Phyre^{2}

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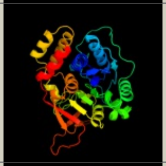
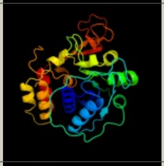
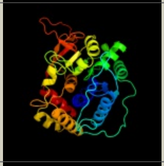
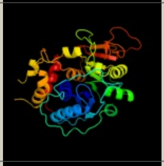
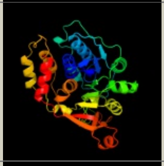
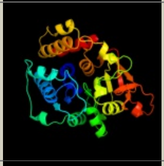
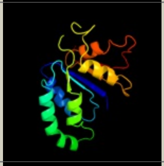
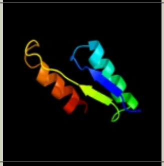
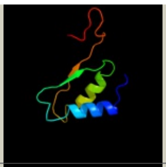
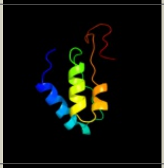
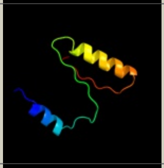
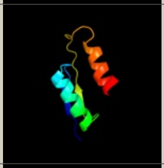
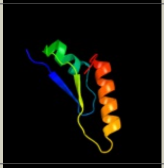
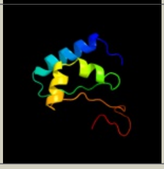
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b9xA_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrimidine-specific ribonucleoside hydrolase rihb; **PDBTitle:** crystal structure of the e. coli pyrimidine nucleoside hydrolase yeik2 in complex with inosine
2	d1q8fa_	Alignment		100.0	38	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
3	d2masa_	Alignment		100.0	37	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
4	c1yoeA_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ybek; **PDBTitle:** crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose
5	d1ezra_	Alignment		100.0	37	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
6	c3fz0C_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nucleoside hydrolase, putative; **PDBTitle:** inosine-guanosine nucleoside hydrolase (ig-nh)
7	c2c40B_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inosine-uridine preferring nucleoside hydrolase family **PDBTitle:** crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
8	d1kica_	Alignment		100.0	21	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
9	c2yhgA_	Alignment		99.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulose-binding protein; **PDBTitle:** ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
10	d1gpma1	Alignment		77.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
11	d2ocda1	Alignment		49.0	22	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase

12	d1o7ja_	Alignment		48.3	14	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
13	d1nnsa_	Alignment		48.1	16	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
14	d1o5za2	Alignment		47.8	15	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
15	d4pgaa_	Alignment		47.0	15	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
16	c2dplA_	Alignment		42.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
17	c3r79B_	Alignment		35.7	15	**PDB header:**structure genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharactertized protein from agrobacterium2 tumefaciens
18	d1pkla3	Alignment		35.4	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
19	d1e0ta3	Alignment		35.0	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
20	d1agxa_	Alignment		34.9	12	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
21	c2z1dA_	Alignment	not modelled	34.1	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
22	d3bula2	Alignment	not modelled	32.4	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
23	c3uowB_	Alignment	not modelled	30.8	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
24	d2b3ya2	Alignment	not modelled	30.5	31	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
25	c2zyiB_	Alignment	not modelled	29.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
26	d1ccwa_	Alignment	not modelled	29.4	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
27	c3tqiB_	Alignment	not modelled	29.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
28	c1wnfA_	Alignment	not modelled	28.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of ph0066 from pyrococcus horikoshii
						PDB header:ligase

29	c3p52B_	Alignment	not modelled	25.1	18	**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
30	c1y80A_	Alignment	not modelled	23.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
31	d2c5sa1	Alignment	not modelled	23.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
32	c2vosA_	Alignment	not modelled	23.5	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
33	d2gc6a2	Alignment	not modelled	22.9	13	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
34	c3dlaD_	Alignment	not modelled	21.5	23	**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
35	c2d6fA_	Alignment	not modelled	20.4	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
36	c1zq1B_	Alignment	not modelled	19.3	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
37	d1wsaa_	Alignment	not modelled	19.1	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
38	c3fiuD_	Alignment	not modelled	18.6	24	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
39	d2nu7b1	Alignment	not modelled	18.0	11	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
40	c1bmtB_	Alignment	not modelled	16.3	18	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
41	c2nu9E_	Alignment	not modelled	16.1	11	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
42	c1w8gA_	Alignment	not modelled	16.0	17	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs; **PDBTitle:** crystal structure of e. coli k-12 yggs
43	c2wltA_	Alignment	not modelled	15.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
44	d1tcaa_	Alignment	not modelled	15.1	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
45	c1w78A_	Alignment	not modelled	14.9	15	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
46	d1ru8a_	Alignment	not modelled	14.6	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
47	c3si9B_	Alignment	not modelled	14.2	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
48	d2vk9a1	Alignment	not modelled	13.9	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycosylating toxin catalytic domain-like
49	c3llxA_	Alignment	not modelled	13.5	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**predicted amino acid aldolase or racemase; **PDBTitle:** crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
50	c2hmaA_	Alignment	not modelled	13.4	7	**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
51	d1d9ea_	Alignment	not modelled	13.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
52	c3nxkE_	Alignment	not modelled	13.0	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
53	d3cx5a2	Alignment	not modelled	12.7	4	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
						PDB header:transferase (glutamine amidotransferase)

54	c1gpmD_	Alignment	not modelled	12.4	13	**Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
55	d3clsc1	Alignment	not modelled	12.2	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
56	d1efvb_	Alignment	not modelled	11.5	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
57	c2derA_	Alignment	not modelled	11.3	8	**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
58	c1xtyD_	Alignment	not modelled	11.3	45	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
59	c3cseA_	Alignment	not modelled	11.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
60	c3bl5E_	Alignment	not modelled	11.0	9	**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
61	c3sz8D_	Alignment	not modelled	11.0	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
62	d1lw7a1	Alignment	not modelled	10.7	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
63	d1vbka1	Alignment	not modelled	10.5	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
64	c2d3kA_	Alignment	not modelled	10.3	55	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structural study on project id ph1539 from pyrococcus2 horikoshii ot3
65	c2yxgD_	Alignment	not modelled	10.2	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
66	d1liua3	Alignment	not modelled	10.2	17	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
67	d1j20a1	Alignment	not modelled	10.1	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
68	d1kqpa_	Alignment	not modelled	10.1	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
69	d2bcea_	Alignment	not modelled	10.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
70	c2zv3E_	Alignment	not modelled	9.7	64	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
71	d1q7sa_	Alignment	not modelled	9.5	45	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
72	d1bd0a2	Alignment	not modelled	9.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
73	d1ik6a2	Alignment	not modelled	9.3	33	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
74	d3erja1	Alignment	not modelled	9.0	55	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
75	d2g50a3	Alignment	not modelled	8.9	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
76	d1xnga1	Alignment	not modelled	8.8	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
77	c1o5zA_	Alignment	not modelled	8.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
78	d1hioa_	Alignment	not modelled	8.7	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
79	d5mdha1	Alignment	not modelled	8.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
80	d2bvla1	Alignment	not modelled	8.4	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases

						Family: Glycosylating toxin catalytic domain-like
81	c1eucB_	Alignment	not modelled	8.4	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
82	c3ezxA_	Alignment	not modelled	8.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
83	d1rlka_	Alignment	not modelled	8.0	36	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
84	d2d6fa2	Alignment	not modelled	8.0	20	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
85	d1t1ra2	Alignment	not modelled	8.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
86	c2dy3B_	Alignment	not modelled	7.8	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
87	c3rg9A_	Alignment	not modelled	7.8	26	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate synthase; **PDBTitle:** trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210
88	c2gc6A_	Alignment	not modelled	7.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase; **PDBTitle:** s73a mutant of l. casei fpgs
89	d1o94c_	Alignment	not modelled	7.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
90	d1k4ya_	Alignment	not modelled	7.4	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
91	c3jz0B_	Alignment	not modelled	7.3	18	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**lincosamide nucleotidyltransferase; **PDBTitle:** linb complexed with clindamycin and ampcpp
92	c3kw3B_	Alignment	not modelled	7.3	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
93	d1qs0b2	Alignment	not modelled	7.3	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
94	d1u35c1	Alignment	not modelled	7.0	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
95	d7reqa2	Alignment	not modelled	7.0	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
96	d2ozlb2	Alignment	not modelled	6.8	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
97	d2pg3a1	Alignment	not modelled	6.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
98	d1qe3a_	Alignment	not modelled	6.6	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
99	c1vl2C_	Alignment	not modelled	6.6	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution