

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2967c_(pca)_3319673_3323056
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vz0D_	 Alignment		100.0	45	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
2	c3hblA_	 Alignment		100.0	46	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
3	c4qskB_	 Alignment		100.0	47	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
4	c3bg5B_	 Alignment		100.0	47	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
5	c3tw6B_	 Alignment		100.0	49	PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
6	c2qf7A_	 Alignment		100.0	48	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
7	c4hnbV_	 Alignment		100.0	47	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
8	c3bg5C_	 Alignment		100.0	47	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
9	c4qslE_	 Alignment		100.0	47	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
10	c4qslC_	 Alignment		100.0	47	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
11	c3va7A_	 Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase

12	c5i8iD_	Alignment		100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
13	c3bg3A_	Alignment		100.0	44	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
14	c5cslA_	Alignment		100.0	36	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
15	c3bg3B_	Alignment		100.0	44	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
16	c6g2dC_	Alignment		100.0	36	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
17	c5cslB_	Alignment		100.0	35	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
18	c5ks8D_	Alignment		100.0	35	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
19	c4rcnA_	Alignment		100.0	55	PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
20	c3n6rK_	Alignment		100.0	42	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
21	c3u9sA_	Alignment	not modelled	100.0	49	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
22	c3u9sE_	Alignment	not modelled	100.0	43	PDB header: ligase Chain: E: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
23	c1w96B_	Alignment	not modelled	100.0	33	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
24	c5ks8B_	Alignment	not modelled	100.0	49	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
25	c3u9sl_	Alignment	not modelled	100.0	46	PDB header: ligase Chain: I: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
26	c2hjwA_	Alignment	not modelled	100.0	34	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
27	c2nx9B_	Alignment	not modelled	100.0	38	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae

28	c5h80A_	Alignment	not modelled	100.0	43	PDB header: ligase Chain: A: PDB Molecule: carboxylase; PDBTitle: biotin carboxylase domain of single-chain bacterial carboxylase
29	c1rr2A_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
30	c5ks8F_	Alignment	not modelled	100.0	39	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from 2 methylcobacillus flagellatus
31	c1ulzA_	Alignment	not modelled	100.0	45	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
32	c5mlkA_	Alignment	not modelled	100.0	42	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
33	c5mlkB_	Alignment	not modelled	100.0	44	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
34	c3ouzA_	Alignment	not modelled	100.0	40	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
35	c3jzfA_	Alignment	not modelled	100.0	47	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
36	c2dzdB_	Alignment	not modelled	100.0	51	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
37	c3g8cB_	Alignment	not modelled	100.0	45	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase in complex with biotin,2 bicarbonate, adp and mg ion
38	c2vpqA_	Alignment	not modelled	100.0	41	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
39	c2gpwC_	Alignment	not modelled	100.0	45	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
40	c3gidB_	Alignment	not modelled	100.0	33	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa carboxylase 22 (acc2) in complex with soraphen a
41	c1m6vE_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
42	c1kja_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
43	c5douC_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
44	d1w96a3	Alignment	not modelled	100.0	37	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
45	c2xd4A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
46	c3uvzB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
47	c3lp8A_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
48	c2yyaB_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
49	c3q2oB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
50	d1rqba2	Alignment	not modelled	100.0	37	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
51	c2qk4A_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
52	c2dvcB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl

52	c2uwCB	Alignment	not modelled	100.0	20	PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
53	c4dimA	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
54	c4mamB	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp
55	c2ip4A	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
56	c3orgA	Alignment	not modelled	100.0	15	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
57	c3wvqA	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein
58	c3ax6C	Alignment	not modelled	100.0	21	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
59	c1vkzA	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
60	c4ffnA	Alignment	not modelled	100.0	16	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
61	c3k5iB	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide
62	c2ys6A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
63	c1gsoA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
64	c3ivuB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
65	c3votB	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase, bI00235; PDBTitle: crystal structure of l-amino acid ligase from bacillus licheniformis
66	c4wd3B	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza
67	c1nvmG	Alignment	not modelled	100.0	16	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
68	c3etjB	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
69	c3vmmA	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: alanine-anticapsin ligase bacd; PDBTitle: crystal structure of bacd, an l-amino acid dipeptide ligase from2 bacillus subtilis
70	c3aw8A	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermus thermophilus hb8
71	c6e1jB	Alignment	not modelled	100.0	20	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
72	c4jn6C	Alignment	not modelled	100.0	19	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
73	c5vevB	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
74	c5dotA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
						PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase;

75	c4lrtC	Alignment	not modelled	100.0	21	PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
76	d1a9xa5	Alignment	not modelled	100.0	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
77	c4ov9A	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
78	c2z04A	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
79	d1nvma2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
80	c3rmjB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
81	d1ulza1	Alignment	not modelled	100.0	37	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
82	c3bleA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
83	c1ydoC	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
84	c2ftpA	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
85	c1ydnA	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
86	c2cw6B	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
87	d2j9ga1	Alignment	not modelled	100.0	34	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
88	c1sr9A	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
89	c3a9iA	Alignment	not modelled	100.0	18	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
90	c3ewbX	Alignment	not modelled	100.0	21	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
91	c3eegB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
92	c2zyfA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
93	d1sr9a2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
94	c1ehiB	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (Imddl2) of vancomycin-resistant2 leuconostoc mesenteroides
95	c4fu0B	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase 7; PDBTitle: crystal structure of vang d-ala:d-ser ligase from enterococcus2 faecalis
96	c2r85B	Alignment	not modelled	100.0	14	PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp
97	c3i12A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
98	d1rqba1	Alignment	not modelled	100.0	28	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: Conserved carboxylase domain
99	c3dviB	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase;

99	c3uxbB	Alignment	not modelled	100.0	14	PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus PDB header: transferase
100	c3hpxB	Alignment	not modelled	100.0	17	Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of mycobacterium tuberculosis leuA active site2 domain 1-425 (truncation mutant delta:426-644)
101	d1w96a1	Alignment	not modelled	100.0	28	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
102	c2i80B	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B; PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
103	c2dlnA	Alignment	not modelled	100.0	21	PDB header: ligase(peptidoglycan synthesis) Chain: A; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution
104	d1ulza3	Alignment	not modelled	100.0	46	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
105	d1ulza2	Alignment	not modelled	100.0	50	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
106	c3lwbA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
107	d2j9ga3	Alignment	not modelled	100.0	49	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
108	c6dgiA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: the crystal structure of d-alanyl-alanine synthetase a from vibrio2 cholerae o1 biovar eltor str. n16961
109	d2j9ga2	Alignment	not modelled	100.0	47	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
110	c1e4eB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B; PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
111	c3e5nA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A; PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
112	c4egqD	Alignment	not modelled	100.0	20	PDB header: ligase Chain: D; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
113	c2pn1A	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A; PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
114	d1w96a2	Alignment	not modelled	100.0	35	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
115	c3k3pA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
116	d1w96c1	Alignment	not modelled	100.0	28	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
117	c2zdgA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
118	d1a9xa6	Alignment	not modelled	100.0	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
119	c3se7A	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A; PDB Molecule: vana; PDBTitle: ancient vana
120	c2pvpB	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B; PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori