



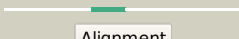
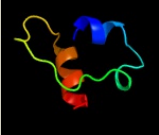



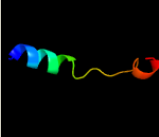







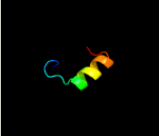





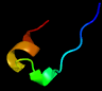




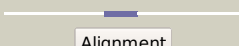
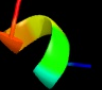
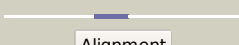

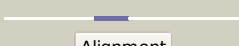








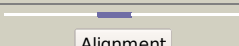




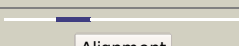



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2414c (-) _2711342_2712886
Date	Wed Aug 7 12:50:03 BST 2019
Unique Job ID	4b11f80663932d75

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1g3a2</a>	 Alignment		57.4	18	<b>Fold:</b> Thiamin pyrophosphokinase, catalytic domain <b>Superfamily:</b> Thiamin pyrophosphokinase, catalytic domain <b>Family:</b> Thiamin pyrophosphokinase, catalytic domain
2	<a href="#">c2hh9A</a>	 Alignment		54.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> thiamin pyrophosphokinase from candida albicans
3	<a href="#">c2f17A</a>	 Alignment		45.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase 1; <b>PDBTitle:</b> mouse thiamin pyrophosphokinase in a ternary complex with2 pyrithiamin pyrophosphate and amp at 2.5 angstrom
4	<a href="#">c3t98A</a>	 Alignment		20.1	36	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
5	<a href="#">c3t98C</a>	 Alignment		19.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
6	<a href="#">c1g0A</a>	 Alignment		18.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of yeast thiamin pyrophosphokinase
7	<a href="#">c3lm8D</a>	 Alignment		18.0	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thiamine pyrophosphokinase; <b>PDBTitle:</b> crystal structure of thiamine pyrophosphokinase from bacillus2 subtilis, northeast structural genomics consortium target sr677
8	<a href="#">c3cq9C</a>	 Alignment		17.4	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein lp_1622; <b>PDBTitle:</b> crystal structure of the lp_1622 protein from lactobacillus plantarum.2 northeast structural genomics consortium target lpr114
9	<a href="#">c2k42A</a>	 Alignment		17.4	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein; <b>PDBTitle:</b> solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
10	<a href="#">d1gwua</a>	 Alignment		16.9	36	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
11	<a href="#">d1rp4a</a>	 Alignment		15.6	50	<b>Fold:</b> ERO1-like <b>Superfamily:</b> ERO1-like <b>Family:</b> ERO1-like

12	<a href="#">c2vzaD_</a>			15.5	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> cell filamentation protein; <b>PDBTitle:</b> type iv secretion system effector protein bepa
13	<a href="#">c2lnhA_</a>			15.3	20	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> neural wiskott-aldrich syndrome protein; <b>PDBTitle:</b> enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
14	<a href="#">c3k94A_</a>			14.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase from geobacillus2 thermodenitrificans, northeast structural genomics consortium target3 gtr2
15	<a href="#">c3ahrA_</a>			14.7	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ero1-like protein alpha; <b>PDBTitle:</b> inactive human ero1
16	<a href="#">c3ihkC_</a>			14.2	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thiamin pyrophosphokinase; <b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase from s.mutans,2 northeast structural genomics consortium target smr83
17	<a href="#">c3melC_</a>			14.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> thiamin pyrophosphokinase family protein; <b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
18	<a href="#">c1ceeB_</a>			13.9	25	<b>PDB header:</b> structural protein regulation <b>Chain:</b> B: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein wasp; <b>PDBTitle:</b> solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
19	<a href="#">c3e0eA_</a>			13.4	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a; <b>PDBTitle:</b> crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
20	<a href="#">d1ig0a2</a>			13.3	21	<b>Fold:</b> Thiamin pyrophosphokinase, catalytic domain <b>Superfamily:</b> Thiamin pyrophosphokinase, catalytic domain <b>Family:</b> Thiamin pyrophosphokinase, catalytic domain
21	<a href="#">d1b80a_</a>		not modelled	11.7	14	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
22	<a href="#">c2kngA_</a>		not modelled	11.5	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> solution structure of c-domain of lsr2
23	<a href="#">c5dniB_</a>		not modelled	10.1	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l(+)-tartrate dehydratase subunit beta; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii fumarate hydratase2 beta subunit
24	<a href="#">c2d0jD_</a>		not modelled	10.0	40	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> galactosylgalactosylxylosylprotein 3-beta- <b>PDBTitle:</b> crystal structure of human glcat-s apo form
25	<a href="#">c3l8mA_</a>		not modelled	9.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiamine pyrophosphokinase; <b>PDBTitle:</b> crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86
26	<a href="#">c1e0aB_</a>		not modelled	9.6	14	<b>PDB header:</b> signalling protein/kinase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak-alpha; <b>PDBTitle:</b> cdc42 complexed with the gtpase binding domain of p212 activated kinase
27	<a href="#">d1lta_</a>		not modelled	9.4	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA replication initiator (cdc21/cdc54) N-terminal domain
28	<a href="#">c1f3mB_</a>		not modelled	9.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak-alpha;

						<b>PDBTitle:</b> crystal structure of human serine/threonine kinase pak1
29	<a href="#">d1scha_</a>	Alignment	not modelled	8.7	27	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
30	<a href="#">c6apxA_</a>	Alignment	not modelled	8.6	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> maltose-binding periplasmic protein,dual specificity <b>PDBTitle:</b> crystal structure of human dual specificity phosphatase 1 catalytic2 domain (c258s) as a maltose binding protein fusion in complex with3 the monobody ysx1
31	<a href="#">c4gs3A_</a>	Alignment	not modelled	8.6	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> dimeric structure of the n-terminal domain of prib protein from2 thermoanaerobacter tencongensis solved ab initio
32	<a href="#">c3hdIA_</a>	Alignment	not modelled	8.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> royal palm tree peroxidase; <b>PDBTitle:</b> crystal structure of highly glycosylated peroxidase from royal palm2 tree
33	<a href="#">d1gawa1</a>	Alignment	not modelled	8.5	17	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
34	<a href="#">c6b3yA_</a>	Alignment	not modelled	8.5	25	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> dennn domain-containing protein 3; <b>PDBTitle:</b> crystal structure of the ph-like domain from denn3
35	<a href="#">c2v6C_</a>	Alignment	not modelled	8.3	4	<b>PDB header:</b> dna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> structural analysis of the sulfobolus solfataricus mcm2 protein n-terminal domain
36	<a href="#">c1ltIE_</a>	Alignment	not modelled	8.2	15	<b>PDB header:</b> replication <b>Chain:</b> E; <b>PDB Molecule:</b> dna replication initiator (cdc21/cdc54); <b>PDBTitle:</b> the dodecamer structure of mcm from archaean m.2 thermoautotrophicum
37	<a href="#">d2vnud1</a>	Alignment	not modelled	8.1	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
38	<a href="#">c4n9nA_</a>	Alignment	not modelled	8.1	29	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> sterol uptake control protein 2, lysozyme; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae upc2 transcription2 factor fused with t4 lysozyme
39	<a href="#">d2cvza1</a>	Alignment	not modelled	8.0	19	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
40	<a href="#">c5n9yB_</a>	Alignment	not modelled	7.9	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
41	<a href="#">d1ej5a_</a>	Alignment	not modelled	7.8	21	<b>Fold:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain <b>Superfamily:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain <b>Family:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
42	<a href="#">c2omkB_</a>	Alignment	not modelled	7.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
43	<a href="#">c4pogC_</a>	Alignment	not modelled	7.7	9	<b>PDB header:</b> replication, dna binding protein/dna <b>Chain:</b> C; <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> mcm-ssdna co-crystal structure
44	<a href="#">d1ijwc_</a>	Alignment	not modelled	7.7	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
45	<a href="#">d1r7ma1</a>	Alignment	not modelled	7.5	33	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Group I mobile intron endonuclease
46	<a href="#">d1ub2a1</a>	Alignment	not modelled	7.3	14	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
47	<a href="#">d3cuma1</a>	Alignment	not modelled	7.0	19	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
48	<a href="#">c4g0dX_</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> X; <b>PDB Molecule:</b> collagenase 3, pro-domain peptide; <b>PDBTitle:</b> human collagenase 3 (mmp-13) full form with peptides from pro-domain
49	<a href="#">c4fu4D_</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> collagenase 3, pro-domain peptide; <b>PDBTitle:</b> human collagenase 3 (mmp-13) with peptide from pro-domain
50	<a href="#">c6msoD_</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> D; <b>PDB Molecule:</b> fumarate hydratase; <b>PDBTitle:</b> crystal structure of mitochondrial fumarate hydratase from leishmania2 major in a complex with inhibitor thiomalate
51	<a href="#">d1lvaa3</a>	Alignment	not modelled	6.9	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
52	<a href="#">c5d7tC_</a>	Alignment	not modelled	6.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> ss-component for folate; <b>PDBTitle:</b> folate ecf transporter: apo state
53	<a href="#">d1hcra_</a>	Alignment	not modelled	6.8	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain

54	<a href="#">c5gqoB</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis
55	<a href="#">c2l6wA</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-type platelet-derived growth factor receptor; <b>PDBTitle:</b> pdgfr beta-tm
56	<a href="#">c2l6wB</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> beta-type platelet-derived growth factor receptor; <b>PDBTitle:</b> pdgfr beta-tm
57	<a href="#">d1vpda1</a>	Alignment	not modelled	6.6	22	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
58	<a href="#">c4me3A</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication licensing factor mcm related protein; <b>PDBTitle:</b> 1.8 angstrom crystal structure of the n-terminal domain of an archaeal2 mcm
59	<a href="#">c3fdFA</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fr253; <b>PDBTitle:</b> crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
60	<a href="#">d1fnda1</a>	Alignment	not modelled	6.4	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
61	<a href="#">c3o2qB</a>	Alignment	not modelled	6.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase ii subunit a c-terminal domain phosphatase <b>PDBTitle:</b> crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
62	<a href="#">c5l2rA</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate hydratase; <b>PDBTitle:</b> crystal structure of fumarate hydratase from leishmania major
63	<a href="#">d2a1xa1</a>	Alignment	not modelled	6.3	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminic synthase-like <b>Family:</b> PhyH-like
64	<a href="#">c2hcnA</a>	Alignment	not modelled	6.3	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rna-directed rna polymerase (ns5); <b>PDBTitle:</b> crystal structure of rna dependent rna polymerase domain from west2 nile virus
65	<a href="#">c3riwA</a>	Alignment	not modelled	6.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ascorbate peroxidase; <b>PDBTitle:</b> the crystal structure of leishmania major peroxidase mutant c197t
66	<a href="#">d2ccaa1</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
67	<a href="#">c5ccvH</a>	Alignment	not modelled	6.2	43	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> rna-directed rna polymerase ns5; <b>PDBTitle:</b> crystal structure of full-length ns5 from dengue virus type 3
68	<a href="#">c5z7cA</a>	Alignment	not modelled	6.1	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 3'3'-cgamp-specific phosphodiesterase 3; <b>PDBTitle:</b> crystal structure of cyclic gmp-amp specific phosphodiesterases in2 v.cholerae (v-cgap3)
69	<a href="#">c4xbzB</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> evdo1; <b>PDBTitle:</b> crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca
70	<a href="#">c6f34C</a>	Alignment	not modelled	6.0	5	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> mgts; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
71	<a href="#">c5oqtC</a>	Alignment	not modelled	6.0	5	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein ynem; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
72	<a href="#">d1pa2a</a>	Alignment	not modelled	5.9	41	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
73	<a href="#">d1mwva1</a>	Alignment	not modelled	5.9	14	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
74	<a href="#">c4ogqE</a>	Alignment	not modelled	5.8	23	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
75	<a href="#">c4h44E</a>	Alignment	not modelled	5.8	23	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
76	<a href="#">c2zt9E</a>	Alignment	not modelled	5.8	23	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
77	<a href="#">c1kqfB</a>	Alignment	not modelled	5.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur <b>PDBTitle:</b> formate dehydrogenase n from e. coli
78	<a href="#">d2ji7a2</a>	Alignment	not modelled	5.7	9	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module

79	<a href="#">d1bg1a2</a>	Alignment	not modelled	5.7	20	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> p53-like transcription factors <b>Family:</b> STAT DNA-binding domain
80	<a href="#">c2latA</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> solution structure of a human minimembrane protein ost4
81	<a href="#">d1k1sa2</a>	Alignment	not modelled	5.6	17	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> Lesion bypass DNA polymerase (Y-family), catalytic domain
82	<a href="#">d2isba1</a>	Alignment	not modelled	5.6	8	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> FumA C-terminal domain-like <b>Family:</b> FumA C-terminal domain-like
83	<a href="#">d1v6ga2</a>	Alignment	not modelled	5.6	21	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
84	<a href="#">d1sm4a1</a>	Alignment	not modelled	5.6	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
85	<a href="#">d1bgpa</a>	Alignment	not modelled	5.6	27	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
86	<a href="#">d2q4qa1</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
87	<a href="#">d1itka1</a>	Alignment	not modelled	5.6	14	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
88	<a href="#">d1ub2a2</a>	Alignment	not modelled	5.5	23	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
89	<a href="#">c4hylB</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation protein; <b>PDBTitle:</b> the crystal structure of an anti-sigma-factor antagonist from <i>2 haliangium ochraceum</i> dsm 14365
90	<a href="#">c2j7uA</a>	Alignment	not modelled	5.5	43	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna dependent rna polymerase; <b>PDBTitle:</b> dengue virus ns5 rna dependent rna polymerase domain
91	<a href="#">d1okra</a>	Alignment	not modelled	5.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
92	<a href="#">c1r7mA</a>	Alignment	not modelled	5.5	35	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> intron-encoded endonuclease i-scei; <b>PDBTitle:</b> the homing endonuclease i-scei bound to its dna recognition2 region
93	<a href="#">c3jc72</a>	Alignment	not modelled	5.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> 2: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
94	<a href="#">c3o2sB</a>	Alignment	not modelled	5.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase ii subunit a c-terminal domain phosphatase <b>PDBTitle:</b> crystal structure of the human symplekin-ssu72 complex
95	<a href="#">d1dzka</a>	Alignment	not modelled	5.3	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Retinol binding protein-like
96	<a href="#">d2e39a1</a>	Alignment	not modelled	5.3	14	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
97	<a href="#">d1v82a</a>	Alignment	not modelled	5.3	45	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> 1,3-glucuronyltransferase
98	<a href="#">c2kctA</a>	Alignment	not modelled	5.3	10	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccme; <b>PDBTitle:</b> solution nmr structure of the ob-fold domain of heme2 chaperone ccme from <i>desulfovibrio vulgaris</i> . northeast3 structural genomics target dvr115g.
99	<a href="#">c4mitE</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> serine/threonine protein kinase pak, putative; <b>PDBTitle:</b> crystal structure of e. histolytica racc bound to the ehpa4 pdb