

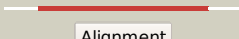

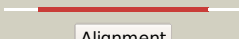








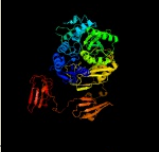

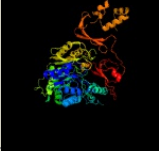








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2501c_(accA1)_2814926_2816890
Date	Wed Aug 7 12:50:13 BST 2019
Unique Job ID	3ff91a67cc3f52a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5cslA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
2	<a href="#">c6g2dC_</a>	 Alignment		100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase 1; <b>PDBTitle:</b> citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
3	<a href="#">c5cskB_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
4	<a href="#">c3n6rK_</a>	 Alignment		100.0	39	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
5	<a href="#">c3u9sA_</a>	 Alignment		100.0	45	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
6	<a href="#">c5vz0D_</a>	 Alignment		100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
7	<a href="#">c3hblA_</a>	 Alignment		100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate carboxylase t908a mutant
8	<a href="#">c3tw6B_</a>	 Alignment		100.0	42	<b>PDB header:</b> ligase/activator <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase protein; <b>PDBTitle:</b> structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
9	<a href="#">c4qskB_</a>	 Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
10	<a href="#">c3bg5B_</a>	 Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase
11	<a href="#">c4rcnA_</a>	 Alignment		100.0	48	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain acyl-coa carboxylase; <b>PDBTitle:</b> structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase

12	<a href="#">c3va7A_</a>	Alignment		100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> klla0e08119p; <b>PDBTitle:</b> crystal structure of the kluyveromyces lactis urea carboxylase
13	<a href="#">c2qf7A_</a>	Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase protein; <b>PDBTitle:</b> crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
14	<a href="#">c3bg5C_</a>	Alignment		100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase
15	<a href="#">c3u9sE_</a>	Alignment		100.0	46	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
16	<a href="#">c4hmvB_</a>	Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of r54e mutant of s. aureus pyruvate carboxylase
17	<a href="#">c5i8iD_</a>	Alignment		100.0	51	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> urea amidolyase; <b>PDBTitle:</b> crystal structure of the k. lactis urea amidolyase
18	<a href="#">c4qslE_</a>	Alignment		100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase
19	<a href="#">c4qslC_</a>	Alignment		100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase
20	<a href="#">c1w96B_</a>	Alignment		100.0	31	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
21	<a href="#">c3u9sl_</a>	Alignment	not modelled	100.0	49	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
22	<a href="#">c2hjwA_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> crystal structure of the bc domain of acc2
23	<a href="#">c5ks8B_</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase subunit alpha; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
24	<a href="#">c1ulzA_</a>	Alignment	not modelled	100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase n-terminal domain; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
25	<a href="#">c5mlkA_</a>	Alignment	not modelled	100.0	48	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
26	<a href="#">c5h80A_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylase; <b>PDBTitle:</b> biotin carboxylase domain of single-chain bacterial carboxylase
27	<a href="#">c2vpqA_</a>	Alignment	not modelled	100.0	46	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
28	<a href="#">c3ouza_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni

29	<a href="#">c3g8cB_</a>	Alignment	not modelled	100.0	46	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase in complex with biotin,2 bicarbonate, adp and mg ion
30	<a href="#">c2gpwC_</a>	Alignment	not modelled	100.0	46	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
31	<a href="#">c5mlkB_</a>	Alignment	not modelled	100.0	50	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> biotin dependent carboxylase acc3a dimer from mycobacterium2 tuberculosis (rv3285)
32	<a href="#">c2dzdB_</a>	Alignment	not modelled	100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
33	<a href="#">c3jzfA_</a>	Alignment	not modelled	100.0	48	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
34	<a href="#">c3gidB_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> the biotin carboxylase (bc) domain of human acetyl-coa carboxylase 22 (acc2) in complex with soraphen a
35	<a href="#">c1m6vE_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
36	<a href="#">c1kjaA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
37	<a href="#">c2xd4A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
38	<a href="#">c3uvzB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
39	<a href="#">c4dimA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide synthetase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
40	<a href="#">c2yyaB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of gar synthetase from aquifex aeolicus
41	<a href="#">c3lp8A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine-glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
42	<a href="#">c2dwcB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl <b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
43	<a href="#">c2qk4A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trifunctional purine biosynthetic protein adenosine-3; <b>PDBTitle:</b> human glycinamide ribonucleotide synthetase
44	<a href="#">c2ip4A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
45	<a href="#">c4mamB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp
46	<a href="#">c3q2oB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
47	<a href="#">c3votB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid ligase, bl00235; <b>PDBTitle:</b> crystal structure of l-amino acid ligase from bacillus licheniformis
48	<a href="#">c3k5iB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide
49	<a href="#">c3orgA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
50	<a href="#">c2ys6A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide synthetase; <b>PDBTitle:</b> crystal structure of gar synthetase from geobacillus kaustophilus
51	<a href="#">d1w96a3</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like

52	<a href="#">c4ffnA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase/substrate <b>Chain:</b> A: <b>PDB Molecule:</b> pylc; <b>PDBTitle:</b> pylc in complex with d-ornithine and amppnp
53	<a href="#">c3ax6C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
54	<a href="#">c1vkzA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
55	<a href="#">c4wd3B</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid ligase; <b>PDBTitle:</b> crystal structure of an l-amino acid ligase riza
56	<a href="#">c3vmmA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine-anticapsin ligase bacd; <b>PDBTitle:</b> crystal structure of bacd, an l-amino acid dipeptide ligase from2 bacillus subtilis
57	<a href="#">c1gsoA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glycinamide ribonucleotide synthetase); <b>PDBTitle:</b> glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
58	<a href="#">c5douC</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
59	<a href="#">c3aw8A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermus thermophilus hb8
60	<a href="#">c3etjB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure e. coli purk in complex with mg, adp, and2 pi
61	<a href="#">c5vevB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
62	<a href="#">c3wvqA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pgm1; <b>PDBTitle:</b> structure of atp grasp protein
63	<a href="#">c2z04A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
64	<a href="#">d1a9xa5</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
65	<a href="#">c5dotA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
66	<a href="#">c1ehiB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine:d-lactate ligase; <b>PDBTitle:</b> d-alanine:d-lactate ligase (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides
67	<a href="#">c4fu0B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase 7; <b>PDBTitle:</b> crystal structure of vang d-ala:d-ser ligase from enterococcus2 faecalis
68	<a href="#">c3i12A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
69	<a href="#">c2i80B</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase; <b>PDBTitle:</b> allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
70	<a href="#">c2r85B</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> purp protein pf1517; <b>PDBTitle:</b> crystal structure of purp from pyrococcus furiosus complexed with amp
71	<a href="#">c3lwbA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
72	<a href="#">d1ulza3</a>	Alignment	not modelled	100.0	47	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
73	<a href="#">c2pn1A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoylphosphate synthase large subunit; <b>PDBTitle:</b> crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
74	<a href="#">c2dlnA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase(peptidoglycan synthesis) <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution
75	<a href="#">d2j9ga3</a>	Alignment	not modelled	100.0	48	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like

76	<a href="#">c6dgiA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> the crystal structure of d-alanyl-alanine synthetase a from vibrio2 cholerae o1 biovar eltor str. n16961
77	<a href="#">c3e5nA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
78	<a href="#">d1ulza1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
79	<a href="#">c1e4eB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> vancomycin/teicoplanin a-type resistance protein vana; <b>PDBTitle:</b> d-alanyl-d-lacate ligase
80	<a href="#">d2j9ga1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
81	<a href="#">d1ulza2</a>	Alignment	not modelled	100.0	54	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
82	<a href="#">d2j9ga2</a>	Alignment	not modelled	100.0	54	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
83	<a href="#">c4egqD</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
84	<a href="#">c2zdqA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
85	<a href="#">c3k3pA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
86	<a href="#">c3se7A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> vana; <b>PDBTitle:</b> ancient vana
87	<a href="#">c2pvpB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> d-alanine-d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
88	<a href="#">c3tqtB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> structure of the d-alanine-d-alanine ligase from coxiella burnetii
89	<a href="#">d1w96a2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
90	<a href="#">d1a9xa6</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
91	<a href="#">c3r23B</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
92	<a href="#">d1w96a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
93	<a href="#">d1kjqA3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
94	<a href="#">c5dmxC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
95	<a href="#">c4iwyA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal protein s6 modification protein; <b>PDBTitle:</b> semet-substituted rimk structure
96	<a href="#">c5i47A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> rimk domain protein atp-grasp; <b>PDBTitle:</b> crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745
97	<a href="#">c4egjD</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
98	<a href="#">d3etja3</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
99	<a href="#">c5csaA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
100	<a href="#">c3df7A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative atp-grasp superfamily protein; <b>PDBTitle:</b> crystal structure of a putative atp-grasp superfamily protein from2 archaeoglobus fulgidus
101	<a href="#">c1uc8B</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> lysine biosynthesis enzyme; <b>PDBTitle:</b> crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
						<b>Fold:</b> ATP-grasp



102	<a href="#">d1vkza3</a>	Alignment	not modelled	99.9	15	<b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
103	<a href="#">c5ig8A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> atp grasp ligase; <b>PDBTitle:</b> crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc
104	<a href="#">c5ig9H_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> atp grasp ligase; <b>PDBTitle:</b> crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc
105	<a href="#">d1w96c1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
106	<a href="#">c3vpbc_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> putative acetylornithine deacetylase; <b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
107	<a href="#">c5k2mG_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> rimk-related lysine biosynthesis protein; <b>PDBTitle:</b> bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa
108	<a href="#">d2r85a2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> PurP ATP-binding domain-like
109	<a href="#">d1ehia2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
110	<a href="#">d2r7ka2</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> PurP ATP-binding domain-like
111	<a href="#">d1gsoa3</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
112	<a href="#">c1i7nA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> synapsin ii; <b>PDBTitle:</b> crystal structure analysis of the c domain of synapsin ii2 from rat brain
113	<a href="#">d1iowa2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
114	<a href="#">c1pk8D_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> rat synapsin i; <b>PDBTitle:</b> crystal structure of rat synapsin i c domain complexed to2 ca.atp
115	<a href="#">d1e4ea2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
116	<a href="#">c2p0aA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> synapsin-3; <b>PDBTitle:</b> the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
117	<a href="#">c5ks8D_</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
118	<a href="#">c5ks8F_</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
119	<a href="#">c3bg3A_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
120	<a href="#">d1uc8a2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Lysine biosynthesis enzyme LysX ATP-binding domain