Phyre2

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Description	P0AA39
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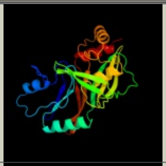
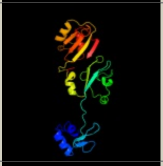
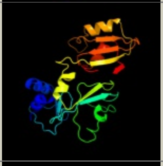
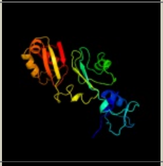
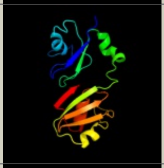
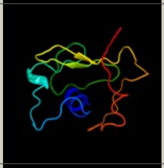
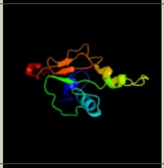
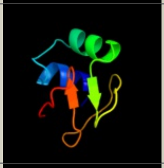
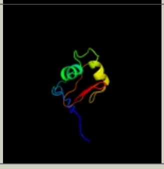
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v9ka_	Alignment		100.0	98	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
2	d1v9fa_	Alignment		100.0	31	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
3	c1v9fA_	Alignment		100.0	31	**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
4	c1qyuA_	Alignment		100.0	31	**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
5	c2i82D_	Alignment		100.0	38	**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
6	c1kskA_	Alignment		100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
7	c1vioA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
8	c3dh3C_	Alignment		100.0	19	**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
9	c2omlA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
10	c2olwB_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
11	d1kska4	Alignment		100.0	23	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD

12	d1vioa1	Alignment		100.0	21	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
13	c2gmlA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of catalytic domain of e.coli rluf
14	c2k6pA_	Alignment		99.5	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
15	d1dm9a_	Alignment		99.0	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
16	c1dm9A_	Alignment		99.0	20	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
17	c3bbnD_	Alignment		98.9	19	**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.
18	d1vioa2	Alignment		98.8	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
19	d1c06a_	Alignment		98.6	12	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
20	d1p9ka_	Alignment		98.5	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
21	d2uubd1	Alignment	not modelled	98.4	19	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
22	d2gy9d1	Alignment	not modelled	98.2	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
23	c2cqjA_	Alignment	not modelled	97.9	18	**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
24	d1k8wa5	Alignment	not modelled	97.7	20	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
25	d2ey4a2	Alignment	not modelled	97.6	27	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
26	d2apoa2	Alignment	not modelled	97.6	20	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
27	d1sgva2	Alignment	not modelled	97.5	27	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
28	c2ey4A_	Alignment	not modelled	97.5	27	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
						Fold: Pseudouridine synthase

29	d1r3ea2	Alignment	not modelled	97.5	24	**Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
30	c3uaiA_	Alignment	not modelled	97.3	17	**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
31	c3hp7A_	Alignment	not modelled	97.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
32	c2apoA_	Alignment	not modelled	97.3	23	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
33	c1k8wA_	Alignment	not modelled	97.3	20	**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	c1sgvA_	Alignment	not modelled	97.3	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
35	d1kska3	Alignment	not modelled	97.1	27	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
36	c1s1hD_	Alignment	not modelled	96.9	11	**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	96.8	10	**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	d1h3fa2	Alignment	not modelled	96.6	11	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
39	d1jh3a_	Alignment	not modelled	95.7	15	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
40	c1ze2B_	Alignment	not modelled	95.7	28	**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
41	c3kbgA_	Alignment	not modelled	95.5	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.
42	c1h3eA_	Alignment	not modelled	95.1	13	**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
43	c2xzmW_	Alignment	not modelled	94.9	25	**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
44	c2janD_	Alignment	not modelled	93.9	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
45	c3iz6D_	Alignment	not modelled	93.9	28	**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
46	c3izbD_	Alignment	not modelled	93.6	25	**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
47	d1fm0d_	Alignment	not modelled	85.2	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
48	c2qieB_	Alignment	not modelled	83.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
49	c3po0A_	Alignment	not modelled	82.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
50	d1vjka_	Alignment	not modelled	82.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
51	c3iz6C_	Alignment	not modelled	81.1	10	**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
52	d2g1la1	Alignment	not modelled	78.5	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
53	d1wgka_	Alignment	not modelled	77.7	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog

54	c2g1eA_	Alignment	not modelled	75.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
55	c3fm8A_	Alignment	not modelled	71.0	20	**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)
56	d1xo3a_	Alignment	not modelled	70.6	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
57	c2eh0A_	Alignment	not modelled	69.0	28	**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
58	c2kmmA_	Alignment	not modelled	67.9	28	**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)
59	c3hvzB_	Alignment	not modelled	66.4	19	**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
60	c2qjlA_	Alignment	not modelled	66.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
61	c1v8cA_	Alignment	not modelled	66.1	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
62	d2affa1	Alignment	not modelled	63.3	26	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
63	c1r21A_	Alignment	not modelled	61.1	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
64	c3dwmA_	Alignment	not modelled	59.7	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
65	d1wlna1	Alignment	not modelled	59.0	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
66	d1v8ca1	Alignment	not modelled	59.0	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
67	c3rpfC_	Alignment	not modelled	57.9	14	**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
68	d1tkea1	Alignment	not modelled	57.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
69	d1rwsa_	Alignment	not modelled	54.7	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
70	c2hj1A_	Alignment	not modelled	53.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
71	d2hj1a1	Alignment	not modelled	53.2	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
72	d2ff4a3	Alignment	not modelled	52.3	36	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
73	c2k9xA_	Alignment	not modelled	50.2	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
74	d1wxqa2	Alignment	not modelled	46.5	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
75	c1yj5C_	Alignment	not modelled	42.2	27	**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
76	c3elsA_	Alignment	not modelled	38.1	24	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204
77	c3gqsB_	Alignment	not modelled	37.8	28	**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	c2jqlA_	Alignment	not modelled	37.7	24	**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
						Fold:beta-Grasp (ubiquitin-like)

79	d1nyra2	Alignment	not modelled	37.5	19	**Superfamily:**TGS-like **Family:**TGS domain
80	c3kt9A_	Alignment	not modelled	36.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
81	c3zrhA_	Alignment	not modelled	35.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1; **PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
82	c3hx1B_	Alignment	not modelled	34.3	25	**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
83	c2l52A_	Alignment	not modelled	33.0	32	**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
84	c3poaA_	Alignment	not modelled	31.1	29	**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	d1lgpa_	Alignment	not modelled	30.6	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
86	d1g6ga_	Alignment	not modelled	28.3	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
87	d1zud21	Alignment	not modelled	27.4	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
88	d2piea1	Alignment	not modelled	26.4	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
89	c2kklA_	Alignment	not modelled	25.8	33	**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).
90	c1gxcA_	Alignment	not modelled	25.8	16	**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
91	d1gxca_	Alignment	not modelled	25.8	16	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
92	c3cwiA_	Alignment	not modelled	23.1	23	**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	c2jkdB_	Alignment	not modelled	23.1	24	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex
94	c2h89B_	Alignment	not modelled	21.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
95	c2zodB_	Alignment	not modelled	20.1	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
96	c2ekiA_	Alignment	not modelled	20.0	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
97	d1k25a2	Alignment	not modelled	19.9	7	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
98	d1g3ga_	Alignment	not modelled	19.8	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
99	d1c1za5	Alignment	not modelled	19.7	29	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain