Phyre2

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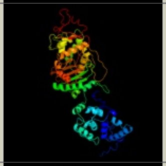
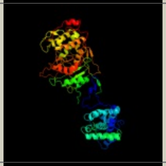
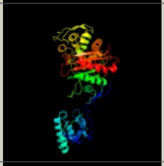
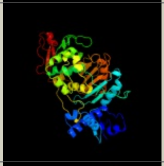
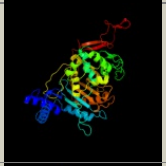
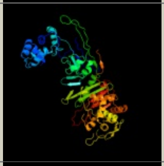
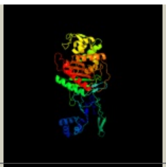
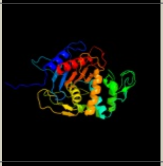
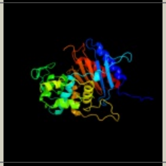
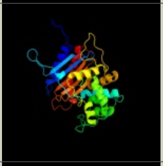
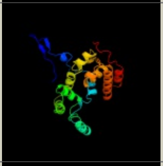
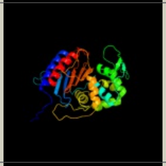
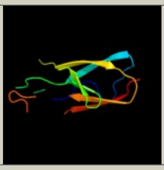
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dwkC_	Alignment		100.0	23	**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	25	**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	22	**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	30	**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	19	**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	c2wadB_	Alignment		100.0	14	**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)
9	d2c5wb1	Alignment		100.0	24	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
10	d2olua2	Alignment		100.0	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
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	c3pbqA_	Alignment		100.0	18	**PDB header:**hydrolase/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of pbp3 complexed with imipenem
13	c3lo7A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein a; **PDBTitle:** crystal structure of pbpa from mycobacterium tuberculosis
14	c3equB_	Alignment		100.0	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
15	c3ue3A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
16	c3oc2A_	Alignment		100.0	20	**PDB header:**penicillin-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
17	d2olua1	Alignment		100.0	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
18	c1qmfA_	Alignment		100.0	16	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**penicillin-binding protein 2x; **PDBTitle:** penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
19	c3hzsA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monofunctional glycosyltransferase; **PDBTitle:** s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
20	d1pyya4	Alignment		100.0	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
21	d1rp5a4	Alignment	not modelled	100.0	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
22	d2oqoa1	Alignment	not modelled	100.0	38	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
23	d1vqqa3	Alignment	not modelled	100.0	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
24	c1mwuA_	Alignment	not modelled	100.0	15	**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	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
26	c2iwdA_	Alignment	not modelled	100.0	12	**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	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
28	d1m6ka_	Alignment	not modelled	100.0	13	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
						PDB header:hydrolase

29	c3if6C_	Alignment	not modelled	100.0	15	**Chain:** C: **PDB Molecule:**oxa-46 oxacillinase; **PDBTitle:** crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
30	d1k55a_	Alignment	not modelled	100.0	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
31	c2jc7A_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase oxa-24; **PDBTitle:** the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
32	d1nrfa_	Alignment	not modelled	100.0	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
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	17	**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	c2qpnA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ges-1; **PDBTitle:** ges-1 beta-lactamase
37	d1g6aa_	Alignment	not modelled	99.9	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
38	d1dy6a_	Alignment	not modelled	99.9	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
39	c2xftA_	Alignment	not modelled	99.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**orf12; **PDBTitle:** structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
40	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
41	d2cc1a1	Alignment	not modelled	99.9	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
42	d1iysa_	Alignment	not modelled	99.9	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
43	c2j7vA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tll2115 protein; **PDBTitle:** structure of pbp-a
44	c2ov5A_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbapenemase; **PDBTitle:** crystal structure of the kpc-2 carbapenemase
45	d1e25a_	Alignment	not modelled	99.8	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
46	d1buea_	Alignment	not modelled	99.8	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
47	c3dw0B_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**class a carbapenemase kpc-2; **PDBTitle:** crystal structure of the class a carbapenemase kpc-2 at 1.62 angstrom resolution
48	c3lezA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of a halotolerant bacterial beta-lactamase
49	d1bsga_	Alignment	not modelled	99.8	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
50	d1o7ea_	Alignment	not modelled	99.8	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
51	d1m40a_	Alignment	not modelled	99.8	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
52	d1djaa_	Alignment	not modelled	99.8	12	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
53	d1n9ba_	Alignment	not modelled	99.8	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
54	c2v20A_	Alignment	not modelled	99.7	18	**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.
55	d1hzoa_	Alignment	not modelled	99.7	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase

56	c1w7fB_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
57	c3qhyA_	Alignment	not modelled	99.7	19	**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	d1alqa_	Alignment	not modelled	99.6	13	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
59	c3cg5A_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
60	d1i2sa_	Alignment	not modelled	99.6	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
61	c1i2sA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** beta-lactamase from bacillus licheniformis bs3
62	c3p09B_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
63	c3cjmA_	Alignment	not modelled	99.4	14	**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
64	c3p09A_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
65	d3beca2	Alignment	not modelled	98.8	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
66	d1xp4a2	Alignment	not modelled	98.8	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
67	d1w79a1	Alignment	not modelled	98.6	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
68	d1es5a_	Alignment	not modelled	98.6	13	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
69	c2bcfA_	Alignment	not modelled	98.4	18	**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.
70	c1xp4C_	Alignment	not modelled	98.3	14	**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
71	d1tvfa2	Alignment	not modelled	98.3	11	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
72	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
73	d2ex2a1	Alignment	not modelled	98.2	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
74	d1w5da1	Alignment	not modelled	98.2	24	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
75	c2pbyB_	Alignment	not modelled	98.1	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
76	c3uo9B_	Alignment	not modelled	98.1	15	**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
77	c3czdA_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaminase kidney isoform; **PDBTitle:** crystal structure of human glutaminase in complex with l-glutamate
78	c2dfwA_	Alignment	not modelled	98.0	16	**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
79	c3ih9A_	Alignment	not modelled	98.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
80	d1u60a_	Alignment	not modelled	98.0	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
						PDB header:hydrolase

81	c3ss4C_	Alignment	not modelled	97.9	16	**Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
82	c3a3jA_	Alignment	not modelled	97.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pbp5; **PDBTitle:** crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
83	c3it9B_	Alignment	not modelled	97.8	17	**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
84	d1mkia_	Alignment	not modelled	97.7	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
85	c3pe9D_	Alignment		97.7	15	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
86	c3humB_	Alignment	not modelled	97.6	13	**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
87	c3mfdB_	Alignment	not modelled	97.6	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
88	c1tvfA_	Alignment	not modelled	97.5	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
89	c1zkjA_	Alignment	not modelled	97.2	16	**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
90	c3pe9B_	Alignment		97.2	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
91	d2dcfa1	Alignment	not modelled	97.2	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
92	d1ci9a_	Alignment	not modelled	97.1	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
93	d1onha_	Alignment	not modelled	97.0	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
94	c3ozhA_	Alignment	not modelled	97.0	20	**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	c3pe9A_	Alignment	not modelled	96.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
96	c3pe9C_	Alignment	not modelled	96.9	19	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
97	d1rgya_	Alignment	not modelled	96.9	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
98	c2wzzA_	Alignment	not modelled	96.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
99	c2qmiH_	Alignment	not modelled	96.6	17	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**pbp related beta-lactamase; **PDBTitle:** structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
100	c2qz6A_	Alignment	not modelled	96.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** first crystal structure of a psychrophile class c beta-2 lactamase
101	c3pdgA_	Alignment	not modelled	96.3	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
102	d2drwa1	Alignment	not modelled	96.1	11	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
103	d2hdsa1	Alignment	not modelled	96.0	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
104	c3a3eB_	Alignment	not modelled	95.8	19	**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)
105	d1yqsa1	Alignment	not modelled	94.7	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
106	c3tg9A_	Alignment	not modelled	93.4	14	**PDB header:**penicillin binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein; **PDBTitle:** the crystal structure of penicillin binding protein from bacillus2 halodurans
107	d1rhfa2	Alignment	not modelled	93.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
108	c3hleA_	Alignment	not modelled	93.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transesterase; **PDBTitle:** simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
109	c3i7jB_	Alignment	not modelled	93.0	21	**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
110	c3o3vB_	Alignment	not modelled	88.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of clbp peptidase domain
111	c2e6pA_	Alignment	not modelled	88.7	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**obscurin-like protein 1; **PDBTitle:** solution structure of the ig-like domain (714-804) from2 human obscurin-like protein 1
112	d2oz4a3	Alignment	not modelled	88.5	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
113	c3pddA_	Alignment	not modelled	87.0	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
114	c2cknA_	Alignment	not modelled	83.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**basic fibroblast growth factor receptor 1; **PDBTitle:** nmr structure of the first ig module of mouse fgfr1
115	d1cs6a1	Alignment	not modelled	82.8	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
116	c2v5mA_	Alignment	not modelled	82.1	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**dscam; **PDBTitle:** structural basis for dscam isoform specificity
117	c2v5rB_	Alignment	not modelled	80.9	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**dscam; **PDBTitle:** structural basis for dscam isoform specificity
118	c3b43A_	Alignment	not modelled	79.9	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**titin; **PDBTitle:** i-band fragment i65-i70 from titin
119	c2dltA_	Alignment	not modelled	79.4	22	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin binding protein c, fast-type; **PDBTitle:** solution structure of the ig-like domain(433- 525) of2 murine myosin-binding protein c, fast-type
120	d1f00i2	Alignment	not modelled	79.3	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments