Phyre2

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Description	P0AAS7
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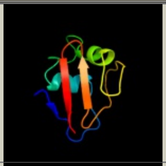
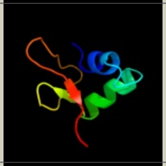
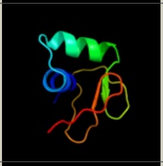
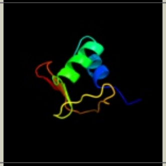
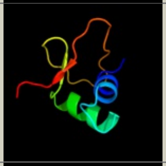
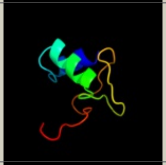
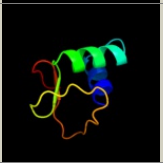
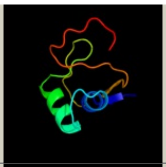
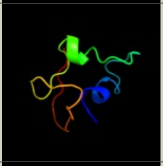
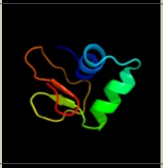
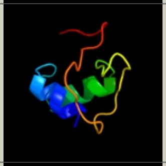
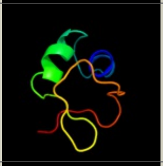
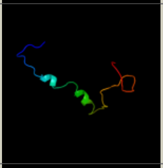
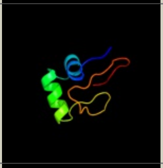
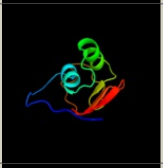
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1p9ka_	Alignment		99.9	100	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
2	d1c06a_	Alignment		99.5	23	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
3	d2uubd1	Alignment		99.5	19	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
4	d1vioa2	Alignment		99.5	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
5	c1dm9A_	Alignment		99.5	18	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
6	d1dm9a_	Alignment		99.5	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
7	d2gy9d1	Alignment		99.5	17	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
8	c3bbnD_	Alignment		99.5	13	**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.
9	c2cqjA_	Alignment		99.4	17	**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
10	c3dh3C_	Alignment		99.4	21	**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
11	c1kskA_	Alignment		99.3	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua

12	c3hp7A_	Alignment		99.2	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
13	c2k6pA_	Alignment		99.1	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
14	c1vioA_	Alignment		99.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
15	c1s1hD_	Alignment		99.1	17	**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.
16	c2xzmD_	Alignment		99.1	14	**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
17	c3iz6C_	Alignment		98.5	16	**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
18	d1h3fa2	Alignment		98.4	21	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
19	d1jh3a_	Alignment		98.3	22	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
20	c2janD_	Alignment		98.2	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
21	c1h3eA_	Alignment	not modelled	98.1	21	**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
22	d1kska3	Alignment	not modelled	98.1	22	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
23	c3kbgA_	Alignment	not modelled	98.0	27	**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.
24	c2xzmW_	Alignment	not modelled	97.5	22	**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
25	c3iz6D_	Alignment	not modelled	97.2	18	**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
26	c3izbD_	Alignment	not modelled	97.0	21	**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
27	c2ktlA_	Alignment	not modelled	85.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of c-terminal domain from mttyrrs of a. nidulans
						Fold:SMAD/FHA domain

28	d2g1la1	Alignment	not modelled	78.9	15	**Superfamily:**SMAD/FHA domain **Family:**FHA domain
29	d1zud21	Alignment	not modelled	74.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
30	d1xnea_	Alignment	not modelled	72.2	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
31	c3poaA_	Alignment	not modelled	71.2	13	**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
32	c2eh0A_	Alignment	not modelled	71.2	12	**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
33	d1s04a_	Alignment	not modelled	71.2	30	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
34	c2qjlA_	Alignment	not modelled	71.1	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
35	c3gqsB_	Alignment	not modelled	66.8	21	**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
36	c3rpfC_	Alignment	not modelled	66.4	8	**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
37	d2affa1	Alignment	not modelled	66.1	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
38	c3hvzB_	Alignment	not modelled	66.1	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
39	d2ff4a3	Alignment	not modelled	63.7	16	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
40	c3cwiA_	Alignment	not modelled	63.0	18	**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
41	d1fm0d_	Alignment	not modelled	62.3	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
42	c3po0A_	Alignment	not modelled	61.8	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
43	c2kmmA_	Alignment	not modelled	61.2	19	**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)
44	c2jqlA_	Alignment	not modelled	59.8	12	**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
45	c3fm8A_	Alignment	not modelled	59.3	12	**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)
46	c1r21A_	Alignment	not modelled	58.5	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
47	c3dwmA_	Alignment	not modelled	58.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
48	d1xo3a_	Alignment	not modelled	53.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
49	d1vjka_	Alignment	not modelled	53.1	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
50	c2qieB_	Alignment	not modelled	51.1	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
51	d1tkea1	Alignment	not modelled	49.7	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
52	d1rwsa_	Alignment	not modelled	49.6	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
53	d1wlna1	Alignment	not modelled	48.2	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain

						Family:FHA domain
54	c2jv2A_	Alignment	not modelled	48.0	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
55	d1v8ca1	Alignment	not modelled	44.2	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
56	c2kklA_	Alignment	not modelled	43.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
57	c2g1eA_	Alignment	not modelled	43.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
58	c1v8cA_	Alignment	not modelled	42.0	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
59	d2hzab1	Alignment	not modelled	41.1	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
60	d2hzaa1	Alignment	not modelled	39.4	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
61	d2cu3a1	Alignment	not modelled	38.8	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
62	c3hx1B_	Alignment	not modelled	37.1	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
63	d2f9ha1	Alignment	not modelled	35.1	5	**Fold:**PTSIIA/GutA-like **Superfamily:**PTSIIA/GutA-like **Family:**PTSIIA/GutA-like
64	c2l52A_	Alignment	not modelled	34.5	4	**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
65	d1wxqa2	Alignment	not modelled	33.8	5	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
66	d1wgka_	Alignment	not modelled	33.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
67	d2bj7a1	Alignment	not modelled	33.1	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
68	c2k9xA_	Alignment	not modelled	31.5	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
69	c3er0A_	Alignment	not modelled	31.0	8	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of the full length eif5a from2 saccharomyces cerevisiae
70	d1nyra2	Alignment	not modelled	30.7	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
71	d1g3ga_	Alignment	not modelled	30.3	8	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
72	c1yj5C_	Alignment	not modelled	29.9	8	**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
73	d1tygb_	Alignment	not modelled	29.9	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
74	d1ueba1	Alignment	not modelled	29.2	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
75	c2ff4B_	Alignment	not modelled	29.1	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
76	d1iz6a1	Alignment	not modelled	29.1	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
77	c3tdqB_	Alignment	not modelled	28.8	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
78	c2kl0A_	Alignment	not modelled	28.2	22	**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

79	d1g6ga_	Alignment	not modelled	28.1	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
80	c1q5vB_	Alignment	not modelled	27.6	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
81	c3kt9A_	Alignment	not modelled	27.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
82	d2piea1	Alignment	not modelled	27.1	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
83	c3a5zF_	Alignment	not modelled	26.8	22	**PDB header:**ligase **Chain:** F: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p
84	c1gxcA_	Alignment	not modelled	26.2	12	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
85	d1gxca_	Alignment	not modelled	26.2	12	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
86	c3elsA_	Alignment	not modelled	25.8	8	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204
87	c1iz6B_	Alignment	not modelled	25.6	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**initiation factor 5a; **PDBTitle:** crystal structure of translation initiation factor 5a from pyrococcus2 horikoshii
88	c2bj3D_	Alignment	not modelled	24.5	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
89	d1ryja_	Alignment	not modelled	24.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
90	d1yjma1	Alignment	not modelled	23.8	7	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
91	d1ed7a_	Alignment	not modelled	23.8	23	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
92	c3hksB_	Alignment	not modelled	23.5	15	**PDB header:**translation, rna binding protein **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
93	d1lgpa_	Alignment	not modelled	22.3	12	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
94	c1xtdA_	Alignment	not modelled	20.8	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic initiation factor 5a; **PDBTitle:** structural analysis of leishmania mexicana eukaryotic initiation2 factor 5a
95	c1tygG_	Alignment	not modelled	20.8	9	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
96	c3gmgB_	Alignment	not modelled	20.0	4	**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
97	c2v9vA_	Alignment	not modelled	19.2	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
98	c1wwtA_	Alignment	not modelled	18.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
99	d1uhta_	Alignment	not modelled	18.3	6	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain