Phyre^2

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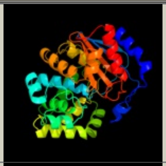
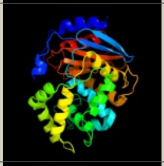
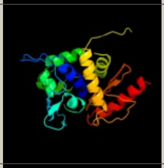
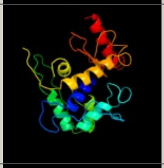
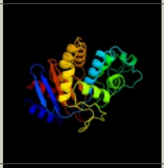
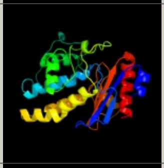
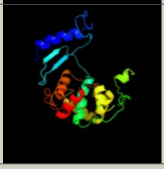
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u60a_	Alignment		100.0	37	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
2	c3ih9A_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
3	c2dfwA_	Alignment		100.0	34	**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
4	c3uo9B_	Alignment		100.0	35	**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
5	c3czdA_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaminase kidney isoform; **PDBTitle:** crystal structure of human glutaminase in complex with l-glutamate
6	c2pbyB_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
7	c3ss4C_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
8	d1mkia_	Alignment		100.0	35	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
9	c3dwkC_	Alignment		97.6	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
10	c3oc2A_	Alignment		97.5	19	**PDB header:**penicillin-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
11	d2dcfa1	Alignment		97.4	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase

12	c2wadB_	Alignment		97.4	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)
13	c3lo7A_	Alignment		97.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein a; **PDBTitle:** crystal structure of pbpa from mycobacterium tuberculosis
14	d1k25a4	Alignment		97.3	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
15	d2c5wb1	Alignment		97.2	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
16	d1vqqa3	Alignment		97.1	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
17	d1buea_	Alignment		97.0	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
18	d1n9ba_	Alignment		96.9	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
19	c2olvA_	Alignment		96.8	17	**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
20	d1rp5a4	Alignment		96.8	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
21	c3qhyA_	Alignment	not modelled	96.8	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
22	c3pbqA_	Alignment	not modelled	96.8	17	**PDB header:**hydrolase/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of pbp3 complexed with imipenem
23	c2jc7A_	Alignment	not modelled	96.6	15	**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
24	d2olua2	Alignment	not modelled	96.6	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
25	d1g6aa_	Alignment	not modelled	96.5	13	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
26	d1pyya4	Alignment	not modelled	96.5	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
27	c1qmfA_	Alignment	not modelled	96.4	19	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**penicillin-binding protein 2x; **PDBTitle:** penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
28	c1w7fB_	Alignment	not modelled	96.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate

29	d1nrfa_	Alignment	not modelled	96.4	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
30	c3udiA_	Alignment	not modelled	96.3	25	**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
31	c2qpnA_	Alignment	not modelled	96.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ges-1; **PDBTitle:** ges-1 beta-lactamase
32	c1i2sA_	Alignment	not modelled	96.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** beta-lactamase from bacillus licheniformis bs3
33	d1i2sa_	Alignment	not modelled	96.3	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
34	c2bg1A_	Alignment	not modelled	96.3	16	**PDB header:**peptidoglycan **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
35	c3cg5A_	Alignment	not modelled	96.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
36	d1alqa_	Alignment	not modelled	96.1	12	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
37	c2ov5A_	Alignment	not modelled	96.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbapenemase; **PDBTitle:** crystal structure of the kpc-2 carbapenemase
38	d1bsga_	Alignment	not modelled	95.6	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
39	c1mwuA_	Alignment	not modelled	95.4	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.
40	c2wuqA_	Alignment	not modelled	95.3	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**beta-lactamase regulatory protein blab; **PDBTitle:** crystal structure of blab protein from streptomyces cacaoi
41	d1djaa_	Alignment	not modelled	95.2	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
42	c3ue3A_	Alignment	not modelled	95.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
43	c3i7jB_	Alignment	not modelled	95.0	22	**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
44	d1e25a_	Alignment	not modelled	94.8	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
45	c3lezA_	Alignment	not modelled	94.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of a halotolerant bacterial beta-lactamase
46	d1dy6a_	Alignment	not modelled	93.2	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
47	d1iysa_	Alignment	not modelled	93.2	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
48	c3p09A_	Alignment	not modelled	92.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
49	d1k55a_	Alignment	not modelled	91.9	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
50	d2cc1a1	Alignment	not modelled	91.4	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
51	c3dw0B_	Alignment	not modelled	91.2	17	**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
52	d1m6ka_	Alignment	not modelled	90.1	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
53	d1m40a_	Alignment	not modelled	90.1	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
54	c2v20A_	Alignment	not modelled	90.0	23	**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	d1xa1a_	Alignment	not modelled	89.7	12	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
56	c2wzzA_	Alignment	not modelled	89.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
57	d1w79a1	Alignment	not modelled	88.6	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
58	c3a3eB_	Alignment	not modelled	88.6	16	**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)
59	c1pmdA_	Alignment	not modelled	88.5	27	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**peptidoglycan synthesis multifunctional enzyme; **PDBTitle:** penicillin-binding protein 2x (pbp-2x)
60	d1w5da1	Alignment	not modelled	88.4	20	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
61	d2ex2a1	Alignment	not modelled	87.9	13	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
62	d2bg1a1	Alignment	not modelled	87.6	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
63	c3hbrD_	Alignment	not modelled	87.3	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**oxa-48; **PDBTitle:** crystal structure of oxa-48 beta-lactamase
64	d3beca2	Alignment	not modelled	87.1	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
65	c2qmiH_	Alignment	not modelled	86.9	23	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**pbp related beta-lactamase; **PDBTitle:** structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
66	c2jciA_	Alignment	not modelled	86.5	21	**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
67	c3cjmA_	Alignment	not modelled	85.7	20	**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
68	d1onha_	Alignment	not modelled	85.2	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
69	d1yqsa1	Alignment	not modelled	85.1	31	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
70	c3fwlA_	Alignment	not modelled	85.0	26	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
71	c3ozhA_	Alignment	not modelled	84.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase/d-alanine carboxypeptidase; **PDBTitle:** crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
72	c3equB_	Alignment	not modelled	83.6	22	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
73	d1hzoa_	Alignment	not modelled	83.5	26	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
74	c2j7vA_	Alignment	not modelled	82.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tll2115 protein; **PDBTitle:** structure of pbp-a
75	d1ci9a_	Alignment	not modelled	82.1	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
76	d2hdsa1	Alignment	not modelled	81.5	30	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
77	c1z6fA_	Alignment	not modelled	80.8	16	**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
78	c3hleA_	Alignment	not modelled	78.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transesterase; **PDBTitle:** simvastatin synthase (lovd), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
79	d1k38a_	Alignment	not modelled	78.7	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
80	d1tvfa2	Alignment	not modelled	77.6	13	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
						PDB header:hydrolase

81	c3p09B_	Alignment	not modelled	77.1	19	**Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
82	c2iwdA_	Alignment	not modelled	76.5	14	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**methicillin resistance mecr1 protein; **PDBTitle:** oxacilloyl-acylated mecr1 extracellular antibiotic-sensor2 domain.
83	d1o7ea_	Alignment	not modelled	76.1	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
84	c1zkjA_	Alignment	not modelled	74.7	36	**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
85	c2bcfA_	Alignment	not modelled	74.3	25	**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.
86	c2qz6A_	Alignment	not modelled	72.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** first crystal structure of a psychrophile class c beta-2 lactamase
87	d1ei5a3	Alignment	not modelled	71.9	24	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
88	c1ei5A_	Alignment	not modelled	71.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminopeptidase; **PDBTitle:** crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
89	c1tvfA_	Alignment	not modelled	71.1	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
90	c2wuqB_	Alignment	not modelled	70.2	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**beta-lactamase regulatory protein blab; **PDBTitle:** crystal structure of blab protein from streptomyces cacaoi
91	d1xp4a2	Alignment	not modelled	66.0	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
92	d2drwa1	Alignment	not modelled	65.4	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
93	d1rgya_	Alignment	not modelled	64.5	26	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
94	c3humB_	Alignment	not modelled	64.5	15	**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
95	c3it9B_	Alignment	not modelled	63.6	21	**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
96	c3a3jA_	Alignment	not modelled	63.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pbp5; **PDBTitle:** crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
97	d1es5a_	Alignment	not modelled	58.5	24	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
98	c3tg9A_	Alignment	not modelled	55.9	21	**PDB header:**penicillin binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein; **PDBTitle:** the crystal structure of penicillin binding protein from bacillus2 halodurans
99	c2cblA_	Alignment	not modelled	55.5	24	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
100	c3bunB_	Alignment	not modelled	54.8	24	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
101	c3if6C_	Alignment	not modelled	54.2	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**oxa-46 oxacillinase; **PDBTitle:** crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
102	c2xftA_	Alignment	not modelled	53.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**orf12; **PDBTitle:** structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
103	c2obvA_	Alignment	not modelled	48.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine synthetase isoform type-1; **PDBTitle:** crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
104	d1qm4a1	Alignment	not modelled	47.2	22	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
105	c3o3vB_	Alignment	not modelled	45.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of clbp peptidase domain
						PDB header:hydrolase **Chain:** B: **PDB Molecule:**d-alanyl-d-alanine carboxypeptidase

106	c3mfdB_	Alignment	not modelled	41.5	26	dacb; **PDBTitle:** the structure of the beta-lactamase superfamily domain of d-alanyl-d-2 alanine carboxypeptidase from bacillus subtilis
107	c1xp4C_	Alignment	not modelled	41.0	23	**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
108	d2p02a1	Alignment	not modelled	38.6	25	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
109	c3rv2B_	Alignment	not modelled	27.3	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
110	c2l02B_	Alignment	not modelled	27.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
111	d1a4ea_	Alignment	not modelled	25.0	16	**Fold:**Heme-dependent catalase-like **Superfamily:**Heme-dependent catalase-like **Family:**Heme-dependent catalases
112	c3ik5A_	Alignment	not modelled	24.5	15	**PDB header:**viral protein/signaling protein **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** sivmac239 nef in complex with tcr zeta itam 1 polypeptide2 (a63-r80)
113	c3so4C_	Alignment	not modelled	24.4	28	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
114	d1efnb_	Alignment	not modelled	22.9	15	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
115	d2g17a2	Alignment	not modelled	22.3	63	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
116	d2nefa_	Alignment	not modelled	21.7	15	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
117	d1chka_	Alignment	not modelled	21.7	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Chitosanase
118	d1dnpa1	Alignment	not modelled	21.1	21	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
119	c2xi1A_	Alignment	not modelled	21.1	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nef; **PDBTitle:** crystal structure of the hiv-1 nef sequenced from a patient's sample
120	d2q49a2	Alignment	not modelled	20.9	75	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like