buea_	Alignment	not modelled	99.7	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
49	d1e25a_	Alignment	not modelled	99.7	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
50	d1m40a_	Alignment	not modelled	99.7	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
51	d1o7ea_	Alignment	not modelled	99.7	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
52	d1n9ba_	Alignment	not modelled	99.7	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
53	c2v20A_	Alignment	not modelled	99.6	14	**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.
54	d1bsga_	Alignment	not modelled	99.6	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
55	c1w7fB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate

56	c3qhyA_	Alignment	not modelled	99.6	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
57	d1hzoa_	Alignment	not modelled	99.6	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
58	d1alqa_	Alignment	not modelled	99.5	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
59	c3cg5A_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
60	c1i2sA_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** beta-lactamase from bacillus licheniformis bs3
61	d1i2sa_	Alignment	not modelled	99.4	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
62	c3p09B_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
63	c3p09A_	Alignment	not modelled	99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
64	d1es5a_	Alignment	not modelled	98.9	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
65	c2bcfA_	Alignment	not modelled	98.9	20	**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.
66	c3cjmA_	Alignment	not modelled	98.9	18	**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
67	d3beca2	Alignment	not modelled	98.6	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
68	d1xp4a2	Alignment	not modelled	98.5	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
69	c3a3jA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pbp5; **PDBTitle:** crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
70	c3d0fA_	Alignment	not modelled	98.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
71	c1z6fA_	Alignment	not modelled	98.3	18	**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
72	c3it9B_	Alignment	not modelled	98.2	15	**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
73	c1xp4C_	Alignment	not modelled	98.1	16	**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
74	d1tvfa2	Alignment	not modelled	98.0	12	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
75	c1tvfA_	Alignment	not modelled	97.9	13	**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
76	c3mfdB_	Alignment	not modelled	97.9	14	**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
77	c3humB_	Alignment	not modelled	97.8	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
78	c3uo9B_	Alignment	not modelled	97.3	18	**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
79	c3ih9A_	Alignment	not modelled	97.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
80	c2pbyB_	Alignment	not modelled	97.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase;

80	c2pbyB_	Alignment	not modelled	97.2	17	**PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
81	c2dfwA_	Alignment	not modelled	97.1	17	**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
82	c3czdA_	Alignment	not modelled	97.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaminase kidney isoform; **PDBTitle:** crystal structure of human glutaminase in complex with l-glutamate
83	c3ss4C_	Alignment	not modelled	96.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
84	d1u60a_	Alignment	not modelled	96.8	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
85	d1mkia_	Alignment	not modelled	96.5	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
86	c3a3eB_	Alignment	not modelled	95.7	20	**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)
87	d2ex2a1	Alignment	not modelled	95.3	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
88	d1w5da1	Alignment	not modelled	95.3	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
89	d1w79a1	Alignment	not modelled	95.2	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
90	d1yqsa1	Alignment	not modelled	94.7	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
91	c3i7jB_	Alignment	not modelled	94.7	23	**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
92	c2qmiH_	Alignment	not modelled	94.2	19	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**pbp related beta-lactamase; **PDBTitle:** structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
93	d2dcfa1	Alignment	not modelled	93.8	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
94	c3ozhA_	Alignment	not modelled	90.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase/d-alanine carboxypeptidase; **PDBTitle:** crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
95	c2qz6A_	Alignment	not modelled	89.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** first crystal structure of a psychrophile class c beta-2 lactamase
96	d1rgya_	Alignment	not modelled	88.8	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
97	c1zkjA_	Alignment	not modelled	88.7	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
98	d2drwa1	Alignment	not modelled	88.3	25	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
99	c3tg9A_	Alignment	not modelled	83.6	18	**PDB header:**penicillin binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein; **PDBTitle:** the crystal structure of penicillin binding protein from bacillus2 halodurans
100	c3hleA_	Alignment	not modelled	82.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transesterase; **PDBTitle:** simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
101	d1ci9a_	Alignment	not modelled	82.0	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
102	d1onha_	Alignment	not modelled	81.2	26	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
103	c2wzzA_	Alignment	not modelled	76.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
104	d2hdsa1	Alignment	not modelled	70.4	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
105	c3o3vB_	Alignment	not modelled	70.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of clbp peptidase domain
						Fold:TK C-terminal domain-like

106	d2ieaa3	Alignment	not modelled	27.7	19	**Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
107	c3zriA_	Alignment	not modelled	27.2	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**clpb protein; **PDBTitle:** n-domain of clpv from vibrio cholerae
108	d1qvra1	Alignment	not modelled	26.2	22	**Fold:**Double Clp-N motif **Superfamily:**Double Clp-N motif **Family:**Double Clp-N motif
109	c2k77A_	Alignment	not modelled	25.6	7	**PDB header:**chaperone, protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence **PDBTitle:** nmr solution structure of the bacillus subtilis clpc n-2 domain
110	c2a6eF_	Alignment	not modelled	25.3	28	**PDB header:**transferase **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** crystal structure of the t. thermophilus rna polymerase2 holoenzyme
111	d1vqqa2	Alignment	not modelled	23.4	17	**Fold:**Penicillin binding protein dimerisation domain **Superfamily:**Penicillin binding protein dimerisation domain **Family:**Penicillin binding protein dimerisation domain
112	c3fesB_	Alignment	not modelled	22.2	5	**PDB header:**atp binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp endopeptidase; **PDBTitle:** crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile