

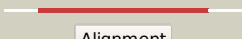

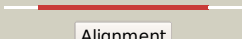

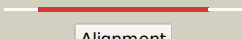


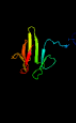

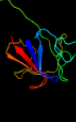








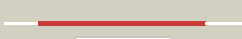


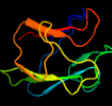

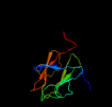



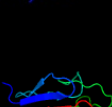



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3360_(-)_3772822_3773190
Date	Fri Aug 9 18:20:02 BST 2019
Unique Job ID	60d4eba849edc9b9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ccdA_</a>	 Alignment		100.0	64	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding/permease protein rv1747; <b>PDBTitle:</b> the crystal structure of mycobacterium tuberculosis rv1747 fha-1
2	<a href="#">c2kkkA_</a>	 Alignment		99.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mb1858; <b>PDBTitle:</b> solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
3	<a href="#">c2kfuA_</a>	 Alignment		99.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rv1827 pthr 22; <b>PDBTitle:</b> pknb-phosphorylated rv1827
4	<a href="#">c2n84A_</a>	 Alignment		99.9	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the fha domain of tbpar42
5	<a href="#">c6cahA_</a>	 Alignment		99.9	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding/permease protein rv1747; <b>PDBTitle:</b> nmr-based structure of the fha-2 domain from mycobacterium2 tuberculosis abc transporter rv1747
6	<a href="#">c3hx1B_</a>	 Alignment		99.8	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> slr1951 protein; <b>PDBTitle:</b> crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
7	<a href="#">c4jonA_</a>	 Alignment		99.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 170 kda; <b>PDBTitle:</b> crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
8	<a href="#">d1mzka_</a>	 Alignment		99.8	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
9	<a href="#">c3vpyA_</a>	 Alignment		99.8	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fha domain-containing protein ddl; <b>PDBTitle:</b> crystal structure of arabidopsis ddl fha domain
10	<a href="#">d1luhta_</a>	 Alignment		99.8	25	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
11	<a href="#">d2ff4a3</a>	 Alignment		99.8	21	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain

12	<a href="#">c5a8iA_</a>	Alignment		99.8	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arna; <b>PDBTitle:</b> crystal structure of the fha domain of arna from sulfobolbus2 acidocaldarius
13	<a href="#">c3poaA_</a>	Alignment		99.8	22	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tb39.8; <b>PDBTitle:</b> structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
14	<a href="#">c2jkdB_</a>	Alignment		99.8	17	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> structure of the yeast pm11 splicing factor and its2 integration into the res complex
15	<a href="#">c2jqIA_</a>	Alignment		99.8	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage response protein kinase dun1; <b>PDBTitle:</b> nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
16	<a href="#">c3elsA_</a>	Alignment		99.8	16	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna leakage protein 1; <b>PDBTitle:</b> crystal structure of yeast pml1p, residues 51-204
17	<a href="#">c4h87A_</a>	Alignment		99.8	19	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kanadaplin; <b>PDBTitle:</b> crystal structure of a fha domain of kanadaplin (slc4a1ap) from homo2 sapiens at 1.55 a resolution
18	<a href="#">c3ounA_</a>	Alignment		99.8	22	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tb39.8; <b>PDBTitle:</b> crystal structure of the fhaa fha domain complexed with the2 intracellular domain of rv3910
19	<a href="#">c5yyxA_</a>	Alignment		99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> meiosis-specific serine/threonine-protein kinase mek1; <b>PDBTitle:</b> crystal structure of the mek1 fha domain
20	<a href="#">c6ar2B_</a>	Alignment		99.8	24	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sarcolemmal membrane-associated protein; <b>PDBTitle:</b> structure of human slmap fha domain in complex with pmst2
21	<a href="#">c1r21A_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> antigen ki-67; <b>PDBTitle:</b> solution structure of human ki67 fha domain
22	<a href="#">d2affa1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
23	<a href="#">c3fm8A_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transport protein/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif13b; <b>PDBTitle:</b> crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
24	<a href="#">c3uotB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> mediator of dna damage checkpoint protein 1; <b>PDBTitle:</b> crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
25	<a href="#">d2piea1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
26	<a href="#">c2jpeA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear inhibitor of protein phosphatase 1; <b>PDBTitle:</b> fha domain of nipp1
27	<a href="#">c3gqsB_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate cyclase-like protein; <b>PDBTitle:</b> crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
28	<a href="#">d1g6ga_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain <b>PDB header:</b> cell cycle

29	<a href="#">c5t2sA</a>	Alignment	not modelled	99.8	14	<b>Chain:</b> A: <b>PDB Molecule:</b> ddk kinase regulatory subunit dbf4.serine/threonine-protein <b>PDBTitle:</b> structure of the fha1 domain of rad53 bound simultaneously to the brct2 domain of dbf4 and a phosphopeptide.
30	<a href="#">d1g3ga</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
31	<a href="#">c2ff4B</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable regulatory protein embr; <b>PDBTitle:</b> mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
32	<a href="#">c4a0eB</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> type iii secretion protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd
33	<a href="#">d1gxca</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
34	<a href="#">c1gxcA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> phosphoprotein-binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase chk2; <b>PDBTitle:</b> fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
35	<a href="#">d1dmza</a>	Alignment	not modelled	99.7	9	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
36	<a href="#">c6a8wA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 64; <b>PDBTitle:</b> crystal structure of the fha domain of far9
37	<a href="#">c5e50A</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> aplf/xrcc4 complex
38	<a href="#">c3kt9A</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin; <b>PDBTitle:</b> aprataxin fha domain
39	<a href="#">d1yjma1</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
40	<a href="#">c5djoB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein; <b>PDBTitle:</b> crystal structure of the cc1-fha tandem of kinesin-3 kif13a
41	<a href="#">d1wlna1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
42	<a href="#">c2eh0A</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1b; <b>PDBTitle:</b> solution structure of the fha domain from human kinesin-2 like protein kif1b
43	<a href="#">c1yj5C</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 5' polynucleotide kinase-3' phosphatase fha domain; <b>PDBTitle:</b> molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
44	<a href="#">d1lgpa</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
45	<a href="#">d1ujxa</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
46	<a href="#">c4eqxA</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a cc1-fha tandem
47	<a href="#">d1qu5a</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
48	<a href="#">d2g1la1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
49	<a href="#">c5z58X</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> smad nuclear-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
50	<a href="#">d2brfa1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
51	<a href="#">c4ejqB</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a c-cc1-fha
52	<a href="#">c3i0mA</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and telomere maintenance protein nbs1; <b>PDBTitle:</b> structure of the s. pombe nbs1 fha/brct-repeat domain
53	<a href="#">c5xzvB</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase rad53; <b>PDBTitle:</b> crystal structure of rad53 1-466 in complex with amp-pnp
54	<a href="#">c3i6uA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase chk2; <b>PDBTitle:</b> structure and activation mechanism of the chk2 dna-damage checkpoint2 kinase
55	<a href="#">c3i6wB</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase chk2; <b>PDBTitle:</b> structure and activation mechanism of the chk2 dna-

						damage checkpoint2 kinase <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> traf-interacting protein with fha domain-containing protein <b>PDBTitle:</b> structure of truncated human tifa
56	<a href="#">c4zgiA</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> essc; <b>PDBTitle:</b> n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
57	<a href="#">c5fwhA</a>	Alignment	not modelled	97.5	25	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> mutator 2, isoform b; <b>PDBTitle:</b> crystal structure of the drosophila mu2 fha domain
58	<a href="#">c3uv0B</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> E: <b>PDB Molecule:</b> nucleoporin nup120; <b>PDBTitle:</b> structure of the yeast coat nucleoporin complex, space group c2
59	<a href="#">c4xmmE</a>	Alignment	not modelled	68.7	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin nup120; <b>PDBTitle:</b> nucleoporin nup120 from s.cerevisiae (aa 1-757)
60	<a href="#">c3hxrA</a>	Alignment	not modelled	66.5	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 9.5 kda culture filtrate antigen cfp10a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyso, an antigen
61	<a href="#">c3dwmA</a>	Alignment	not modelled	55.7	33	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
62	<a href="#">d1xo3a</a>	Alignment	not modelled	50.8	10	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
63	<a href="#">d1dm9a</a>	Alignment	not modelled	48.2	17	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic <b>PDBTitle:</b> heat shock protein 15 kd
64	<a href="#">c1dm9A</a>	Alignment	not modelled	48.2	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-related modifier 1; <b>PDBTitle:</b> crystal structure of urm1
65	<a href="#">c2qjlA</a>	Alignment	not modelled	46.3	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 15; <b>PDBTitle:</b> trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
66	<a href="#">c5z81A</a>	Alignment	not modelled	45.8	24	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> this/moad family protein; <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex
67	<a href="#">c4n6eB</a>	Alignment	not modelled	45.0	38	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
68	<a href="#">d1wgka</a>	Alignment	not modelled	43.5	10	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
69	<a href="#">d1c06a</a>	Alignment	not modelled	42.5	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of urm1 from trypanosoma brucei
70	<a href="#">c2k9xA</a>	Alignment	not modelled	42.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895; <b>PDBTitle:</b> solution structure of ta0895
71	<a href="#">c2g1eA</a>	Alignment	not modelled	41.8	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> Moad
72	<a href="#">d1v8ca1</a>	Alignment	not modelled	41.3	24	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> nucleoporin nup120; <b>PDBTitle:</b> structure of nup120
73	<a href="#">c3h7nD</a>	Alignment	not modelled	41.0	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
74	<a href="#">d1wxqa2</a>	Alignment	not modelled	40.6	15	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
75	<a href="#">d2uubd1</a>	Alignment	not modelled	40.5	24	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rhp9/crb2; <b>PDBTitle:</b> crystal structure of crb2 tandem tudor domains
76	<a href="#">c2fhdA</a>	Alignment	not modelled	40.2	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> crystal structure of translation elongation factor p from2 thermus thermophilus hb8
77	<a href="#">c1uebB</a>	Alignment	not modelled	37.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
78	<a href="#">c3hvxzB</a>	Alignment	not modelled	35.8	32	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin converting factor subunit 1; <b>PDBTitle:</b> solution structure of the haloferax volcanii hvo 2177 protein
79	<a href="#">c2m19A</a>	Alignment	not modelled	34.4	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> Moad
80	<a href="#">d1vjka</a>	Alignment	not modelled	33.3	29	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> structure of a translation elongation factor p (efp) from coxiella2 burnetii
81	<a href="#">c3treA</a>	Alignment	not modelled	33.1	9	<b>PDB header:</b> ribosome

82	<a href="#">c3bbnD_</a>	Alignment	not modelled	31.3	20	<b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s4; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
83	<a href="#">c5o5jD_</a>	Alignment	not modelled	31.3	20	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 30s ribosomal protein s4; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
84	<a href="#">c3po0A_</a>	Alignment	not modelled	30.6	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> small archaeal modifier protein 1; <b>PDBTitle:</b> crystal structure of samp1 from haloferax volcanii
85	<a href="#">d1h3fa2</a>	Alignment	not modelled	30.4	20	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
86	<a href="#">c3mm1E_</a>	Alignment	not modelled	29.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> allophanate hydrolase subunit 2; <b>PDBTitle:</b> allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
87	<a href="#">c2k6pA_</a>	Alignment	not modelled	28.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp_1423; <b>PDBTitle:</b> solution structure of hypothetical protein, hp1423
88	<a href="#">c6jzbD_</a>	Alignment	not modelled	28.4	33	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> moad/this family protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
89	<a href="#">c1ybyB_</a>	Alignment	not modelled	27.5	9	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation elongation factor p; <b>PDBTitle:</b> conserved hypothetical protein cth-95 from clostridium thermocellum
90	<a href="#">d2gy9d1</a>	Alignment	not modelled	27.4	20	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
91	<a href="#">d1p9ka_</a>	Alignment	not modelled	26.5	29	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> YbcJ-like
92	<a href="#">c2i52A_</a>	Alignment	not modelled	26.2	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> methanosarcina acetivorans samp1 homolog; <b>PDBTitle:</b> solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
93	<a href="#">d1fm0d_</a>	Alignment	not modelled	25.9	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
94	<a href="#">d1zud21</a>	Alignment	not modelled	25.1	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
95	<a href="#">c5mpoA_</a>	Alignment	not modelled	25.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin synthase sulfur carrier subunit; <b>PDBTitle:</b> crystal structure of human molybdopterin synthase complex
96	<a href="#">c2kmmA_</a>	Alignment	not modelled	24.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine-3',5'-bis(diphosphate) 3'- <b>PDBTitle:</b> solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
97	<a href="#">c1v8cA_</a>	Alignment	not modelled	24.6	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> moad related protein; <b>PDBTitle:</b> crystal structure of moad related protein from thermus2 thermophilus hb8
98	<a href="#">c6jc0A_</a>	Alignment	not modelled	24.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein d2 <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
99	<a href="#">c3a5zD_</a>	Alignment	not modelled	22.3	12	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> crystal structure of escherichia coli genx in complex with elongation2 factor p