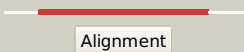

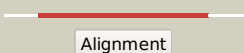

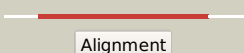

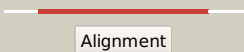





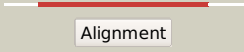

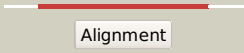





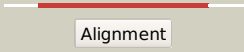



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0389_(purT)_468338_469597
Date	Tue Jul 23 14:50:46 BST 2019
Unique Job ID	92c3eb2fc7372b43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kja_	 Alignment		100.0	40	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
2	c2dwcB_	 Alignment		100.0	33	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
3	c3bg5C_	 Alignment		100.0	17	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
4	c4mamB_	 Alignment		100.0	21	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
5	c3g8cB_	 Alignment		100.0	15	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
6	c3uvzB_	 Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
7	c3ouzA_	 Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
8	c1ulzA_	 Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
9	c2dzdB_	 Alignment		100.0	18	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
10	c3orgA_	 Alignment		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
11	c1m6vE_	 Alignment		100.0	16	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

12	c2vpqA_	Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
13	c2hjaA_	Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
14	c3q2oB_	Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
15	c1w96B_	Alignment		100.0	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
16	c3tw6B_	Alignment		100.0	19	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
17	c5vz0D_	Alignment		100.0	15	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
18	c3gidB_	Alignment		100.0	13	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
19	c3etjB_	Alignment		100.0	20	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
20	c3ax6C_	Alignment		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
21	c2gpwC_	Alignment	not modelled	100.0	15	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.
22	c4qslE_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
23	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
24	c3aw8A_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermus thermophilus hb8
25	c3u9sA_	Alignment	not modelled	100.0	19	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
26	c3k5iB_	Alignment	not modelled	100.0	20	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
27	c3n6rK_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc) PDB header: ligase

28	c2xd4A	Alignment	not modelled	100.0	16	Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
29	c3u9sE	Alignment	not modelled	100.0	18	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
30	c5mlkA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
31	c3hblA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
32	c3lp8A	Alignment	not modelled	100.0	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
33	c4qslC	Alignment	not modelled	100.0	15	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
34	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
35	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
36	c4dimA	Alignment	not modelled	100.0	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
37	c2ip4A	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
38	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
39	c4ffnA	Alignment	not modelled	100.0	15	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
40	c6g2dC	Alignment	not modelled	100.0	13	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
41	c5douC	Alignment	not modelled	100.0	16	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
42	c5cskB	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
43	c5vevB	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
44	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.
45	c2z04A	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
46	c5cslA	Alignment	not modelled	100.0	13	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
47	c5h80A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: carboxylase; PDBTitle: biotin carboxylase domain of single-chain bacterial carboxylase
48	c3vmmA	Alignment	not modelled	100.0	15	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
49	c3jzfA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
50	c4wd3B	Alignment	not modelled	100.0	13	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza
51	c5dotA	Alignment	not modelled	100.0	16	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
52	c5mlkB	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from

						mycobacterium2 tuberculosis (rv3285)
53	c3u9sl	Alignment	not modelled	100.0	19	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
54	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
55	c5ks8B	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
56	d1a9xa5	Alignment	not modelled	100.0	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
57	c4qskB	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
58	c2pn1A	Alignment	not modelled	100.0	14	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
59	c5i8iD	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
60	c3va7A	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
61	c3bg5B	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
62	c4fu0B	Alignment	not modelled	100.0	14	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
63	c2qf7A	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
64	c4rcnA	Alignment	not modelled	100.0	19	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
65	c3i12A	Alignment	not modelled	100.0	17	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
66	c4hmvB	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
67	c2i80B	Alignment	not modelled	100.0	16	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
68	c3lwbA	Alignment	not modelled	100.0	18	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
69	c1ehiB	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdd2) of vancomycin-resistant2 leuconostoc mesenteroides
70	c2dlnA	Alignment	not modelled	100.0	18	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
71	c6dgiA	Alignment	not modelled	100.0	16	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
72	d1a9xa6	Alignment	not modelled	100.0	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
73	c2r85B	Alignment	not modelled	100.0	15	PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp
74	d1kjqa3	Alignment	not modelled	100.0	41	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
75	c1e4eB	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
76	d1w96a3	Alignment	not modelled	100.0	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
77	c2zdqA	Alignment	not modelled	100.0	16	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
78	c3e5nA_	Alignment	not modelled	100.0	19 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
79	c2pvpB_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
80	c3tqtB_	Alignment	not modelled	100.0	14 PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
81	c3r23B_	Alignment	not modelled	100.0	13 PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
82	c3se7A_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
83	d3etja3	Alignment	not modelled	100.0	20 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
84	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
85	c4iwyA_	Alignment	not modelled	100.0	15 PDB header: ligase Chain: A: PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure
86	c3k3pA_	Alignment	not modelled	100.0	14 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
87	d2j9ga3	Alignment	not modelled	100.0	17 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
88	c3wvqA_	Alignment	not modelled	100.0	16 PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein
89	c5i47A_	Alignment	not modelled	100.0	18 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
90	c5dmxC_	Alignment	not modelled	100.0	22 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
91	d1ulza3	Alignment	not modelled	100.0	15 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
92	d1vkza3	Alignment	not modelled	100.0	14 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
93	c3df7A_	Alignment	not modelled	100.0	14 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	c4egjD_	Alignment	not modelled	100.0	24 PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
95	c5k2mG_	Alignment	not modelled	100.0	14 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
96	c3vpbC_	Alignment	not modelled	100.0	12 PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
97	c1uc8B_	Alignment	not modelled	100.0	16 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
98	c5ig8A_	Alignment	not modelled	99.9	15 PDB header: ligase Chain: A: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc
99	c5ig9H_	Alignment	not modelled	99.9	14 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
100	d1ehia2	Alignment	not modelled	99.9	17 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
101	d2r85a2	Alignment	not modelled	99.9	16 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
102	d2r7ka2	Alignment	not modelled	99.9	13 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
103	d1iowa2	Alignment	not modelled	99.9	20 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
					Fold: ATP-grasp

104	d1e4ea2	Alignment	not modelled	99.9	21	Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
105	d1uc8a2	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
106	d1gsoa3	Alignment	not modelled	99.9	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
107	c3ln6A_	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
108	c1i7nA_	Alignment	not modelled	99.9	13	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
109	c1z2pX_	Alignment	not modelled	99.8	13	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
110	c2p0aA_	Alignment	not modelled	99.8	15	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
111	c1pk8D_	Alignment	not modelled	99.8	14	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
112	c3ln7A_	Alignment	not modelled	99.8	18	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurrella multocida
113	d1kjqaz	Alignment	not modelled	99.8	42	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
114	d1pk8a2	Alignment	not modelled	99.8	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
115	d1i7na2	Alignment	not modelled	99.8	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
116	c2qb5B_	Alignment	not modelled	99.8	17	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+
117	c1gshA_	Alignment	not modelled	99.8	14	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
118	c4yakD_	Alignment	not modelled	99.7	14	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)
119	d1gsaa2	Alignment	not modelled	99.6	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
120	c3t9aA_	Alignment	not modelled	99.6	16	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