Phyre2

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Description	P17854
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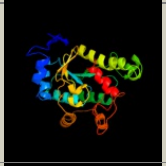
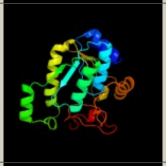
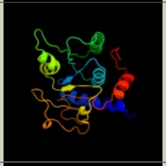
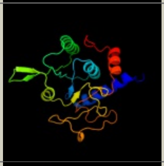
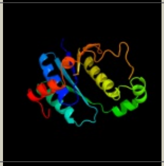
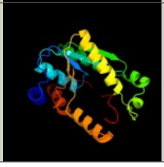
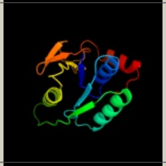
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o8vA_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
2	c2oq2B_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
3	c2goyC_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
4	d1sura_	Alignment		100.0	100	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
5	c3g59A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp
6	c2wsiA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fad synthetase; **PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad
7	c1zunA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
8	d1zuna1	Alignment		100.0	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
9	c3bl5E_	Alignment		99.9	7	**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
10	c3a2kB_	Alignment		99.9	17	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
11	d1wy5a1	Alignment		99.8	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase

12	d1k92a1	Alignment		99.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
13	c2e21A_	Alignment		99.8	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
14	c1ni5A_	Alignment		99.8	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
15	d1ni5a1	Alignment		99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
16	d1j20a1	Alignment		99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
17	c2dplA_	Alignment		99.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
18	d1vl2a1	Alignment		99.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
19	d1gpma1	Alignment		99.7	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
20	d2c5sa1	Alignment		99.7	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
21	c3p52B_	Alignment	not modelled	99.7	13	**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
22	c1vl2C_	Alignment	not modelled	99.7	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
23	c1kh2D_	Alignment	not modelled	99.6	17	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
24	c2e18B_	Alignment	not modelled	99.6	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
25	c2nz2A_	Alignment	not modelled	99.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
26	c3tqiB_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
27	c2ywcC_	Alignment	not modelled	99.6	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
28	c1k97A_	Alignment	not modelled	99.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline

29	c2derA_	Alignment	not modelled	99.6	17	**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
30	c3fiuD_	Alignment	not modelled	99.6	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
31	c2hmaA_	Alignment	not modelled	99.5	13	**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
32	c2c5sA_	Alignment	not modelled	99.5	17	**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
33	c3k32D_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
34	d2pg3a1	Alignment	not modelled	99.5	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
35	d1xnga1	Alignment	not modelled	99.5	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
36	c1gpmD_	Alignment	not modelled	99.5	17	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
37	c3uowB_	Alignment	not modelled	99.4	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
38	c2vxoB_	Alignment	not modelled	99.3	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
39	d1vbka1	Alignment	not modelled	99.2	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
40	d1kqpa_	Alignment	not modelled	98.9	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
41	d1ru8a_	Alignment	not modelled	98.9	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
42	c3q4gA_	Alignment	not modelled	98.8	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
43	c3dpiA_	Alignment	not modelled	98.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
44	d1wxia1	Alignment	not modelled	98.6	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
45	d2d13a1	Alignment	not modelled	98.5	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
46	c3n05B_	Alignment	not modelled	98.3	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
47	c1ct9D_	Alignment	not modelled	98.0	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
48	d1jgta1	Alignment	not modelled	97.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
49	d1q15a1	Alignment	not modelled	97.8	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
50	d1ct9a1	Alignment	not modelled	97.7	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
51	c1vbkA_	Alignment	not modelled	97.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
52	c1q15A_	Alignment	not modelled	97.6	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
53	c1m1zB_	Alignment	not modelled	97.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
54	c3ilvA_	Alignment	not modelled	97.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii

55	c3dlaD_	Alignment	not modelled	96.3	10	**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
56	c2cb1A_	Alignment	not modelled	78.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-actetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
57	c3bq7A_	Alignment	not modelled	64.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)
58	c3e15D_	Alignment	not modelled	64.4	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** 6-phosphogluconolactonase from plasmodium vivax
59	c3bs7A_	Alignment	not modelled	59.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
60	d1pk1c1	Alignment	not modelled	56.4	20	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
61	c3lwdA_	Alignment	not modelled	49.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
62	c3bs5A_	Alignment	not modelled	49.3	10	**PDB header:**signaling protein/membrane protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of hcnk2-sam/dhyp-sam complex
63	c2iy3A_	Alignment	not modelled	48.7	13	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
64	c1pbtA_	Alignment	not modelled	45.9	11	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
65	d1wwva1	Alignment	not modelled	39.9	15	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
66	c2j0eA_	Alignment	not modelled	39.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
67	c3nbmA_	Alignment	not modelled	39.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
68	c1pk1A_	Alignment	not modelled	39.3	20	**PDB header:**transcription repression **Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein; **PDBTitle:** hetero sam domain structure of ph and scm.
69	c3ndnC_	Alignment	not modelled	37.8	7	**PDB header:**lyase **Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
70	c3loqA_	Alignment	not modelled	37.4	17	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
71	c1v85A_	Alignment	not modelled	37.3	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
72	d1kw4a_	Alignment	not modelled	36.4	20	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
73	c3nwpA_	Alignment	not modelled	34.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
74	c3lhiA_	Alignment	not modelled	34.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
75	c1pk1B_	Alignment	not modelled	32.4	33	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
76	c3dm5A_	Alignment	not modelled	31.3	15	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
77	d1dv5a_	Alignment	not modelled	28.7	7	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**apo-D-alanyl carrier protein
78	c3bolB_	Alignment	not modelled	28.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
79	d1fsfa_	Alignment	not modelled	27.9	9	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like

						Family: NagB-like
80	d1tx2a_	Alignment	not modelled	27.1	3	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
81	c1tx2A_	Alignment	not modelled	27.1	3	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
82	d1pjqa3	Alignment	not modelled	24.9	19	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
83	c2pa6A_	Alignment	not modelled	24.5	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of mj0232 from methanococcus jannaschii
84	d1q77a_	Alignment	not modelled	23.7	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
85	c2o2jA_	Alignment	not modelled	23.3	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
86	c2dkzA_	Alignment	not modelled	22.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical protein loc64762; **PDBTitle:** solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
87	c2l5yA_	Alignment	not modelled	22.4	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**stromal interaction molecule 2; **PDBTitle:** nmr structure of calcium-loaded stim2 ef-sam.
88	d3bofa1	Alignment	not modelled	22.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
89	d1uqva_	Alignment	not modelled	22.0	3	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
90	c3oc6A_	Alignment	not modelled	21.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
91	d1sv0c_	Alignment	not modelled	21.7	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
92	c3hn6D_	Alignment	not modelled	21.6	11	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
93	c3lqkA_	Alignment	not modelled	21.6	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
94	c2k60A_	Alignment	not modelled	21.3	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein (stromal interaction molecule 1); **PDBTitle:** nmr structure of calcium-loaded stim1 ef-sam
95	d1ne7a_	Alignment	not modelled	21.1	7	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
96	d1ad1a_	Alignment	not modelled	20.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
97	d1xpja_	Alignment	not modelled	20.3	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
98	c2ycbA_	Alignment	not modelled	20.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
99	d1s8na_	Alignment	not modelled	20.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related