Phyre2

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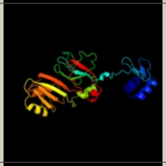
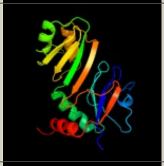
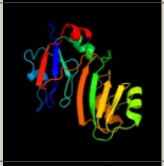
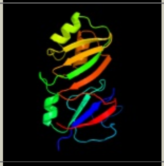
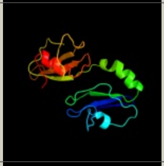
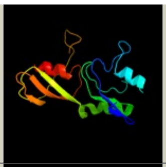
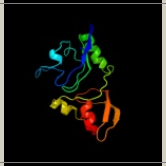
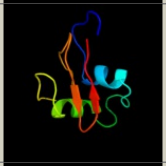
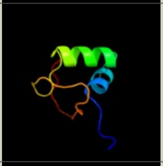
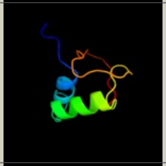
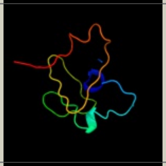
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dh3C_	Alignment		100.0	100	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
2	c1kskA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
3	c1vioA_	Alignment		100.0	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
4	c2gmlA_	Alignment		100.0	98	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of catalytic domain of e.coli rluf
5	d1kska4	Alignment		100.0	29	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
6	d1vioa1	Alignment		100.0	31	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
7	c2omlA_	Alignment		100.0	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
8	c2olwB_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
9	d1v9ka_	Alignment		100.0	19	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
10	c2i82D_	Alignment		99.9	15	**PDB header:**lyase/rna **Chain:** D: **PDB Molecule:**ribosomal large subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
11	c1v9fA_	Alignment		99.9	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli

12	d1v9fa_	Alignment		99.9	20	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
13	c1qyuA_	Alignment		99.9	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
14	d1vioa2	Alignment		99.4	29	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
15	d1p9ka_	Alignment		99.3	21	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
16	d1dm9a_	Alignment		99.2	29	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
17	c1dm9A_	Alignment		99.2	29	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
18	c3bbnD_	Alignment		99.0	22	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
19	c2k6pA_	Alignment		99.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
20	d1c06a_	Alignment		99.0	24	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
21	c2cqjA_	Alignment	not modelled	99.0	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein **PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
22	d2uubd1	Alignment	not modelled	98.9	31	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
23	d2gy9d1	Alignment	not modelled	98.7	27	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
24	d2apoa2	Alignment	not modelled	98.6	22	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
25	d2ey4a2	Alignment	not modelled	98.6	21	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
26	c2ey4A_	Alignment	not modelled	98.5	23	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
27	d1r3ea2	Alignment	not modelled	98.5	27	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
28	d1k8wa5	Alignment	not modelled	98.5	20	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
						PDB header:isomerase/rna binding protein

29	c2apoA_	Alignment	not modelled	98.4	21	**Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
30	d1sgva2	Alignment	not modelled	98.3	22	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
31	c1sgvA_	Alignment	not modelled	98.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
32	c3uaiA_	Alignment	not modelled	98.2	19	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
33	c1k8wA_	Alignment	not modelled	98.1	18	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
34	c3hp7A_	Alignment	not modelled	98.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
35	d1kska3	Alignment	not modelled	97.9	26	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
36	c1s1hD_	Alignment	not modelled	97.6	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s9-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
37	c2xzmD_	Alignment	not modelled	97.6	12	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
38	d1jh3a_	Alignment	not modelled	97.5	22	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
39	d1h3fa2	Alignment	not modelled	97.5	23	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
40	c2janD_	Alignment	not modelled	97.1	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
41	c1h3eA_	Alignment	not modelled	97.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
42	c1ze2B_	Alignment	not modelled	93.9	23	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
43	c3iz6C_	Alignment	not modelled	93.6	17	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**40s ribosomal protein s9 (s4p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
44	c3kbgA_	Alignment	not modelled	93.5	26	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
45	c2xzmW_	Alignment	not modelled	92.8	23	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
46	c3iz6D_	Alignment	not modelled	91.2	23	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
47	c3izbD_	Alignment	not modelled	91.0	24	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
48	d2g1la1	Alignment	not modelled	70.3	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
49	d1fm0d_	Alignment	not modelled	64.5	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
50	c3fm8A_	Alignment	not modelled	63.3	24	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
51	c3hvzB_	Alignment	not modelled	59.6	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
52	c2eh0A_	Alignment	not modelled	58.3	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b; **PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
53	c3h7hA_	Alignment	not modelled	58.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4;

53	c3h7hA_	Alignment	not modelled	58.3	22	**PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
54	c3po0A_	Alignment	not modelled	58.1	35	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
55	c2qieB_	Alignment	not modelled	55.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
56	d1rwsa_	Alignment	not modelled	55.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
57	c2kmmA_	Alignment	not modelled	54.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
58	d1tkea1	Alignment	not modelled	48.7	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
59	d2hzab1	Alignment	not modelled	47.9	22	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
60	d1wlna1	Alignment	not modelled	47.3	12	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
61	d1vjka_	Alignment	not modelled	46.5	39	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
62	d2hzaa1	Alignment	not modelled	44.9	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
63	c1z4hA_	Alignment	not modelled	43.9	27	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
64	d2affa1	Alignment	not modelled	42.2	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
65	c3gmgB_	Alignment	not modelled	41.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
66	c2exuA_	Alignment	not modelled	39.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
67	d2ff4a3	Alignment	not modelled	35.4	11	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
68	c3dwmA_	Alignment	not modelled	34.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
69	d1nyra2	Alignment	not modelled	33.8	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
70	c1q5vB_	Alignment	not modelled	33.4	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
71	c2bj3D_	Alignment	not modelled	32.6	28	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
72	c1r21A_	Alignment	not modelled	31.6	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
73	c3rpfC_	Alignment	not modelled	30.8	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
74	d1wxqa2	Alignment	not modelled	30.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
75	d1xo3a_	Alignment	not modelled	27.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
76	c2qjlA_	Alignment	not modelled	27.1	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
77	c3gqsB_	Alignment	not modelled	26.7	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
78	d1zud21	Alignment	not modelled	25.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
79	d2cu3a1	Alignment	not modelled	24.8	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS

80	c2g1eA_	Alignment	not modelled	24.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
81	d1v8ca1	Alignment	not modelled	24.4	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
82	c1wwtA_	Alignment	not modelled	24.3	5	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
83	d1c1za5	Alignment	not modelled	24.0	21	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
84	c3poaA_	Alignment	not modelled	23.9	20	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
85	d2piea1	Alignment	not modelled	23.4	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
86	d2bj7a1	Alignment	not modelled	23.1	38	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
87	c2jqlA_	Alignment	not modelled	22.2	28	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
88	c3kt9A_	Alignment	not modelled	22.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
89	c2kl0A_	Alignment	not modelled	21.4	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
90	c2ca9B_	Alignment	not modelled	21.3	28	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
91	c1yj5C_	Alignment	not modelled	21.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
92	c3cwiA_	Alignment	not modelled	20.7	41	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
93	c2r9qD_	Alignment	not modelled	20.5	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**2'-deoxycytidine 5'-triphosphate deaminase; **PDBTitle:** crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
94	c1tygG_	Alignment	not modelled	20.2	9	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
95	c1f5nA_	Alignment	not modelled	19.5	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1; **PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
96	d1ryja_	Alignment	not modelled	18.5	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
97	d1xnea_	Alignment	not modelled	18.2	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
98	c2l52A_	Alignment	not modelled	18.1	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**methanosarcina acetivorans samp1 homolog; **PDBTitle:** solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
99	d1wgka_	Alignment	not modelled	18.0	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog