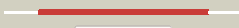




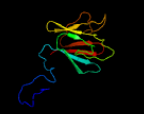


















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1267c_(embR)_1416187_1417353
Date	Wed Jul 31 22:05:36 BST 2019
Unique Job ID	63bd6fc05da5160d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ff4B_</a>	 Alignment		100.0	100	<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
2	<a href="#">d2ff4a2</a>	 Alignment		100.0	100	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> BTAD-like
3	<a href="#">c2kkIA_</a>	 Alignment		99.8	26	<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).
4	<a href="#">c2kfuA_</a>	 Alignment		99.8	25	<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="#">d2ff4a1</a>	 Alignment		99.7	100	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
6	<a href="#">c2n84A_</a>	 Alignment		99.7	21	<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
7	<a href="#">d2ff4a3</a>	 Alignment		99.7	100	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
8	<a href="#">d2affa1</a>	 Alignment		99.7	24	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
9	<a href="#">c6cahA_</a>	 Alignment		99.7	40	<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="#">c3uotB_</a>	 Alignment		99.7	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
11	<a href="#">c1r21A_</a>	 Alignment		99.7	25	<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

12	<a href="#">c4jonA_</a>	Alignment		99.7	29	<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)
13	<a href="#">c3vpyA_</a>	Alignment		99.6	20	<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
14	<a href="#">c3poaA_</a>	Alignment		99.6	34	<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
15	<a href="#">c3ounA_</a>	Alignment		99.6	34	<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
16	<a href="#">c6ccdA_</a>	Alignment		99.6	22	<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
17	<a href="#">d1mzka_</a>	Alignment		99.6	25	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
18	<a href="#">c4h87A_</a>	Alignment		99.6	22	<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 (slc4a1ap) from homo2 sapiens at 1.55 a resolution
19	<a href="#">c3hx1B_</a>	Alignment		99.6	26	<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
20	<a href="#">c4a0eB_</a>	Alignment		99.6	16	<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
21	<a href="#">c5a8iA_</a>	Alignment	not modelled	99.6	21	<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 sulfobolus2 acidocaldarius
22	<a href="#">c3qqsB_</a>	Alignment	not modelled	99.6	29	<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
23	<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)
24	<a href="#">d1uhta_</a>	Alignment	not modelled	99.6	29	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
25	<a href="#">c2jqIA_</a>	Alignment	not modelled	99.5	22	<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
26	<a href="#">c2jpeA_</a>	Alignment	not modelled	99.5	15	<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="#">c2jkdB_</a>	Alignment	not modelled	99.5	28	<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 pml1 splicing factor and its2 integration into the res complex
28	<a href="#">d2piea1</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain

29	<a href="#">c3elsA_</a>	Alignment	not modelled	99.5	28	<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
30	<a href="#">c5yyxA_</a>	Alignment	not modelled	99.5	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
31	<a href="#">c6ar2B_</a>	Alignment	not modelled	99.5	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
32	<a href="#">c5e50A_</a>	Alignment	not modelled	99.5	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> aplf/xrcc4 complex
33	<a href="#">d1wlna1</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
34	<a href="#">c5t2sA_</a>	Alignment	not modelled	99.4	20	<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.
35	<a href="#">c5djoB_</a>	Alignment	not modelled	99.4	17	<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
36	<a href="#">c3kt9A_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin; <b>PDBTitle:</b> aprataxin fha domain
37	<a href="#">c6a8wA_</a>	Alignment	not modelled	99.4	34	<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
38	<a href="#">d1yjma1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
39	<a href="#">d1ujxa_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
40	<a href="#">d1g6ga_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
41	<a href="#">d1g3ga_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
42	<a href="#">d1dmza_</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
43	<a href="#">c1vj5C_</a>	Alignment	not modelled	99.4	13	<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="#">d1lqpa_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
45	<a href="#">c2eh0A_</a>	Alignment	not modelled	99.3	25	<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
46	<a href="#">c4eqxA_</a>	Alignment	not modelled	99.3	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
47	<a href="#">d2q1la1</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
48	<a href="#">d1gxca_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
49	<a href="#">c1qxA_</a>	Alignment	not modelled	99.3	17	<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
50	<a href="#">d2brfa1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
51	<a href="#">c5z58X_</a>	Alignment	not modelled	99.2	25	<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.
52	<a href="#">d1qu5a_</a>	Alignment	not modelled	99.2	24	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
53	<a href="#">c4ejqB_</a>	Alignment	not modelled	99.2	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
54	<a href="#">c5ju7A_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator cadc; <b>PDBTitle:</b> dna binding domain of e.coli cadc
						<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> kdp operon transcriptional regulatory

55	<a href="#">c3zq7A_</a>	Alignment	not modelled	98.9	21	protein kdpe; <b>PDBTitle:</b> the structure of dna-binding domain of response regulator from2 escherichia coli k-12
56	<a href="#">c2hvvA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator vicr; <b>PDBTitle:</b> crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
57	<a href="#">c4ixaA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator saer; <b>PDBTitle:</b> structure of dna-binding domain of the response regulator saer from2 staphylococcus epidermidis
58	<a href="#">c2pmuD_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> transcription regulation <b>Chain:</b> D: <b>PDB Molecule:</b> response regulator phop; <b>PDBTitle:</b> crystal structure of the dna-binding domain of phop
59	<a href="#">c2hqnA_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
60	<a href="#">c5dcmB_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> phob family transcriptional regulator; <b>PDBTitle:</b> structure of a lantibiotic response regulator: c-terminal domain of2 the nisin resistance regulator nsrr
61	<a href="#">c4uhtA_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cpxr; <b>PDBTitle:</b> crystal structure of the dna binding domain of cpxr from e. coli
62	<a href="#">c2k4jA_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> arsr dna binding domain
63	<a href="#">c2zxbB_</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein walr; <b>PDBTitle:</b> crystal structure of yycf dna-binding domain from staphylococcus2 aureus
64	<a href="#">d1opca_</a>	Alignment	not modelled	98.8	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
65	<a href="#">d1ys7a1</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
66	<a href="#">d1p2fa1</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
67	<a href="#">c2jzyA_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein pcor; <b>PDBTitle:</b> solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
68	<a href="#">d1gxqa_</a>	Alignment	not modelled	98.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
69	<a href="#">c2rv8A_</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
70	<a href="#">c3i0mA_</a>	Alignment	not modelled	98.7	23	<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
71	<a href="#">c3q9vB_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
72	<a href="#">c3rjpA_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> covr; <b>PDBTitle:</b> crystal structure of the dna binding domain of covr from streptococcus2 pyogenes
73	<a href="#">c2m87A_</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein basr/pmra; <b>PDBTitle:</b> structural basis of dna recognition by the effector domain of2 klebsiella pneumoniae pmra
74	<a href="#">c2m1bA_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein, c terminal family <b>PDBTitle:</b> solution structure of the chxr dna-binding domain
75	<a href="#">c5xzvB_</a>	Alignment	not modelled	98.6	27	<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
76	<a href="#">d1kgsa1</a>	Alignment	not modelled	98.5	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
77	<a href="#">c2nazA_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein rsta; <b>PDBTitle:</b> the solution nmr structure of the c-terminal effector domain of bfmr2 from acinetobacter baumannii
78	<a href="#">c4kfcB_</a>	Alignment	not modelled	98.5	23	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> B: <b>PDB Molecule:</b> kdp operon transcriptional regulatory protein kdpe; <b>PDBTitle:</b> crystal structure of a hyperactive mutant of response regulator kdpe2 complexed to its promoter dna
79	<a href="#">c2oqrA_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> transcription,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory transduction protein regx3; <b>PDBTitle:</b> the structure of the response regulator regx3 from mycobacterium2 tuberculosis

80	<a href="#">c5x5IM</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> M: <b>PDB Molecule:</b> ader; <b>PDBTitle:</b> crystal structure of response regulator ader dna binding domain in2 complex with an intercistronic region
81	<a href="#">c1ys7B</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed2 with mg2+
82	<a href="#">c2hqrA</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
83	<a href="#">c4i2wA</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> chaperone/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein unc-45; <b>PDBTitle:</b> crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
84	<a href="#">c2gwrA</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator mtra; <b>PDBTitle:</b> crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
85	<a href="#">c5djsA</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide tpr_2 repeat protein; <b>PDBTitle:</b> thermobaculum terrenum o-glcnaC transferase mutant -k341m
86	<a href="#">d2hr2a1</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> CT2138-like
87	<a href="#">c5ompA</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp5; <b>PDBTitle:</b> human fkbp5 protein
88	<a href="#">c1kt0A</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 51 kda fk506-binding protein; <b>PDBTitle:</b> structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
89	<a href="#">c2if4A</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> atfkbp42; <b>PDBTitle:</b> crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
90	<a href="#">c5u8mA</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
91	<a href="#">c3i6uA</a>	Alignment	not modelled	97.9	22	<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
92	<a href="#">c4aifA</a>	Alignment	not modelled	97.9	8	<b>PDB header:</b> signaling protein/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> ah receptor-interacting protein; <b>PDBTitle:</b> aip tpr domain in complex with human hsp90 peptide
93	<a href="#">c3pe3D</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcnaC transferase and its complex with a peptide2 substrate
94	<a href="#">c4s05B</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding transcriptional regulator basr; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
95	<a href="#">c4b09F</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein baer; <b>PDBTitle:</b> structure of unphosphorylated baer dimer
96	<a href="#">c1qz2B</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> isomerase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> fk506-binding protein 4; <b>PDBTitle:</b> crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
97	<a href="#">c1p2fA</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
98	<a href="#">c1ihgA</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclophilin 40; <b>PDBTitle:</b> bovine cyclophilin 40, monoclinic form
99	<a href="#">c5dseC</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> tetratricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
100	<a href="#">c2c2ID</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> carboxy terminus of hsp70-interacting protein; <b>PDBTitle:</b> crystal structure of the chip u-box e3 ubiquitin ligase
101	<a href="#">c3r0jA</a>	Alignment	not modelled	97.6	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> possible two component system response transcriptional <b>PDBTitle:</b> structure of phop from mycobacterium tuberculosis
102	<a href="#">c3rkvA</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidylprolyl isomerase; <b>PDBTitle:</b> c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans
103	<a href="#">c1wao4</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> serine/threonine protein phosphatase 5; <b>PDBTitle:</b> pp5 structure
104	<a href="#">c2y4tA</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 3; <b>PDBTitle:</b> crystal structure of the human co-chaperone p58(ipk)
105	<a href="#">c6hftA</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hsp70/hsp90 co-chaperone cns1; <b>PDBTitle:</b> hsp90 co-chaperone cns1 from saccharomyces cerevisiae (delta69)



106	<a href="#">c5dseA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tetratricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
107	<a href="#">c6n3qF_</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> translocation protein sec72; <b>PDBTitle:</b> cryo-em structure of the yeast sec complex
108	<a href="#">c3i6wB_</a>	Alignment	not modelled	97.5	22	<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
109	<a href="#">c4j8dC_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> middle domain of hsc70-interacting protein, crystal form ii
110	<a href="#">c2xpiA_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> anaphase-promoting complex subunit cut9; <b>PDBTitle:</b> crystal structure of apc/c hetero-tetramer cut9-hcn1
111	<a href="#">c5jitA_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein phosphatase 5; <b>PDBTitle:</b> crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
112	<a href="#">c2vsnB_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of f3 intracellular glycosylation
113	<a href="#">c5mgxG_</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase fkbp8; <b>PDBTitle:</b> the structure of fkbp38 in complex with the meevd tetratricopeptide2 binding-motif of hsp90
114	<a href="#">c5wftA_</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> pelb; <b>PDBTitle:</b> pelb 319-436 from pseudomonas aeruginosa pao1
115	<a href="#">c5fzqB_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> designed tpr protein; <b>PDBTitle:</b> designed tpr protein m4n
116	<a href="#">c2dbaA_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> smooth muscle cell associated protein-1, isoform <b>PDBTitle:</b> the solution structure of the tetratricopeptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
117	<a href="#">d1hxia_</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
118	<a href="#">c2xcba_</a>	Alignment	not modelled	97.3	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein pcrh; <b>PDBTitle:</b> crystal structure of pcrh in complex with the chaperone2 binding region of popd
119	<a href="#">c5nnrD_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n-terminal acetyltransferase-like protein; <b>PDBTitle:</b> structure of naa15/naa10 bound to hypk-thb
120	<a href="#">c2gw1A_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial precursor proteins import receptor; <b>PDBTitle:</b> crystal structure of the yeast tom70