

Phyre2

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Description	RVBD0973c_(accA2)_1083751_1085754
Date	Wed Jul 31 22:05:04 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5cslA_	Alignment		100.0	28	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
2	c6g2dC_	Alignment		100.0	30	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
3	c5cslB_	Alignment		100.0	28	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
4	c3n6rK_	Alignment		100.0	36	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
5	c3u9sA_	Alignment		100.0	45	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
6	c5vz0D_	Alignment		100.0	40	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
7	c4rcnA_	Alignment		100.0	46	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
8	c3hblA_	Alignment		100.0	39	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
9	c3tw6B_	Alignment		100.0	39	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
10	c3bg5B_	Alignment		100.0	39	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
11	c4qskB_	Alignment		100.0	42	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp

12	c3va7A_	Alignment		100.0	41	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
13	c2qf7A_	Alignment		100.0	37	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
14	c3bg5C_	Alignment		100.0	37	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
15	c4hmvB_	Alignment		100.0	40	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
16	c4qslC_	Alignment		100.0	38	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
17	c5i8iD_	Alignment		100.0	45	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
18	c3u9sE_	Alignment		100.0	44	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
19	c4qslE_	Alignment		100.0	38	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
20	c1w96B_	Alignment		100.0	32	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
21	c3u9sl_	Alignment	not modelled	100.0	47	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
22	c2hvwA_	Alignment	not modelled	100.0	33	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
23	c5ks8B_	Alignment	not modelled	100.0	41	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
24	c5h80A_	Alignment	not modelled	100.0	38	PDB header: ligase Chain: A: PDB Molecule: carboxylase; PDBTitle: biotin carboxylase domain of single-chain bacterial carboxylase
25	c5m1kA_	Alignment	not modelled	100.0	44	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
26	c1ulzA_	Alignment	not modelled	100.0	43	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
27	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
28	c2vpqA_	Alignment	not modelled	100.0	40	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp

29	c5mlkB_	Alignment	not modelled	100.0	45	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acc3a dimer from mycobacterium2 tuberculosis (rv3285)
30	c3g8cB_	Alignment	not modelled	100.0	43	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
31	c2dzdB_	Alignment	not modelled	100.0	41	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
32	c2gpwC_	Alignment	not modelled	100.0	42	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.
33	c3jzfA_	Alignment	not modelled	100.0	44	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
34	c3gidB_	Alignment	not modelled	100.0	31	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
35	c1m6vE_	Alignment	not modelled	100.0	20	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
36	c1kjaA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
37	c3uvzB_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
38	c3lp8A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
39	c2xd4A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
40	c2yyaB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
41	c4dimA_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
42	c2qk4A_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
43	c3q2oB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
44	c4ffnA_	Alignment	not modelled	100.0	17	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
45	c3ax6C_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
46	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
47	c2dwcB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
48	c2ip4A_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
49	c3votB_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase, bl00235; PDBTitle: crystal structure of l-amino acid ligase from bacillus licheniformis
50	c4mamB_	Alignment	not modelled	100.0	16	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
51	c4wd3B_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza
						PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole

52	c3k5iB	Alignment	not modelled	100.0	18	carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from <i>Aspergillus clavatus</i> in complex with adp and 5-aminoimidazole3 ribonucleotide
53	c1gsoA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A; PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from <i>E. coli</i> .
54	c2ys6A	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A; PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from <i>Geobacillus kaustophilus</i>
55	c1vkzA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A; PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from <i>Thermotoga maritima</i> at 2.30 Å resolution
56	c3etjB	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B; PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure <i>E. coli</i> purk in complex with mg, adp, and 2 pi
57	d1w96a3	Alignment	not modelled	100.0	36	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
58	c3aw8A	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A; PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from <i>Thermus thermophilus</i> hb8
59	c5vevB	Alignment	not modelled	100.0	18	Chain: B; PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from <i>Neisseria2 gonorrhoeae</i>
60	c5douC	Alignment	not modelled	100.0	19	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
61	c3vmmA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A; PDB Molecule: alanine-anticapsin ligase bacd; PDBTitle: crystal structure of bacd, an L-amino acid dipeptide ligase from <i>Bacillus subtilis</i>
62	c2z04A	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A; PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from <i>Aquifex aeolicus</i>
63	c3wvqA	Alignment	not modelled	100.0	21	PDB header: biosynthetic protein Chain: A; PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein
64	d1a9xa5	Alignment	not modelled	100.0	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
65	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 (lmdl2) of vancomycin-resistant2 <i>Leuconostoc mesenteroides</i>
66	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 from <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar typhimurium str. lt2
67	c4fu0B	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B; PDB Molecule: d-alanine--d-alanine ligase 7; PDBTitle: crystal structure of vang d-ala:d-ser ligase from <i>Enterococcus2 faecalis</i>
68	c2i80B	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B; PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of <i>Staphylococcus aureus</i> d-alanine:d-alanine2 ligase revealed by crystallographic studies
69	c2r85B	Alignment	not modelled	100.0	14	PDB header: unknown function Chain: B; PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from <i>Pyrococcus furiosus</i> complexed with amp
70	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
71	c3lwbA	Alignment	not modelled	100.0	26	PDB header: ligase Chain: A; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from <i>Mycobacterium tuberculosis</i>
72	c2dlnA	Alignment	not modelled	100.0	26	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 Å resolution
73	c2pn1A	Alignment	not modelled	100.0	17	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 <i>Exiguobacterium</i> sp. 255-15 at 2.00 Å resolution
74	c1e4eB	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B; PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lactate ligase
75	c6dgiA	Alignment	not modelled	100.0	17	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
76	c2zdgA_	Alignment	not modelled	100.0	25	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
77	c3e5nA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structure of d-alanine-d-alanine ligase from xanthomonas oryzae pv. oryzae kacc10331
78	d1ulza1	Alignment	not modelled	100.0	31	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
79	d2j9ga1	Alignment	not modelled	100.0	31	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
80	c3se7A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
81	c3tqtB_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
82	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
83	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
84	c4egqD_	Alignment	not modelled	100.0	25	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
85	d1ulza2	Alignment	not modelled	100.0	49	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
86	d1ulza3	Alignment	not modelled	100.0	47	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
87	c3r23B_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
88	d2j9ga2	Alignment	not modelled	100.0	47	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
89	d2j9ga3	Alignment	not modelled	100.0	46	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
90	d1w96a1	Alignment	not modelled	100.0	21	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
91	c5dmxC_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: C: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
92	d1w96a2	Alignment	not modelled	100.0	32	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
93	c3df7A_	Alignment	not modelled	100.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative atp-grasp superfamily protein; PDBTitle: crystal structure of a putative atp-grasp superfamily protein from2 archaeoglobus fulgidus
94	c4iwyA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure
95	c4egjD_	Alignment	not modelled	100.0	26	PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
96	d1a9xa6	Alignment	not modelled	100.0	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
97	c5csaA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
98	c5i47A_	Alignment	not modelled	99.9	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: rimk domain protein atp-grasp; PDBTitle: crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745
99	c5ig8A_	Alignment	not modelled	99.9	14	PDB header: ligase Chain: A: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc
100	d1kjq3	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
101	d1w96c1	Alignment	not modelled	99.9	21	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
						Fold: ATP-grasp

102	d1vkza3	Alignment	not modelled	99.9	17	Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
103	d3etja3	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
104	c3vpbc	Alignment	not modelled	99.9	13	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
105	c1uc8B	Alignment	not modelled	99.9	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: lysine biosynthesis enzyme; PDBTitle: crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
106	d2r85a2	Alignment	not modelled	99.9	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
107	c5ig9H	Alignment	not modelled	99.9	12	PDB header: ligase Chain: H: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc
108	c5k2mG	Alignment	not modelled	99.9	17	PDB header: biosynthetic protein Chain: G: PDB Molecule: rimk-related lysine biosynthesis protein; PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa
109	d2r7ka2	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
110	d1ehia2	Alignment	not modelled	99.9	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
111	c1i7nA	Alignment	not modelled	99.9	17	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
112	c1pk8D	Alignment	not modelled	99.9	16	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
113	d1iowa2	Alignment	not modelled	99.9	25	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
114	c2p0aA	Alignment	not modelled	99.9	17	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
115	d1e4ea2	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
116	d1gsoa3	Alignment	not modelled	99.9	20	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
117	c5ks8D	Alignment	not modelled	99.9	31	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
118	d1a9xa4	Alignment	not modelled	99.9	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
119	c5ks8F	Alignment	not modelled	99.8	30	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
120	c3bg3A	Alignment	not modelled	99.8	23	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)