Phyre^2

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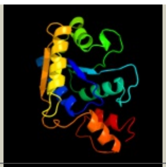
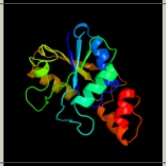
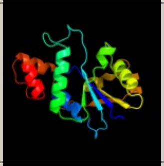
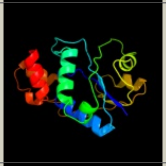
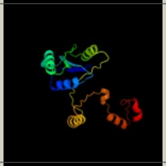
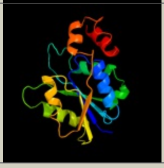
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k4ma_	Alignment		100.0	100	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
2	c1yunB_	Alignment		100.0	37	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
3	d1kama_	Alignment		100.0	40	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
4	d1nuua_	Alignment		100.0	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
5	d1kr2a_	Alignment		100.0	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
6	c3e27B_	Alignment		100.0	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate (nicotinamide) nucleotide **PDBTitle:** nicotinic acid mononucleotide (namn) adenylyltransferase2 from bacillus anthracis: product complex
7	c2h29A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
8	c3f3mA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** six crystal structures of two phosphopantetheine2 adenylyltransferases reveal an alternative ligand binding3 mode and an associated structural change
9	d1tfua_	Alignment		100.0	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
10	c3nd5D_	Alignment		100.0	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
11	c3ikzA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei

12	d1od6a_	Alignment		100.0	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
13	d1o6ba_	Alignment		100.0	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
14	d1vlha_	Alignment		100.0	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
15	d1qjca_	Alignment		100.0	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
16	c3h05A_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vpa0413; **PDBTitle:** the crystal structure of a putative nicotinate-nucleotide2 adenylyltransferase from vibrio parahaemolyticus
17	d1f9aa_	Alignment		100.0	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
18	c3nv7A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of h.pylori phosphopantetheine adenylyltransferase2 mutant i4v/n76y
19	d1ej2a_	Alignment		100.0	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
20	c2qjoB_	Alignment		100.0	20	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase; **PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
21	d1lw7a1	Alignment	not modelled	99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
22	c2r5wA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
23	c1lw7A_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulator nadr; **PDBTitle:** nadr protein from haemophilus influenzae
24	c3gmiA_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0348 protein mj0951; **PDBTitle:** crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
25	d1mrza2	Alignment	not modelled	99.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
26	d1coza_	Alignment	not modelled	99.7	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Cytidylyltransferase
27	c2b7lD_	Alignment	not modelled	99.7	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol-3-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ctp:glycerol-3-phosphate2 cytidylyltransferase from staphylococcus aureus
						PDB header:biosynthetic protein **Chain:** B: **PDB Molecule:**lipopolysaccharide core biosynthesis

28	c3glvB_	Alignment	not modelled	99.2	17	protein; **PDBTitle:** crystal structure of the lipopolysaccharide core biosynthesis protein2 from thermoplasma volcanium gss1
29	c3do8B_	Alignment	not modelled	99.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** the crystal structure of the protein with unknown function2 from archaeoglobus fulgidus
30	c3elbA_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ethanolamine-phosphate cytidylyltransferase; **PDBTitle:** human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
31	c3op1A_	Alignment	not modelled	99.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
32	c2x0kB_	Alignment	not modelled	99.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
33	c1t6zB_	Alignment	not modelled	99.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
34	c3hl4B_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline-phosphate cytidylyltransferase a; **PDBTitle:** crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
35	d1jhda2	Alignment	not modelled	98.8	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
36	d1x6va2	Alignment	not modelled	98.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
37	c1jhdA_	Alignment	not modelled	98.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
38	c1g8gB_	Alignment	not modelled	98.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
39	c2qjfB_	Alignment	not modelled	98.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'- **PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
40	d1g8fa2	Alignment	not modelled	98.5	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
41	c1xnjB_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
42	c1r6xA_	Alignment	not modelled	98.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase; **PDBTitle:** the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
43	c3cr8C_	Alignment	not modelled	98.4	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
44	c1m8pB_	Alignment	not modelled	98.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of p. chrysogenum atp sulfurylase in the t-state
45	d1v47a2	Alignment	not modelled	98.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
46	d1m8pa2	Alignment	not modelled	98.3	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
47	c2gksB_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
48	c1v47B_	Alignment	not modelled	97.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp sulfurylase; **PDBTitle:** crystal structure of atp sulfurylase from thermus2 thermophillus hb8 in complex with aps
49	c3guzB_	Alignment	not modelled	96.3	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
50	c3ag5A_	Alignment	not modelled	90.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus
51	c3innB_	Alignment	not modelled	89.9	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
52	d1ihoa_	Alignment	not modelled	89.6	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
53	c3uk2B_	Alignment	not modelled	89.3	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase;

53	[illegible]	Alignment	not modelled	[illegible]	14	**PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis
54	c3n8hA_	Alignment	not modelled	89.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
55	c2ejcA_	Alignment	not modelled	88.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
56	d1v8fa_	Alignment	not modelled	88.5	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
57	d2a84a1	Alignment	not modelled	84.2	28	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
58	c3mxtA_	Alignment	not modelled	77.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
59	c3dzcA_	Alignment	not modelled	72.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
60	c3focB_	Alignment	not modelled	66.7	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
61	c2dlnA_	Alignment	not modelled	53.7	14	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
62	c3c8zB_	Alignment	not modelled	50.5	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
63	c1zuwA_	Alignment	not modelled	44.5	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
64	c2q4dB_	Alignment	not modelled	36.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
65	c3s81A_	Alignment	not modelled	35.7	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
66	d2d5ba2	Alignment	not modelled	35.5	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
67	c2el7A_	Alignment	not modelled	34.7	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
68	c3sp1B_	Alignment	not modelled	33.9	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
69	d1ydha_	Alignment	not modelled	33.0	11	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
70	d1f74a_	Alignment	not modelled	29.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
71	d1jfla1	Alignment	not modelled	28.0	44	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
72	c2dx7B_	Alignment	not modelled	26.2	44	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
73	d1iowa1	Alignment	not modelled	25.3	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
74	c2q4oA_	Alignment	not modelled	24.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
75	d2q4oa1	Alignment	not modelled	24.7	10	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
76	d1rqga2	Alignment	not modelled	24.6	29	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
77	c3hv0A_	Alignment	not modelled	23.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
78	d1iq0a2	Alignment	not modelled	21.1	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain

79	c2zskA_	Alignment	not modelled	20.5	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
80	c1woyA_	Alignment	not modelled	20.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
81	d1n3la_	Alignment	not modelled	20.2	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
82	c1znyA_	Alignment	not modelled	19.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
83	c2ct8A_	Alignment	not modelled	19.3	16	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 anologue
84	c1u0bB_	Alignment	not modelled	18.4	21	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
85	d1q0qa2	Alignment	not modelled	18.2	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
86	c2k4nA_	Alignment	not modelled	18.1	43	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein pf0246; **PDBTitle:** nmr structure of protein pf0246 from pyrococcus furiosus:2 target pfr75 from the northeast structural genomics3 consortium
87	c2qx7A_	Alignment	not modelled	17.8	64	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
88	c3jxeB_	Alignment	not modelled	17.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
89	d1hx6a2	Alignment	not modelled	17.1	56	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Coat protein p3
90	d1v31a_	Alignment	not modelled	17.1	13	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
91	d1jila_	Alignment	not modelled	16.8	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
92	c2gzmB_	Alignment	not modelled	15.8	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
93	d1v32a_	Alignment	not modelled	15.3	19	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
94	d1uhra_	Alignment	not modelled	14.8	13	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
95	c3akcA_	Alignment	not modelled	14.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
96	c3dhnA_	Alignment	not modelled	14.3	30	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
97	c2ts1A_	Alignment	not modelled	14.1	22	**PDB header:**ligase (synthetase) **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of tyrosyl-t/rna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
98	d2ts1a_	Alignment	not modelled	14.1	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
99	c3tqoA_	Alignment	not modelled	13.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.