























Phyre2

Email	mdejesus@rockefeller.edu
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gpmD_	 Alignment		100.0	49	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
2	c5tw7E_	 Alignment		100.0	50	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
3	c2vx0B_	 Alignment		100.0	40	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
4	c3uowB_	 Alignment		100.0	40	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
5	c2ywcC_	 Alignment		100.0	52	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
6	c3tqiB_	 Alignment		100.0	48	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
7	c2dplA_	 Alignment		100.0	53	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
8	d1gpmA3	 Alignment		100.0	55	Fold: Alpha-lytic protease prodomain-like Superfamily: GMP synthetase C-terminal dimerisation domain Family: GMP synthetase C-terminal dimerisation domain
9	c2vpiA_	 Alignment		100.0	41	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
10	d1gpmA2	 Alignment		100.0	42	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
11	d1wl8a1	 Alignment		100.0	34	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	c1keeH_	Alignment		100.0	24	PDB header: ligase Chain: H; PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
13	c3r74B_	Alignment		100.0	17	PDB header: lyase, biosynthetic protein Chain: B; PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
14	d1i7qb_	Alignment		100.0	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
15	d2a9va1	Alignment		100.0	31	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
16	d1qdlb_	Alignment		100.0	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
17	d1a9xb2	Alignment		100.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	c2lxaA_	Alignment		100.0	34	PDB header: ligase Chain: A; PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit a; PDBTitle: solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
19	c5dotA_	Alignment		100.0	18	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
20	c6qurA_	Alignment		100.0	24	PDB header: transferase Chain: A; PDB Molecule: glutaminase; PDBTitle: mapping the allosteric communication network of aminodeoxychorismate2 synthase
21	c5douC_	Alignment	not modelled	100.0	17	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
22	d1i1qb_	Alignment	not modelled	100.0	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
23	d1gpma1	Alignment	not modelled	100.0	55	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
24	c4xfdA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A; PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
25	c3q4gA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A; PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
26	c5hujB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B; PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nade from streptococcus pyogenes
27	c1jvnB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B; PDB Molecule: bifunctional histidine biosynthesis protein hisf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
28	d1kqpa_	Alignment	not modelled	100.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases

29	d1wxia1	Alignment	not modelled	100.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
30	c3dpiA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
31	c3l83A_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
32	c3l7nA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
33	c2derA_	Alignment	not modelled	100.0	24	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
34	d1jvna2	Alignment	not modelled	100.0	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c4gudA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
36	c2hmaA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
37	d1o1ya_	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
38	c3fiuD_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
39	c4q16C_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
40	d1ka9h_	Alignment	not modelled	100.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	c3p52B_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
42	c3d54D_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
43	d2nv0a1	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
44	d1k9vf_	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
45	c2e18B_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
46	c3fijD_	Alignment	not modelled	99.9	25	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
47	d1s1ma1	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
48	c4f4hA_	Alignment	not modelled	99.9	27	PDB header: ligase Chain: A: PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
49	c5udwB_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
50	d1q7ra_	Alignment	not modelled	99.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
51	d1vcoa1	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
52	c2issF_	Alignment	not modelled	99.9	13	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
53	c4l8fA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
54	c2ywjA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii

55	c2ywdA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
56	c1l9xA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
57	d1l9xa	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
58	c5khaA	Alignment	not modelled	99.9	21	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
59	c4kr7A	Alignment	not modelled	99.9	21	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
60	c3nvaB	Alignment	not modelled	99.9	23	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
61	c2c5sA	Alignment	not modelled	99.9	20	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
62	c2w7tA	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound acivicin
63	c3n05B	Alignment	not modelled	99.9	22	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
64	c2v4uA	Alignment	not modelled	99.9	15	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
65	c1vcnA	Alignment	not modelled	99.9	23	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
66	c2ad5B	Alignment	not modelled	99.9	22	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
67	c4zdiE	Alignment	not modelled	99.9	21	PDB header: ligase Chain: E: PDB Molecule: ctp synthase; PDBTitle: crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
68	d1xnga1	Alignment	not modelled	99.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
69	d2abwa1	Alignment	not modelled	99.9	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
70	d2c5sa1	Alignment	not modelled	99.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
71	d2ghra1	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
72	c5u03C	Alignment	not modelled	99.9	20	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
73	d1t3ta2	Alignment	not modelled	99.9	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
74	c5udtD	Alignment	not modelled	99.9	23	PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
75	c2h2wA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
76	c3bl5E	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
77	d1wy5a1	Alignment	not modelled	99.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
78	c3a2kB	Alignment	not modelled	99.8	18	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
79	c2e21A	Alignment	not modelled	99.8	15	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
						Fold: Adenine nucleotide alpha hydrolase-like

80	d1j20a1	Alignment	not modelled	99.8	16	Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
81	c3vrhA	Alignment	not modelled	99.8	20	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
82	c3ilvA	Alignment	not modelled	99.8	14	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
83	c6mtgB	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
84	d1ni5a1	Alignment	not modelled	99.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
85	d1vl2a1	Alignment	not modelled	99.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
86	c5ghaC	Alignment	not modelled	99.8	14	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
87	d2pg3a1	Alignment	not modelled	99.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
88	c3k32D	Alignment	not modelled	99.8	17	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
89	c3dlaD	Alignment	not modelled	99.8	15	PDB header: ligase Chain: D: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
90	c1ni5A	Alignment	not modelled	99.7	19	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
91	c1kh2D	Alignment	not modelled	99.7	16	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
92	c2nz2A	Alignment	not modelled	99.7	13	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
93	c1vl2C	Alignment	not modelled	99.7	15	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
94	d1k92a1	Alignment	not modelled	99.7	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
95	c4u7jB	Alignment	not modelled	99.7	18	PDB header: ligase Chain: B: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
96	d1vbka1	Alignment	not modelled	99.7	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
97	c1k97A	Alignment	not modelled	99.6	12	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
98	d1sura	Alignment	not modelled	99.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
99	c4nzpA	Alignment	not modelled	99.6	16	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
100	c2o8vA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
101	c1vbka	Alignment	not modelled	99.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
102	c2goyC	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
103	c6fqeE	Alignment	not modelled	99.3	16	PDB header: ligase Chain: E: PDB Molecule: cobyrinic acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
104	c5n9mA	Alignment	not modelled	99.3	15	PDB header: transferase Chain: A: PDB Molecule: cobyrinic acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
105	d1zuna1	Alignment	not modelled	99.2	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
						PDB header: transferase

106	c1zunA_	Alignment	not modelled	99.2	15	Chain: A: PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
107	d1ru8a_	Alignment	not modelled	99.0	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
108	c4bvwvB_	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine-phosphosulphate reductase; PDBTitle: structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
109	c2oq2B_	Alignment	not modelled	98.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
110	c3g59A_	Alignment	not modelled	98.9	15	PDB header: transferase Chain: A: PDB Molecule: fmn adenylyltransferase; PDBTitle: crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
111	c2wsiA_	Alignment	not modelled	98.6	16	PDB header: transferase Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
112	c1ct9D_	Alignment	not modelled	98.5	12	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
113	d1ct9a1	Alignment	not modelled	98.5	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
114	c1t3tA_	Alignment	not modelled	98.4	20	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
115	d1jgta1	Alignment	not modelled	98.3	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
116	d1q15a1	Alignment	not modelled	98.2	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
117	c1m1zB_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
118	d2d13a1	Alignment	not modelled	98.1	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
119	c1q15A_	Alignment	not modelled	98.0	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
120	c1sy7B_	Alignment	not modelled	97.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.