







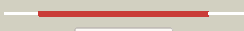
















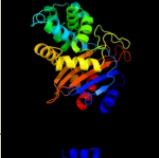
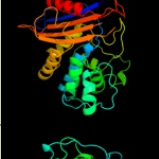
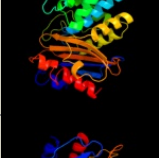
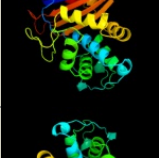
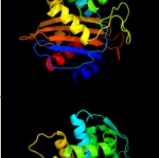
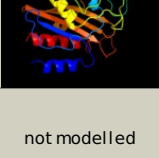
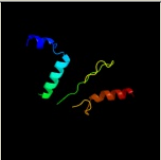


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ex2a1	 Alignment		100.0	100	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
2	d1w5da1	 Alignment		100.0	28	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
3	d1w79a1	 Alignment		100.0	28	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Dac-like
4	c3a3eB	 Alignment		100.0	42	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)
5	c2j7vA	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: tll2115 protein; PDBTitle: structure of pbp-a
6	c3qhyA	 Alignment		99.9	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: beta-lactamase; PDBTitle: structural, thermodynamic and kinetic analysis of the picomolar binding affinity interaction of the beta-lactamase inhibitor protein-3 ii (blip-ii) with class a beta-lactamases
7	c3cg5A	 Alignment		99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
8	c2v20A	 Alignment		99.9	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.
9	d1hzoa	 Alignment		99.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
10	d1n9ba	 Alignment		99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
11	d2cc1a1	 Alignment		99.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

12	c2ov5A_	Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: carbapenemase; PDBTitle: crystal structure of the kpc-2 carbapenemase
13	c1w7fB_	Alignment		99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the class a beta-lactamase bs32 inhibited with isocitrate
14	c3dw0B_	Alignment		99.9	20	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
15	d1bsga_	Alignment		99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
16	d1dy6a_	Alignment		99.9	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
17	d1m40a_	Alignment		99.9	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
18	d1i2sa_	Alignment		99.9	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
19	cli2sa_	Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from bacillus licheniformis bs3
20	c2wuqA_	Alignment		99.9	22	PDB header: transcription Chain: A: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
21	c3cjmA_	Alignment	not modelled	99.9	19	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
22	d1buea_	Alignment	not modelled	99.9	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
23	d1g6aa_	Alignment	not modelled	99.9	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
24	c2wuqB_	Alignment	not modelled	99.9	21	PDB header: transcription Chain: B: PDB Molecule: beta-lactamase regulatory protein blab; PDBTitle: crystal structure of blab protein from streptomyces cacaoi
25	c3leza_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of a halotolerant bacterial beta-lactamase
26	d1e25a_	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
27	d1o7ea_	Alignment	not modelled	99.9	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
28	d1iysa_	Alignment	not modelled	99.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase

29	c2qpnA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
30	d1xp4a2	Alignment	not modelled	99.9	27	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
31	c3p09B	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
32	d1djaa	Alignment	not modelled	99.9	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
33	d3beca2	Alignment	not modelled	99.8	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
34	c3p09A	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of beta-lactamase from francisella tularensis
35	d1alga	Alignment	not modelled	99.8	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
36	d1es5a	Alignment	not modelled	99.8	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
37	c2bcfA	Alignment	not modelled	99.8	21	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.
38	d1tvfa2	Alignment	not modelled	99.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
39	c3a3jA	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: pbp5; PDBTitle: crystal structures of penicillin binding protein 5 from2 haemophilus influenzae
40	c1z6fA	Alignment	not modelled	99.8	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
41	c3it9B	Alignment	not modelled	99.8	20	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
42	c3humB	Alignment	not modelled	99.8	23	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
43	c3mfdB	Alignment	not modelled	99.7	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
44	c1tvfA	Alignment	not modelled	99.7	21	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
45	c1xp4C	Alignment	not modelled	99.7	25	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
46	c2xftA	Alignment	not modelled	99.6	24	PDB header: hydrolase Chain: A: PDB Molecule: orf12; PDBTitle: structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
47	c2jc7A	Alignment	not modelled	99.4	19	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
48	d1nrfa	Alignment	not modelled	99.2	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
49	d1vqqa3	Alignment	not modelled	98.8	21	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
50	d1k38a	Alignment	not modelled	98.5	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
51	c3hbrD	Alignment	not modelled	98.5	13	PDB header: hydrolase Chain: D: PDB Molecule: oxa-48; PDBTitle: crystal structure of oxa-48 beta-lactamase
52	d1xa1a	Alignment	not modelled	98.4	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
53	c3if6C	Alignment	not modelled	98.4	18	PDB header: hydrolase Chain: C: PDB Molecule: oxa-46 oxacillinase; PDBTitle: crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
						Fold: beta-lactamase/transpeptidase-like

54	d1m6ka_	Alignment	not modelled	98.2	21	Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
55	d1k55a_	Alignment	not modelled	98.2	14	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
56	d1pyya4	Alignment	not modelled	98.1	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
57	c2iwdA_	Alignment	not modelled	98.0	15	PDB header: antibiotic resistance Chain: A: PDB Molecule: methicillin resistance mecR1 protein; PDBTitle: oxacilloyl-acylated mecR1 extracellular antibiotic-sensor2 domain.
58	c3lo7A_	Alignment	not modelled	98.0	24	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein a; PDBTitle: crystal structure of pbpa from mycobacterium tuberculosis
59	d1rp5a4	Alignment	not modelled	98.0	19	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
60	c1mwuA_	Alignment	not modelled	97.5	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.
61	c2wadB_	Alignment	not modelled	97.5	16	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)
62	c3equB_	Alignment	not modelled	97.4	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
63	c3oc2A_	Alignment	not modelled	97.0	16	PDB header: penicillin-binding protein Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
64	d2c5wb1	Alignment	not modelled	96.8	16	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
65	c3pbqA_	Alignment	not modelled	96.7	19	PDB header: hydrolase/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 3; PDBTitle: crystal structure of pbp3 complexed with imipenem
66	c1qmfA_	Alignment	not modelled	96.2	17	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
67	c3ue3A_	Alignment	not modelled	96.1	19	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
68	c3fwlA_	Alignment	not modelled	95.4	21	PDB header: transferase, hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
69	c1pmdA_	Alignment	not modelled	94.9	27	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
70	d1k25a4	Alignment	not modelled	94.8	11	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
71	d1ci9a_	Alignment	not modelled	94.6	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
72	c2qmiH_	Alignment	not modelled	94.1	17	PDB header: hydrolase Chain: H: PDB Molecule: pbp related beta-lactamase; PDBTitle: structure of the octameric penicillin-binding protein2 homologue from pyrococcus abyssi
73	c3udiA_	Alignment	not modelled	94.1	20	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
74	c2qlvA_	Alignment	not modelled	94.0	21	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
75	c3hleA_	Alignment		93.8	10	PDB header: transferase Chain: A: PDB Molecule: transesterase; PDBTitle: simvastatin synthase (lovD), from aspergillus terreus, s5 mutant, s76a2 mutant, complex with monacolin j acid
76	c3i7jB_	Alignment	not modelled	93.6	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
77	c1ei5A_	Alignment	not modelled	93.4	13	PDB header: hydrolase Chain: A: PDB Molecule: d-aminopeptidase; PDBTitle: crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
78	c2qz6A_	Alignment	not modelled	93.1	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: first crystal structure of a psychrophile class c beta-2 lactamase
						PDB header: hydrolase

79	c1zkjA_	Alignment	not modelled	92.9	20	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
80	d2bg1a1	Alignment	not modelled	92.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
81	d2drwa1	Alignment	not modelled	92.6	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
82	c2jciA_	Alignment	not modelled	92.5	17	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
83	c2wzzA_	Alignment	not modelled	92.4	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: amp-c beta-lactamase (pseudomonas aeruginosa)in complex2 with compound m-03
84	d1ei5a3	Alignment	not modelled	91.9	13	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
85	c3dwkC_	Alignment	not modelled	91.5	19	PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
86	c2bg1A_	Alignment	not modelled	91.4	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)
87	d1u60a_	Alignment	not modelled	90.2	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
88	d1rgya_	Alignment	not modelled	90.1	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
89	d1yqsa1	Alignment	not modelled	88.9	11	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
90	d2hdsa1	Alignment	not modelled	88.9	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
91	c3czdA_	Alignment	not modelled	88.9	15	PDB header: hydrolase Chain: A: PDB Molecule: glutaminase kidney isoform; PDBTitle: crystal structure of human glutaminase in complex with l-glutamate
92	c3uo9B_	Alignment	not modelled	88.8	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
93	d2olua2	Alignment	not modelled	88.6	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
94	c2dfwA_	Alignment	not modelled	88.5	13	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
95	c2pbyB_	Alignment	not modelled	88.5	17	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase; PDBTitle: probable glutaminase from geobacillus kaustophilus hta426
96	d1onha_	Alignment	not modelled	87.8	18	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
97	c3ozhA_	Alignment	not modelled	87.8	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
98	c3ss4C_	Alignment	not modelled	87.6	15	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
99	c3ih9A_	Alignment	not modelled	87.5	15	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
100	c3o3vB_	Alignment	not modelled	82.5	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of clbp peptidase domain
101	c3tg9A_	Alignment	not modelled	81.6	13	PDB header: penicillin binding protein Chain: A: PDB Molecule: penicillin-binding protein; PDBTitle: the crystal structure of penicillin binding protein from bacillus2 halodurans
102	d1mkia_	Alignment	not modelled	79.5	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
103	c3canA_	Alignment	not modelled	77.0	17	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
104	d2dcfa1	Alignment	not modelled	76.9	11	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						PDB header: metal binding protein

105	c2yx0A_	Alignment	not modelled	56.3	17	Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
106	d1m53a2	Alignment	not modelled	56.2	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
107	c2z2uA_	Alignment	not modelled	56.2	17	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
108	d1mxga2	Alignment	not modelled	51.7	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
109	c3cw4A_	Alignment	not modelled	47.3	27	PDB header: transferase Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2
110	d1e43a2	Alignment	not modelled	43.5	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
111	d1n8fa_	Alignment	not modelled	41.3	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
112	c2wskA_	Alignment	not modelled	40.4	27	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
113	d1ob0a2	Alignment	not modelled	38.2	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
114	c3faxA_	Alignment	not modelled	37.2	15	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
115	c2a5hC_	Alignment	not modelled	36.5	20	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
116	c1ud8A_	Alignment	not modelled	36.3	21	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
117	c1e40A_	Alignment	not modelled	35.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
118	d2gipa2	Alignment	not modelled	34.7	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	d1hvxa2	Alignment	not modelled	32.6	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
120	d1gcyA2	Alignment	not modelled	32.1	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain