
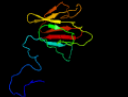


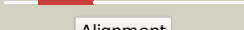

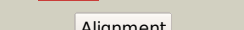

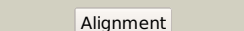
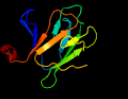
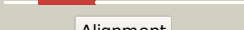

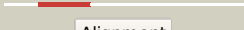





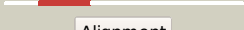

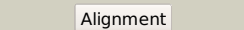

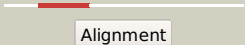

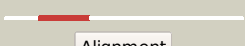
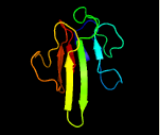
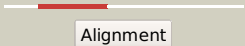
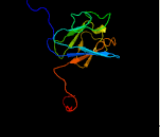
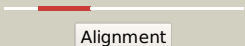





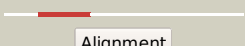

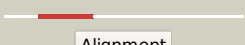
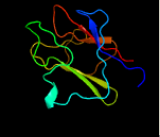
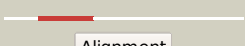

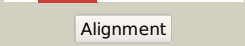
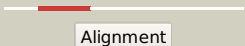
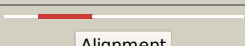

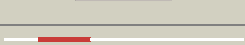
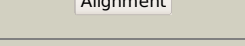
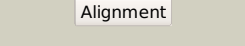
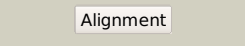
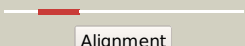


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3863_(-)_4339027_4340205
Date	Sat Aug 10 22:05:04 BST 2019
Unique Job ID	834f3550f089d9e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kkIA_</a>	 Alignment		99.9	15	<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).
2	<a href="#">c2kfuA_</a>	 Alignment		99.9	10	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> rv1827 pthr 22; <b>PDBTitle:</b> pknb-phosphorylated rv1827
3	<a href="#">c6ccdA_</a>	 Alignment		99.9	28	<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
4	<a href="#">c2n84A_</a>	 Alignment		99.9	17	<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="#">c4jonA_</a>	 Alignment		99.8	19	<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)
6	<a href="#">c3vpyA_</a>	 Alignment		99.8	15	<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
7	<a href="#">c3poaA_</a>	 Alignment		99.8	20	<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
8	<a href="#">c4h87A_</a>	 Alignment		99.8	18	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> kanadapтин; <b>PDBTitle:</b> crystal structure of a fha domain of kanadapтин (slc4a1ap) from homo2 sapiens at 1.55 a resolution
9	<a href="#">c3ounA_</a>	 Alignment		99.8	20	<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
10	<a href="#">c3hx1B_</a>	 Alignment		99.8	17	<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
11	<a href="#">c3uotB_</a>	 Alignment		99.8	18	<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

12	<a href="#">c6cahA_</a>	 Alignment		99.8	21	<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
13	<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
14	<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
15	<a href="#">d2ff4a3</a>	 Alignment		99.8	19	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
16	<a href="#">c2jkdB_</a>	 Alignment		99.8	13	<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
17	<a href="#">c3elsA_</a>	 Alignment		99.8	13	<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 pm1p, residues 51-204
18	<a href="#">c3kt9A_</a>	 Alignment		99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin; <b>PDBTitle:</b> aprataxin fha domain
19	<a href="#">c5yyxA_</a>	 Alignment		99.8	15	<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="#">d2piea1</a>	 Alignment		99.8	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
21	<a href="#">d1dmza_</a>	 Alignment	not modelled	99.8	16	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
22	<a href="#">d2affa1</a>	 Alignment	not modelled	99.8	12	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
23	<a href="#">c1r21A_</a>	 Alignment	not modelled	99.8	11	<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
24	<a href="#">c5a8iA_</a>	 Alignment	not modelled	99.8	18	<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 sulfolobus2 acidocaldarius
25	<a href="#">c4a0eB_</a>	 Alignment	not modelled	99.7	15	<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
26	<a href="#">c2jpeA_</a>	 Alignment	not modelled	99.7	19	<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="#">c5e50A_</a>	 Alignment	not modelled	99.7	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> aplf/xrcc4 complex
28	<a href="#">c6ar2B_</a>	 Alignment	not modelled	99.7	21	<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
		 Alignment				<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 5' polynucleotide kinase-3' phosphatase

29	<a href="#">c1yj5C_</a>	Alignment	not modelled	99.7	18	fha domain; <b>PDBTitle:</b> molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
30	<a href="#">d1uhta_</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
31	<a href="#">c5t2sA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> cell cycle <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.
32	<a href="#">d1g3ga_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
33	<a href="#">d1yjma1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
34	<a href="#">d1qu5a_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
35	<a href="#">c3fm8A_</a>	Alignment	not modelled	99.7	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)
36	<a href="#">c3gqsB_</a>	Alignment	not modelled	99.7	18	<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
37	<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
38	<a href="#">d1g6ga_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
39	<a href="#">c1gxcA_</a>	Alignment	not modelled	99.7	14	<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
40	<a href="#">d1gxca_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
41	<a href="#">d1ujxa_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
42	<a href="#">c6a8wA_</a>	Alignment	not modelled	99.7	22	<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
43	<a href="#">d2brfa1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
44	<a href="#">d1lqpa_</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
45	<a href="#">c5z58X_</a>	Alignment	not modelled	99.6	14	<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.
46	<a href="#">d1wlna1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
47	<a href="#">c5djoB_</a>	Alignment	not modelled	99.6	11	<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
48	<a href="#">c2eh0A_</a>	Alignment	not modelled	99.6	18	<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
49	<a href="#">c4eqxA_</a>	Alignment	not modelled	99.6	15	<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
50	<a href="#">d2g1la1</a>	Alignment	not modelled	99.6	15	<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	17	<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="#">c5xzvB_</a>	Alignment	not modelled	99.4	19	<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
53	<a href="#">c3i0mA_</a>	Alignment	not modelled	99.2	17	<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
54	<a href="#">c3i6uA_</a>	Alignment	not modelled	99.1	14	<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	98.9	16	<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

56	<a href="#">c4zgiA_</a>	Alignment	not modelled	98.0	14	<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
57	<a href="#">c5fwhA_</a>	Alignment	not modelled	97.2	10	<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
58	<a href="#">c3uv0B_</a>	Alignment	not modelled	96.9	18	<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
59	<a href="#">c3egbA_</a>	Alignment	not modelled	85.7	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein pellino homolog 2; <b>PDBTitle:</b> structure of pellino2 fha domain at 3.3 angstroms resolution.
60	<a href="#">c4xmmE_</a>	Alignment	not modelled	85.7	12	<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
61	<a href="#">c3hxrA_</a>	Alignment	not modelled	80.1	12	<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)
62	<a href="#">c3dwmA_</a>	Alignment	not modelled	70.9	14	<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
63	<a href="#">c2qjlA_</a>	Alignment	not modelled	70.2	14	<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
64	<a href="#">d1xo3a_</a>	Alignment	not modelled	69.6	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
65	<a href="#">d1dm9a_</a>	Alignment	not modelled	68.7	17	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
66	<a href="#">c1dm9A_</a>	Alignment	not modelled	68.7	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
67	<a href="#">c3hvxB_</a>	Alignment	not modelled	67.4	27	<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 cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
68	<a href="#">c2k9xA_</a>	Alignment	not modelled	65.7	14	<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
69	<a href="#">c3h7nD_</a>	Alignment	not modelled	65.5	12	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> nucleoporin nup120; <b>PDBTitle:</b> structure of nup120
70	<a href="#">d1c06a_</a>	Alignment	not modelled	65.1	24	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
71	<a href="#">d2uubd1</a>	Alignment	not modelled	64.9	28	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
72	<a href="#">d1wxqa2</a>	Alignment	not modelled	64.1	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
73	<a href="#">c5lo7B_</a>	Alignment	not modelled	62.3	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> fimbrial protein myfa,fimbrial protein myfa; <b>PDBTitle:</b> crystal structure of self-complemented myfa, the major subunit of myf2 fimbriae from yersinia enterocolitica
74	<a href="#">d1wgka_</a>	Alignment	not modelled	62.2	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> C9orf74 homolog
75	<a href="#">c1v8cA_</a>	Alignment	not modelled	61.7	17	<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
76	<a href="#">c4n6eB_</a>	Alignment	not modelled	60.7	19	<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
77	<a href="#">c2g1eA_</a>	Alignment	not modelled	59.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0895; <b>PDBTitle:</b> solution structure of ta0895
78	<a href="#">d1v8ca1</a>	Alignment	not modelled	59.7	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> Moad
79	<a href="#">c5o5jD_</a>	Alignment	not modelled	57.1	24	<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
80	<a href="#">d1vjka_</a>	Alignment	not modelled	56.9	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> Moad
81	<a href="#">c2kmmA_</a>	Alignment	not modelled	56.9	14	<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)

82	<a href="#">c3bbnD</a>	Alignment	not modelled	55.8	24	<b>PDB header:</b> ribosome <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="#">d2gy9d1</a>	Alignment	not modelled	55.4	24	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
84	<a href="#">c5nj3B</a>	Alignment	not modelled	54.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 2; <b>PDBTitle:</b> structure of an abc transporter: complete structure
85	<a href="#">c2m19A</a>	Alignment	not modelled	52.6	14	<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
86	<a href="#">c3po0A</a>	Alignment	not modelled	50.8	5	<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
87	<a href="#">c5z81A</a>	Alignment	not modelled	48.9	17	<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
88	<a href="#">d1fm0d</a>	Alignment	not modelled	47.7	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/This <b>Family:</b> MoaD
89	<a href="#">c2i52A</a>	Alignment	not modelled	46.9	14	<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
90	<a href="#">c6jzbD</a>	Alignment	not modelled	46.4	19	<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
91	<a href="#">d1zud21</a>	Alignment	not modelled	46.0	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/This <b>Family:</b> This
92	<a href="#">d1tkea1</a>	Alignment	not modelled	45.9	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
93	<a href="#">c3u7zA</a>	Alignment	not modelled	43.5	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal binding protein rumgna_00854; <b>PDBTitle:</b> crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
94	<a href="#">c5mpoA</a>	Alignment	not modelled	42.6	10	<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
95	<a href="#">d1tygb</a>	Alignment	not modelled	40.3	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/This <b>Family:</b> This
96	<a href="#">c2qieB</a>	Alignment	not modelled	39.8	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin synthase small subunit; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
97	<a href="#">c6jc0A</a>	Alignment	not modelled	39.1	0	<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
98	<a href="#">d1jh3a</a>	Alignment	not modelled	39.0	27	<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
99	<a href="#">d1vioa2</a>	Alignment	not modelled	38.3	26	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsuA N-terminal domain
100	<a href="#">c2ki0A</a>	Alignment	not modelled	38.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiamine biosynthesis this; <b>PDBTitle:</b> solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
101	<a href="#">d1p9ka</a>	Alignment	not modelled	38.1	11	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ybcj-like
102	<a href="#">d2cu3a1</a>	Alignment	not modelled	37.3	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/This <b>Family:</b> This
103	<a href="#">c3cwiA</a>	Alignment	not modelled	36.2	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-biosynthesis protein this; <b>PDBTitle:</b> crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
104	<a href="#">c5dudA</a>	Alignment	not modelled	35.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ybgk; <b>PDBTitle:</b> crystal structure of e. coli ybgk
105	<a href="#">c5xjyA</a>	Alignment	not modelled	34.9	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family a member 1; <b>PDBTitle:</b> cryo-em structure of human abca1
106	<a href="#">c2ekiA</a>	Alignment	not modelled	34.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> developmentally-regulated gtp-binding protein 1;

						<b>PDBTitle:</b> solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
107	<a href="#">c5do7B_</a>	Alignment	not modelled	33.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 8; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
108	<a href="#">d1udxa3</a>	Alignment	not modelled	33.7	25	<b>Fold:</b> Obg GTP-binding protein C-terminal domain <b>Superfamily:</b> Obg GTP-binding protein C-terminal domain <b>Family:</b> Obg GTP-binding protein C-terminal domain
109	<a href="#">d1h3fa2</a>	Alignment	not modelled	33.0	23	<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
110	<a href="#">c2k6pA_</a>	Alignment	not modelled	32.7	15	<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
111	<a href="#">c5do7A_</a>	Alignment	not modelled	28.5	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 5; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
112	<a href="#">c4i86A_</a>	Alignment	not modelled	27.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose synthase 1; <b>PDBTitle:</b> crystal structure of pilz domain of cesa from cellulose synthesizing2 bacterium
113	<a href="#">c1tygG_</a>	Alignment	not modelled	27.0	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> yjbs; <b>PDBTitle:</b> structure of the thiazole synthase/this complex
114	<a href="#">d2ia9a1</a>	Alignment	not modelled	26.3	19	<b>Fold:</b> SpoVG-like <b>Superfamily:</b> SpoVG-like <b>Family:</b> SpoVG-like
115	<a href="#">c3oepA_</a>	Alignment	not modelled	25.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha0988; <b>PDBTitle:</b> crystal structure of ttha0988 in space group p43212
116	<a href="#">c4pu4C_</a>	Alignment	not modelled	24.8	17	<b>PDB header:</b> toxin/antitoxin/dna <b>Chain:</b> C: <b>PDB Molecule:</b> toxin-antitoxin system antidote transcriptional repressor <b>PDBTitle:</b> shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
117	<a href="#">d2oq0a1</a>	Alignment	not modelled	24.3	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> HIN-2000 domain-like <b>Family:</b> HIN-200/F120x domain
118	<a href="#">d2i9xa1</a>	Alignment	not modelled	24.1	24	<b>Fold:</b> SpoVG-like <b>Superfamily:</b> SpoVG-like <b>Family:</b> SpoVG-like
119	<a href="#">c2i9zB_</a>	Alignment	not modelled	24.1	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative septation protein spovg; <b>PDBTitle:</b> structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
120	<a href="#">c1uebB_</a>	Alignment	not modelled	23.2	9	<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