

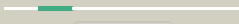






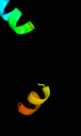







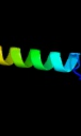

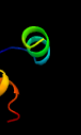

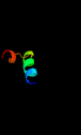


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2169c (- )_2431573_2431977
Date	Mon Aug 5 13:25:29 BST 2019
Unique Job ID	7afeb1bfbcbb7cbf

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4b4yA_</a>	 Alignment		59.6	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> neuroglobin; <b>PDBTitle:</b> crystal structure of the neuroglobin from the photosymbiotic2 marine acoeel symsagittifera roscoffensis
2	<a href="#">d1civa2</a>	 Alignment		47.7	24	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
3	<a href="#">d1lvaa3</a>	 Alignment		45.9	17	<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
4	<a href="#">c5fqdA_</a>	 Alignment		43.5	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage-binding protein 1; <b>PDBTitle:</b> structural basis of lenalidomide induced ck1a degradation by the2 cri4crbn ubiquitin ligase
5	<a href="#">d1fhjb_</a>	 Alignment		40.8	16	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
6	<a href="#">c2pjpA_</a>	 Alignment		40.4	18	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
7	<a href="#">c6cfzB_</a>	 Alignment		39.7	50	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> dad3; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
8	<a href="#">c2x9qA_</a>	 Alignment		39.0	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclodipeptide synthetase; <b>PDBTitle:</b> structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
9	<a href="#">d1fsla_</a>	 Alignment		38.0	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
10	<a href="#">c5firtC_</a>	 Alignment		36.7	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dimeric (2fe-2s) protein; <b>PDBTitle:</b> structure of the fesii (shethna) protein of azotobacter vinelandii
11	<a href="#">c3oqvA_</a>	 Alignment		35.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> albc; <b>PDBTitle:</b> albc, a cyclodipeptide synthase from streptomyces noursei

12	<a href="#">c1ciiA_</a>	Alignment		34.9	21	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
13	<a href="#">d3bj1b1</a>	Alignment		34.4	15	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
14	<a href="#">c2kq9A_</a>	Alignment		34.0	32	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> dnak suppressor protein; <b>PDBTitle:</b> solution structure of dnak suppressor protein from agrobacterium2 tumefaciens c58. northeast structural genomics consortium target3 att12/ontario center for structural proteomics target atc0888
15	<a href="#">c6adqC_</a>	Alignment		33.5	33	<b>PDB header:</b> electron transport <b>Chain:</b> C; <b>PDB Molecule:</b> cytochrome bc1 complex cytochrome c subunit; <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
16	<a href="#">c6eojA_</a>	Alignment		32.6	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein cft1; <b>PDBTitle:</b> poly polymerase module of the cleavage and polyadenylation factor2 (cpf) from saccharomyces cerevisiae
17	<a href="#">c5nvkF_</a>	Alignment		30.5	50	<b>PDB header:</b> translation <b>Chain:</b> F; <b>PDB Molecule:</b> grb10-interacting gyf protein 1; <b>PDBTitle:</b> crystal structure of the human 4ehp-gigyf1 complex
18	<a href="#">c5zm9D_</a>	Alignment		30.3	10	<b>PDB header:</b> oxygen transport <b>Chain:</b> D; <b>PDB Molecule:</b> globin protein; <b>PDBTitle:</b> crystal structure of hexacoordinated heme protein from anhydrobiotic2 tardigrade at ph 7
19	<a href="#">c3oqhB_</a>	Alignment		30.1	15	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein yvmc; <b>PDBTitle:</b> crystal structure of b. licheniformis cdps yvmc-blic
20	<a href="#">c1tjID_</a>	Alignment		29.5	26	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> dnak suppressor protein; <b>PDBTitle:</b> crystal structure of transcription factor dksa from e. coli
21	<a href="#">c1wsuA_</a>	Alignment	not modelled	29.3	16	<b>PDB header:</b> translation/rna <b>Chain:</b> A; <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> c-terminal domain of elongation factor selb complexed with2 secis rna
22	<a href="#">c4o8wE_</a>	Alignment	not modelled	27.1	43	<b>PDB header:</b> structural protein, signaling protein <b>Chain:</b> E; <b>PDB Molecule:</b> spore germination protein; <b>PDBTitle:</b> crystal structure of the gerd spore germination protein
23	<a href="#">c6ptgB_</a>	Alignment	not modelled	26.0	41	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> dnak suppressor; <b>PDBTitle:</b> structure of rna polymerase binding protein and transcriptional2 regulator dks from chlamydia trachomatis d/uw-3/cx
24	<a href="#">c3mvcB_</a>	Alignment	not modelled	25.0	10	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> globin protein 6; <b>PDBTitle:</b> high resolution crystal structure of the heme domain of glb-6 from c.2 elegans
25	<a href="#">d1wmub_</a>	Alignment	not modelled	25.0	8	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
26	<a href="#">c6bm0A_</a>	Alignment	not modelled	24.1	27	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor subunit 1; <b>PDBTitle:</b> cryo-em structure of human cpsf-160-wdr33 complex at 3.8 a resolution
27	<a href="#">d1spgb_</a>	Alignment	not modelled	22.7	15	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
28	<a href="#">c3fewX_</a>	Alignment	not modelled	21.6	8	<b>PDB header:</b> immune system <b>Chain:</b> X; <b>PDB Molecule:</b> colicin s4; <b>PDBTitle:</b> structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain

29	<a href="#">d1b8db_</a>	Alignment	not modelled	21.4	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
30	<a href="#">c4tlgB_</a>	Alignment	not modelled	20.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sec14-like protein 4; <b>PDBTitle:</b> crystal structure of sec14-like protein 4 (sec1414)
31	<a href="#">c6et5b_</a>	Alignment	not modelled	20.0	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
32	<a href="#">c1xrdA_</a>	Alignment	not modelled	19.6	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> light-harvesting protein b-880, alpha chain; <b>PDBTitle:</b> light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
33	<a href="#">d1xrda1</a>	Alignment	not modelled	19.6	22	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
34	<a href="#">c6fahD_</a>	Alignment	not modelled	19.4	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit carc; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
35	<a href="#">d1xg0c_</a>	Alignment	not modelled	19.4	16	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
36	<a href="#">c2gs0B_</a>	Alignment	not modelled	19.3	55	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> nmr structure of the complex between the ph domain of the2 tfb1 subunit from tfiih and the activation domain of p53
37	<a href="#">c3ei1A_</a>	Alignment	not modelled	19.0	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna damage-binding protein 1; <b>PDBTitle:</b> structure of hsddb1-drddb2 bound to a 14 bp 6-42 photoproduct containing dna-duplex
38	<a href="#">c1o6uA_</a>	Alignment	not modelled	18.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sec14-like protein 2; <b>PDBTitle:</b> the crystal structure of human supernatant protein factor
39	<a href="#">c4uf2A_</a>	Alignment	not modelled	17.1	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> antiapoptotic membrane protein; <b>PDBTitle:</b> deerpox virus dpv022 in complex with bax bh3
40	<a href="#">c5kk2E_</a>	Alignment	not modelled	17.1	13	<b>PDB header:</b> membrane protein, transport protein, sig <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-2 subunit; <b>PDBTitle:</b> architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
41	<a href="#">c4hvpA_</a>	Alignment	not modelled	16.8	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from sulfolobus2 solfataricus
42	<a href="#">d1hlba_</a>	Alignment	not modelled	16.1	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
43	<a href="#">c2d46A_</a>	Alignment	not modelled	15.7	38	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> calcium channel, voltage-dependent, beta 4 <b>PDBTitle:</b> solution structure of the human beta4a-a domain
44	<a href="#">c4ijjA_</a>	Alignment	not modelled	15.7	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative c4-type zinc finger protein, dkxa/trar family; <b>PDBTitle:</b> structure of transcription factor dkxa2 from pseudomonas aeruginosa
45	<a href="#">d1ln4a_</a>	Alignment	not modelled	15.6	29	<b>Fold:</b> IF3-like <b>Superfamily:</b> YhbY-like <b>Family:</b> YhbY-like
46	<a href="#">c3rq9B_</a>	Alignment	not modelled	15.4	22	<b>PDB header:</b> tse2-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> type vi secretion immunity protein; <b>PDBTitle:</b> structure of tsi2, a tse2-immunity protein from pseudomonas aeruginosa
47	<a href="#">d1ha7b_</a>	Alignment	not modelled	15.4	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
48	<a href="#">d1tc3c_</a>	Alignment	not modelled	15.2	40	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
49	<a href="#">d1phnb_</a>	Alignment	not modelled	15.1	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
50	<a href="#">c2kncA_</a>	Alignment	not modelled	14.8	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
51	<a href="#">c2jo1A_</a>	Alignment	not modelled	14.6	28	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxd1 in2 micelles
52	<a href="#">d1s29a_</a>	Alignment	not modelled	14.2	40	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> La domain
53	<a href="#">c3wmmY_</a>	Alignment	not modelled	14.0	26	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> lh1 alpha polypeptide; <b>PDBTitle:</b> crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
54	<a href="#">c3b7qA_</a>	Alignment	not modelled	13.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ykl091c; <b>PDBTitle:</b> crystal structure of yeast sec14 homolog sfh1 in complex

						with2 phosphatidylcholine <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fyxd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
55	<a href="#">c2jp3A</a>	Alignment	not modelled	13.1	25	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> type iii export protein psce; <b>PDBTitle:</b> structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
56	<a href="#">c2uwjE</a>	Alignment	not modelled	13.1	29	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> characterization of the p300 taz2-p53 tad2 complex and comparison with2 the p300 taz2-p53 tad1 complex
57	<a href="#">c2mzdB</a>	Alignment	not modelled	13.1	55	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor protein, alpha chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
58	<a href="#">c2bg9A</a>	Alignment	not modelled	13.1	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor subunit alpha; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
59	<a href="#">c4aq5A</a>	Alignment	not modelled	13.1	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein prenyltransferase alpha subunit repeat-containing <b>PDBTitle:</b> crystal structure of ggase3-fbxl2-skp1 complex
60	<a href="#">c6o60A</a>	Alignment	not modelled	12.9	29	<b>PDB header:</b> fluorescent protein <b>Chain:</b> C: <b>PDB Molecule:</b> smurfp; <b>PDBTitle:</b> smurfp-y56f mutant
61	<a href="#">c6fzoC</a>	Alignment	not modelled	12.9	17	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
62	<a href="#">c2zxeG</a>	Alignment	not modelled	12.5	27	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
63	<a href="#">d1b8da</a>	Alignment	not modelled	12.3	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> F: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
64	<a href="#">c5ol2F</a>	Alignment	not modelled	11.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RPO3F domain-like
65	<a href="#">d2dk5a1</a>	Alignment	not modelled	11.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
66	<a href="#">d2cg4a1</a>	Alignment	not modelled	11.8	5	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
67	<a href="#">c4zmuD</a>	Alignment	not modelled	11.7	20	<b>Fold:</b> KRAB domain (Kruppel-associated box) <b>Superfamily:</b> KRAB domain (Kruppel-associated box) <b>Family:</b> KRAB domain (Kruppel-associated box)
68	<a href="#">d1v65a</a>	Alignment	not modelled	11.6	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> cyclo(l-leucyl-l-leucyl) synthase; <b>PDBTitle:</b> structure of cdps from staphylococcus haemolyticus
69	<a href="#">c6ez3C</a>	Alignment	not modelled	11.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein glb-12; <b>PDBTitle:</b> globin-like protein glb-12 from c.elegans
70	<a href="#">c4bjaA</a>	Alignment	not modelled	11.5	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
71	<a href="#">c2e1cA</a>	Alignment	not modelled	11.4	12	<b>Fold:</b> DinB/YfiT-like putative metalloenzymes <b>Superfamily:</b> DinB/YfiT-like putative metalloenzymes <b>Family:</b> DinB-like
72	<a href="#">d2f22a1</a>	Alignment	not modelled	11.3	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
73	<a href="#">c2l8sA</a>	Alignment	not modelled	11.3	14	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> hypothetical protein pa2703 pseudomonas aeruginosa pao1
74	<a href="#">c3stqC</a>	Alignment	not modelled	11.3	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> myocilin; <b>PDBTitle:</b> mouse myocilin leucine zipper c-terminal 7 heptad repeat
75	<a href="#">c5vr2A</a>	Alignment	not modelled	11.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ent; <b>PDBTitle:</b> crystal structure of ent domain from t. brucei
76	<a href="#">c5zx1A</a>	Alignment	not modelled	11.1	24	<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
77	<a href="#">d2j7pe1</a>	Alignment	not modelled	11.1	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> claudin-15; <b>PDBTitle:</b> crystal structure of mouse claudin-15
78	<a href="#">c4p79A</a>	Alignment	not modelled	10.9	11	<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
79	<a href="#">d1okkd1</a>	Alignment	not modelled	10.8	32	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit beta, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3
80	<a href="#">c6fkib</a>	Alignment	not modelled	10.8	17	

81	<a href="#">d2a26a1</a>	Alignment	not modelled	10.6	24	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Calcyclin-binding protein-like <b>Family:</b> Siah interacting protein N terminal domain-like
82	<a href="#">c6gygA_</a>	Alignment	not modelled	10.6	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator reg576; <b>PDBTitle:</b> x-ray structure of the apo form of the establishment gene regulator2 reg576 of the g+ plasmid p576
83	<a href="#">d3bz6a1</a>	Alignment	not modelled	10.5	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PSPTO2686-like
84	<a href="#">c2vigC_</a>	Alignment	not modelled	10.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short-chain specific acyl-coa dehydrogenase,; <b>PDBTitle:</b> crystal structure of human short-chain acyl coa dehydrogenase
85	<a href="#">c2lt3A_</a>	Alignment	not modelled	10.2	45	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, card family; <b>PDBTitle:</b> solution nmr structure of the c-terminal domain of cdnl from2 myxococcus xanthus
86	<a href="#">c3l9kX_</a>	Alignment	not modelled	10.0	42	<b>PDB header:</b> motor protein <b>Chain:</b> X: <b>PDB Molecule:</b> dynein intermediate chain, cytosolic; <b>PDBTitle:</b> insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
87	<a href="#">c3l9kZ_</a>	Alignment	not modelled	10.0	42	<b>PDB header:</b> motor protein <b>Chain:</b> Z: <b>PDB Molecule:</b> dynein intermediate chain, cytosolic; <b>PDBTitle:</b> insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
88	<a href="#">d1jbob_</a>	Alignment	not modelled	10.0	18	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
89	<a href="#">c5w1sM_</a>	Alignment	not modelled	10.0	17	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> protein trar; <b>PDBTitle:</b> x-ray crystal structure of escherichia coli rna polymerase and trar2 complex
90	<a href="#">c5j0hA_</a>	Alignment	not modelled	9.9	38	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> design construct 2l6hc3_13; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
91	<a href="#">c2k1aA_</a>	Alignment	not modelled	9.9	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iib) transmembrane segment
92	<a href="#">c3ux4C_</a>	Alignment	not modelled	9.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> acid-activated urea channel; <b>PDBTitle:</b> crystal structure of the urea channel from the human gastric pathogen2 helicobacter pylori
93	<a href="#">d1knlA_</a>	Alignment	not modelled	9.9	22	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
94	<a href="#">c2jr5A_</a>	Alignment	not modelled	9.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0350 protein vc_2471; <b>PDBTitle:</b> solution structure of upf0350 protein vc_2471. northeast structural2 genomics target vcr36
95	<a href="#">c1q90M_</a>	Alignment	not modelled	9.8	35	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome b6f complex subunit petm; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
96	<a href="#">d1q90m_</a>	Alignment	not modelled	9.8	35	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetM subunit of the cytochrome b6f complex <b>Family:</b> PetM subunit of the cytochrome b6f complex
97	<a href="#">c5v1eA_</a>	Alignment	not modelled	9.8	42	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> guavanin 2; <b>PDBTitle:</b> suboptimization of a glycine rich peptide allows the combinatorial2 space exploration for designing novel antimicrobial peptides
98	<a href="#">c2l14B_</a>	Alignment	not modelled	9.7	55	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cellular tumor antigen p53; <b>PDBTitle:</b> structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
99	<a href="#">d1pzqa_</a>	Alignment	not modelled	9.7	55	<b>Fold:</b> Dimerisation interlock <b>Superfamily:</b> Docking domain A of the erythromycin polyketide synthase (DEBS) <b>Family:</b> Docking domain A of the erythromycin polyketide synthase (DEBS)