

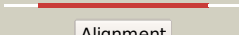
















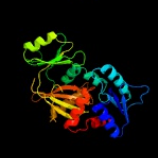
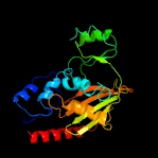


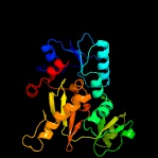


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1455_(-)_1640686_1641549
Date	Fri Aug 2 13:30:03 BST 2019
Unique Job ID	fb070529da61ee7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dlnA_	 Alignment		100.0	16	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
2	c2i80B_	 Alignment		100.0	14	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
3	c1ehiB_	 Alignment		100.0	16	PDB header: ligase Chain: B; PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdld2) of vancomycin-resistant2 leuconostoc mesenteroides
4	c3r23B_	 Alignment		100.0	11	PDB header: ligase Chain: B; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
5	c5dmxC_	 Alignment		100.0	15	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
6	c3i12A_	 Alignment		100.0	15	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
7	c6dgiA_	 Alignment		100.0	11	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
8	c2zdqA_	 Alignment		100.0	17	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
9	c4eggD_	 Alignment		100.0	15	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
10	c2pvpB_	 Alignment		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
11	c3tqtB_	 Alignment		100.0	13	PDB header: ligase Chain: B; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii

12	c4fu0B_	Alignment		100.0	12	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
13	c3e5nA_	Alignment		100.0	16	PDB header: ligase Chain: A; PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
14	c4egjD_	Alignment		100.0	15	PDB header: ligase Chain: D; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
15	c3se7A_	Alignment		100.0	15	PDB header: ligase Chain: A; PDB Molecule: vana; PDBTitle: ancient vana
16	c4iwvyA_	Alignment		100.0	17	PDB header: ligase Chain: A; PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure
17	c1i7nA_	Alignment		100.0	9	PDB header: neuropeptide Chain: A; PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
18	c1e4eB_	Alignment		100.0	12	PDB header: ligase Chain: B; PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
19	c2p0aA_	Alignment		100.0	10	PDB header: neuropeptide Chain: A; PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
20	c5i47A_	Alignment		100.0	15	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
21	c3lwbA_	Alignment	not modelled	100.0	16	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
22	c1pk8D_	Alignment	not modelled	100.0	10	PDB header: membrane protein Chain: D; PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
23	c5k2mG_	Alignment	not modelled	100.0	10	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
24	c1uc8B_	Alignment	not modelled	99.9	13	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
25	c3vpbC_	Alignment	not modelled	99.9	16	PDB header: ligase Chain: C; PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
26	c3ln6A_	Alignment	not modelled	99.9	17	PDB header: ligase Chain: A; PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
27	c1gshA_	Alignment	not modelled	99.9	13	PDB header: glutathione biosynthesis ligase Chain: A; PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
28	c5iq8A_	Alignment	not modelled	99.9	13	PDB header: ligase Chain: A; PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis

					aeruginosa mrc
29	c3k3pA_	Alignment	not modelled	99.9	12 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
30	c2qb5B_	Alignment	not modelled	99.9	13 PDB header: transferase Chain: B: PDB Molecule: inositol-tetrakisphosphate 1-kinase; PDBTitle: crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
31	c1z2pX_	Alignment	not modelled	99.9	12 PDB header: transferase Chain: X: PDB Molecule: inositol 1,3,4-trisphosphate 5/6-kinase; PDBTitle: inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3
32	c3ln7A_	Alignment	not modelled	99.9	17 PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida
33	c5ig9H_	Alignment	not modelled	99.9	11 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
34	d1pk8a2	Alignment	not modelled	99.9	10 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
35	c1kja_	Alignment	not modelled	99.9	16 PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
36	c3t9aA_	Alignment	not modelled	99.9	10 PDB header: transferase Chain: A: PDB Molecule: inositol pyrophosphate kinase; PDBTitle: crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
37	c1m6vE_	Alignment	not modelled	99.9	14 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
38	c1vkzA_	Alignment	not modelled	99.9	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
39	c4wd3B_	Alignment	not modelled	99.9	12 PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza
40	c2dzdB_	Alignment	not modelled	99.9	12 PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
41	c2vpqA_	Alignment	not modelled	99.9	12 PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
42	c2yyaB_	Alignment	not modelled	99.9	14 PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
43	c2xd4A_	Alignment	not modelled	99.9	13 PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
44	d1i7na2	Alignment	not modelled	99.9	10 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
45	c3ouza_	Alignment	not modelled	99.9	12 PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
46	c3bg5C_	Alignment	not modelled	99.9	10 PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
47	c4mamB_	Alignment	not modelled	99.9	13 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
48	c1ulza_	Alignment	not modelled	99.9	14 PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
49	c3g8cB_	Alignment	not modelled	99.9	14 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
50	c3lp8A_	Alignment	not modelled	99.9	15 PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
51	c4ffnA_	Alignment	not modelled	99.9	13 PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
52	c3df7A_	Alignment	not modelled	99.9	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
					PDB header: lyase

53	c3etjB_	Alignment	not modelled	99.9	17	Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
54	c2hfwA_	Alignment	not modelled	99.9	16	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
55	c2ip4A_	Alignment	not modelled	99.9	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
56	c1w96B_	Alignment	not modelled	99.9	15	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
57	c3vmmA_	Alignment	not modelled	99.9	13	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
58	d1iowa2	Alignment	not modelled	99.9	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
59	c3orqA_	Alignment	not modelled	99.9	12	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
60	c3uvzB_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
61	c3tw6B_	Alignment	not modelled	99.8	14	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
62	d1e4ea2	Alignment	not modelled	99.8	12	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
63	c3q2oB_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
64	c3votB_	Alignment	not modelled	99.8	10	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase, bl00235; PDBTitle: crystal structure of l-amino acid ligase from bacillus licheniformis
65	d1ehia2	Alignment	not modelled	99.8	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
66	c3k5iB_	Alignment	not modelled	99.8	12	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
67	c3gidB_	Alignment	not modelled	99.8	14	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
68	c4dimA_	Alignment	not modelled	99.8	11	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
69	c5mlkA_	Alignment	not modelled	99.8	13	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
70	c3u9sA_	Alignment	not modelled	99.8	15	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
71	c3ax6C_	Alignment	not modelled	99.8	13	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
72	c3aw8A_	Alignment	not modelled	99.8	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermus thermophilus hb8
73	d1uc8a2	Alignment	not modelled	99.8	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
74	c2gpwC_	Alignment	not modelled	99.8	14	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.
75	c2ys6A_	Alignment	not modelled	99.8	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
76	c3u9sE_	Alignment	not modelled	99.8	15	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
77	c2qk4A	Alignment	not modelled	99.8	17	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenose-3; PDBTitle: human glycinamide ribonucleotide synthetase
78	c4qslC	Alignment	not modelled	99.8	12	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
79	c2pn1A	Alignment	not modelled	99.8	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
80	d1vkza3	Alignment	not modelled	99.7	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
81	c3n6rK	Alignment	not modelled	99.7	13	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
82	c3hblA	Alignment	not modelled	99.7	11	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
83	c2dwcB	Alignment	not modelled	99.7	13	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
84	c5vz0D	Alignment	not modelled	99.7	12	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
85	d1a9xa5	Alignment	not modelled	99.7	10	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
86	d1w96a3	Alignment	not modelled	99.7	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
87	c5h80A	Alignment	not modelled	99.7	14	PDB header: ligase Chain: A: PDB Molecule: carboxylase; PDBTitle: biotin carboxylase domain of single-chain bacterial carboxylase
88	c5vevB	Alignment	not modelled	99.7	10	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
89	c3wvqA	Alignment	not modelled	99.7	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein
90	d3etja3	Alignment	not modelled	99.7	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
91	c1gsoA	Alignment	not modelled	99.7	12	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
92	d2j9ga3	Alignment	not modelled	99.7	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
93	d2r85a2	Alignment	not modelled	99.7	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
94	c4qslE	Alignment	not modelled	99.6	12	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
95	d1gsaa2	Alignment	not modelled	99.6	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
96	d2r7ka2	Alignment	not modelled	99.6	12	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
97	c6g2dC	Alignment	not modelled	99.6	16	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
98	d1ulza3	Alignment	not modelled	99.6	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
99	c5cskB	Alignment	not modelled	99.6	18	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
100	c2z04A	Alignment	not modelled	99.6	14	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
101	d1kja3	Alignment	not modelled	99.6	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like

102	d1gsoa3	Alignment	not modelled	99.6	12	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
103	c2r85B	Alignment	not modelled	99.6	12	PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp
104	d1a9xa6	Alignment	not modelled	99.5	7	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
105	c5cslA	Alignment	not modelled	99.2	16	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
106	c5douC	Alignment	not modelled	99.2	14	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
107	c5dotA	Alignment	not modelled	99.0	14	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
108	c3jzfA	Alignment	not modelled	99.0	12	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
109	c2cqyA	Alignment	not modelled	98.9	18	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
110	c5mlkB	Alignment	not modelled	98.9	17	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
111	c3u9sl	Alignment	not modelled	98.9	17	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
112	c4yakD	Alignment	not modelled	98.8	13	PDB header: ligase Chain: D: PDB Molecule: beta subunit of acyl-coa synthetase (ndp forming); PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 in complex with coenzyme a, acetyl-coenzyme a and with3 phosphorylated phosphohistidine segment (site i orientation)
113	c5ks8B	Alignment	not modelled	98.7	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
114	d1iowa1	Alignment	not modelled	98.3	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
115	c4hmvB	Alignment	not modelled	98.2	12	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
116	c3bg5B	Alignment	not modelled	98.1	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
117	c4rcnA	Alignment	not modelled	98.1	21	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
118	c5i8iD	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
119	c4qskB	Alignment	not modelled	98.0	12	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
120	c6no2B	Alignment	not modelled	98.0	24	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta; PDBTitle: adp bound to k114bd mutant atp-grasp fold of blastocystis hominis2 succinyl-coa synthetase