

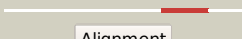
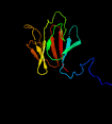
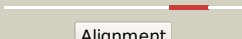

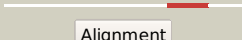

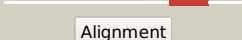



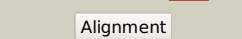

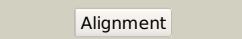

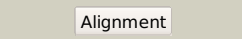
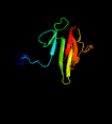
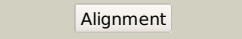

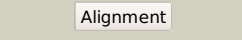




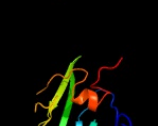

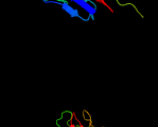
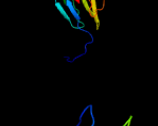

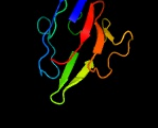


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0020c\_TB39.8\_23861\_25444  
 Date Tue Jul 23 14:50:04 BST 2019  
 Unique Job ID d7fb6a00fe3492bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lc0A_</a>	 Alignment		100.0	100	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tb39.8; <b>PDBTitle:</b> rv0020c_nter structure
2	<a href="#">c2kklA_</a>	 Alignment		99.8	28	<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="#">c2n84A_</a>	 Alignment		99.8	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
4	<a href="#">c2kfuA_</a>	 Alignment		99.8	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rv1827 pthr 22; <b>PDBTitle:</b> pknb-phosphorylated rv1827
5	<a href="#">c3poaA_</a>	 Alignment		99.8	100	<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
6	<a href="#">c3ouaA_</a>	 Alignment		99.8	100	<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
7	<a href="#">c4jonA_</a>	 Alignment		99.8	27	<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="#">c6ccdA_</a>	 Alignment		99.8	23	<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
9	<a href="#">c6cahA_</a>	 Alignment		99.8	29	<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
10	<a href="#">c2ff4B_</a>	 Alignment		99.7	33	<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
11	<a href="#">c3vpyA_</a>	 Alignment		99.7	24	<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

12	<a href="#">c3uotB</a>	Alignment		99.7	26	<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
13	<a href="#">d2ff4a3</a>	Alignment		99.7	33	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
14	<a href="#">c4h87A</a>	Alignment		99.7	27	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kanadaptn; <b>PDBTitle:</b> crystal structure of a fha domain of kanadaptn (sic4a1ap) from homo2 sapiens at 1.55 a resolution
15	<a href="#">c2jkdB</a>	Alignment		99.7	34	<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
16	<a href="#">c3hx1B</a>	Alignment		99.7	31	<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
17	<a href="#">d1uhta</a>	Alignment		99.7	34	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
18	<a href="#">d1mzka</a>	Alignment		99.7	30	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
19	<a href="#">c2jqlA</a>	Alignment		99.7	21	<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
20	<a href="#">c5a8iA</a>	Alignment		99.7	31	<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
21	<a href="#">d2affa1</a>	Alignment	not modelled	99.7	28	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
22	<a href="#">c3elsA</a>	Alignment	not modelled	99.7	30	<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 pm11p, residues 51-204
23	<a href="#">c1r21A</a>	Alignment	not modelled	99.7	27	<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="#">c5e50A</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> aplf/xrcc4 complex
25	<a href="#">c3fm8A</a>	Alignment	not modelled	99.6	20	<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)
26	<a href="#">d2piea1</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
27	<a href="#">c3gqsB</a>	Alignment	not modelled	99.6	28	<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="#">c2jpeA</a>	Alignment	not modelled	99.6	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
29	<a href="#">c6ar2B</a>	Alignment	not modelled	99.6	23	<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
30	<a href="#">c5yyxA</a>	Alignment	not modelled	99.6	22	<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
31	<a href="#">c4a0eB</a>	Alignment	not modelled	99.6	21	<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
32	<a href="#">c3kt9A</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin; <b>PDBTitle:</b> aprataxin fha domain
33	<a href="#">d1g6ga</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
34	<a href="#">d1yjma1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
35	<a href="#">d1gxca</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
36	<a href="#">c1gxcA</a>	Alignment	not modelled	99.6	18	<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
37	<a href="#">d1g3ga</a>	Alignment	not modelled	99.6	27	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
38	<a href="#">d1dmza</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
39	<a href="#">c5djoB</a>	Alignment	not modelled	99.5	19	<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
40	<a href="#">c2eh0A</a>	Alignment	not modelled	99.5	24	<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
41	<a href="#">d1wlna1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
42	<a href="#">c5t2sA</a>	Alignment	not modelled	99.5	28	<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.
43	<a href="#">d1lqpa</a>	Alignment	not modelled	99.5	29	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
44	<a href="#">d2g1la1</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
45	<a href="#">c4eqxA</a>	Alignment	not modelled	99.5	23	<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
46	<a href="#">d1ujxa</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
47	<a href="#">c6a8wA</a>	Alignment	not modelled	99.5	27	<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
48	<a href="#">c1vj5C</a>	Alignment	not modelled	99.5	20	<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
49	<a href="#">c5z58X</a>	Alignment	not modelled	99.5	21	<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="#">d1qu5a</a>	Alignment	not modelled	99.4	28	<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	24	<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="#">d2brfa1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
53	<a href="#">c5xzvB</a>	Alignment	not modelled	99.0	28	<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-ppn
54	<a href="#">c3i0mA</a>	Alignment	not modelled	99.0	24	<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
55	<a href="#">c3i6uA</a>	Alignment	not modelled	98.7	21	<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 <b>PDB header:</b> transferase

56	<a href="#">c3i6wB_</a>	Alignment	not modelled	98.4	24	<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
57	<a href="#">c3egbA_</a>	Alignment	not modelled	95.0	41	<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.
58	<a href="#">c5fwhA_</a>	Alignment	not modelled	94.6	14	<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
59	<a href="#">c5b0oG_</a>	Alignment	not modelled	94.4	17	<b>PDB header:</b> hydrolase/motor protein <b>Chain:</b> G: <b>PDB Molecule:</b> flagellar assembly protein flih; <b>PDBTitle:</b> structure of the flih-flii complex
60	<a href="#">c4zgiA_</a>	Alignment	not modelled	94.1	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
61	<a href="#">c5b0oH_</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> hydrolase/motor protein <b>Chain:</b> H: <b>PDB Molecule:</b> flagellar assembly protein flih; <b>PDBTitle:</b> structure of the flih-flii complex
62	<a href="#">c3uv0B_</a>	Alignment	not modelled	91.6	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
63	<a href="#">c1vraB_</a>	Alignment	not modelled	76.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine biosynthesis bifunctional protein argj; <b>PDBTitle:</b> crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
64	<a href="#">c2vzkD_</a>	Alignment	not modelled	74.5	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamate n-acetyltransferase 2 beta chain; <b>PDBTitle:</b> structure of the acyl-enzyme complex of an n-terminal nucleophile2 (ntn) hydrolase, oat2
65	<a href="#">c6avhA_</a>	Alignment	not modelled	70.6	10	<b>PDB header:</b> ligase, plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> gh3.15 acyl acid amido synthetase; <b>PDBTitle:</b> gh3.15 acyl acid amido synthetase
66	<a href="#">c5kodA_</a>	Alignment	not modelled	68.5	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-acetic acid-amido synthetase gh3.5; <b>PDBTitle:</b> crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
67	<a href="#">c2y27B_</a>	Alignment	not modelled	68.4	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
68	<a href="#">d1vz6a_</a>	Alignment	not modelled	67.0	16	<b>Fold:</b> DmpA/Argj-like <b>Superfamily:</b> DmpA/Argj-like <b>Family:</b> Argj-like
69	<a href="#">d1dm9a_</a>	Alignment	not modelled	67.0	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
70	<a href="#">c1dm9A_</a>	Alignment	not modelled	67.0	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
71	<a href="#">c3oepA_</a>	Alignment	not modelled	63.9	10	<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
72	<a href="#">c5dudA_</a>	Alignment	not modelled	63.7	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ybgk; <b>PDBTitle:</b> crystal structure of e. coli ybgk
73	<a href="#">c2y4oA_</a>	Alignment	not modelled	63.6	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak2 in complex with phenylacetyl adenylate
74	<a href="#">c5z81A_</a>	Alignment	not modelled	58.0	24	<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
75	<a href="#">c3dwmA_</a>	Alignment	not modelled	56.6	33	<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
76	<a href="#">c3mmlE_</a>	Alignment	not modelled	55.3	26	<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
77	<a href="#">c2g1eA_</a>	Alignment	not modelled	53.4	29	<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="#">d1p9ka_</a>	Alignment	not modelled	52.9	15	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ybcj-like
79	<a href="#">c3f6tA_</a>	Alignment	not modelled	52.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
80	<a href="#">d1v8ca1</a>	Alignment	not modelled	52.4	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
81	<a href="#">c4n6aB</a>	Alignment	not modelled	52.0	25	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> this/moad family protein;

81	<a href="#">c4t0eB_</a>	Alignment	not modelled	52.0	33	<b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex
82	<a href="#">d1xo3a_</a>	Alignment	not modelled	49.8	33	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> C9orf74 homolog
83	<a href="#">c2k9xA_</a>	Alignment	not modelled	49.3	38	<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
84	<a href="#">d1wgka_</a>	Alignment	not modelled	48.3	33	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> C9orf74 homolog
85	<a href="#">c2zy4F_</a>	Alignment	not modelled	47.0	14	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
86	<a href="#">d1leara1</a>	Alignment	not modelled	45.9	22	<b>Fold:</b> Urease metallochaperone UreE, N-terminal domain <b>Superfamily:</b> Urease metallochaperone UreE, N-terminal domain <b>Family:</b> Urease metallochaperone UreE, N-terminal domain
87	<a href="#">c3hvvB_</a>	Alignment	not modelled	45.8	21	<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
88	<a href="#">c2m19A_</a>	Alignment	not modelled	45.7	29	<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
89	<a href="#">c1v8cA_</a>	Alignment	not modelled	44.7	24	<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
90	<a href="#">c3kxwA_</a>	Alignment	not modelled	44.7	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> saframycin mx1 synthetase b; <b>PDBTitle:</b> the crystal structure of fatty acid amp ligase from legionella2 pneumophila
91	<a href="#">c4nz3A_</a>	Alignment	not modelled	44.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deacetylase da1; <b>PDBTitle:</b> structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
92	<a href="#">d2o5aa1</a>	Alignment	not modelled	43.9	12	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> !ojap/YbeB-like
93	<a href="#">c2qjlA_</a>	Alignment	not modelled	43.2	33	<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
94	<a href="#">c3pfnB_</a>	Alignment	not modelled	43.1	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nad kinase; <b>PDBTitle:</b> crystal structure of human nad kinase
95	<a href="#">d1zud21</a>	Alignment	not modelled	43.1	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
96	<a href="#">d1vjka_</a>	Alignment	not modelled	43.1	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
97	<a href="#">c1eb0A_</a>	Alignment	not modelled	42.7	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> urease accessory protein uree; <b>PDBTitle:</b> crystal structure of bacillus pasteurii uree at 1.85 a, phased by2 siras. type i crystal form.
98	<a href="#">d2i0ka1</a>	Alignment	not modelled	41.7	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cholesterol oxidase
99	<a href="#">c3it4B_</a>	Alignment	not modelled	41.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine biosynthesis bifunctional protein argj <b>PDBTitle:</b> the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
100	<a href="#">c2p0aA_</a>	Alignment	not modelled	41.2	13	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> synapsin-3; <b>PDBTitle:</b> the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
101	<a href="#">c3po0A_</a>	Alignment	not modelled	41.1	25	<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
102	<a href="#">c5m3iB_</a>	Alignment	not modelled	41.0	14	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> rnase iii inhibitor; <b>PDBTitle:</b> macrodomain of mycobacterium tuberculosis darg
103	<a href="#">c6jc0A_</a>	Alignment	not modelled	40.7	8	<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
104	<a href="#">c2kmmA_</a>	Alignment	not modelled	40.2	32	<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)
105	<a href="#">c5lwxA_</a>	Alignment	not modelled	39.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> multicopper oxidase; <b>PDBTitle:</b> crystal structure of the h253d mutant of mcog from aspergillus niger
106	<a href="#">c6jzbD_</a>	Alignment	not modelled	39.5	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> moad/thi family protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens <b>PDB header:</b> glutathione biosynthesis ligase

107	<a href="#">c1gshA_</a>	Alignment	not modelled	39.5	7	<b>Chain:</b> A; <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
108	<a href="#">d2pbdp1</a>	Alignment	not modelled	39.4	18	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
109	<a href="#">c5mpoA_</a>	Alignment	not modelled	39.4	35	<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
110	<a href="#">c2l52A_</a>	Alignment	not modelled	38.5	29	<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
111	<a href="#">c2q9oA_</a>	Alignment	not modelled	38.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> laccase-1; <b>PDBTitle:</b> near-atomic resolution structure of a melanocarpus albomyces laccase
112	<a href="#">c2jg6A_</a>	Alignment	not modelled	38.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dna-3-methyladenine glycosidase; <b>PDBTitle:</b> crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
113	<a href="#">c6qyyD_</a>	Alignment	not modelled	37.6	22	<b>PDB header:</b> virus <b>Chain:</b> D; <b>PDB Molecule:</b> capsid fiber protein; <b>PDBTitle:</b> the crystal structure of head fiber gp8.5 n base in bacteriophage2 phi29
114	<a href="#">d1vmaa1</a>	Alignment	not modelled	37.6	22	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
115	<a href="#">c4wcbB_</a>	Alignment	not modelled	37.4	13	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal silencing factor rsfs; <b>PDBTitle:</b> ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis
116	<a href="#">c3rpfC_</a>	Alignment	not modelled	36.6	40	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> molybdopterin converting factor, subunit 1 (moad); <b>PDBTitle:</b> protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
117	<a href="#">d1c06a_</a>	Alignment	not modelled	36.3	19	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
118	<a href="#">c4hhuA_</a>	Alignment	not modelled	36.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> or280; <b>PDBTitle:</b> crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
119	<a href="#">c2ig3A_</a>	Alignment	not modelled	36.0	16	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> A; <b>PDB Molecule:</b> group iii truncated haemoglobin; <b>PDBTitle:</b> crystal structure of group iii truncated hemoglobin from campylobacter2 jejuni
120	<a href="#">c3eynB_</a>	Alignment	not modelled	36.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acyl-coenzyme a synthetase acsm2a; <b>PDBTitle:</b> crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa