

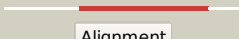











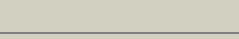



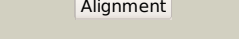




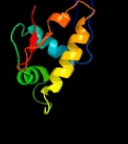






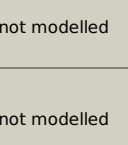


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3124 (-)_3489503_3490372
Date	Thu Aug 8 16:20:30 BST 2019
Unique Job ID	8600b938944439b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ff4B_	 Alignment		100.0	51	PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
2	d2ff4a2	 Alignment		100.0	54	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
3	d2ff4a1	 Alignment		99.8	53	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
4	c2hwwA_	 Alignment		99.2	26	PDB header: transcription Chain: A: PDB Molecule: dna-binding response regulator vicr; PDBTitle: crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
5	c3zq7A_	 Alignment		99.1	21	PDB header: transcription Chain: A: PDB Molecule: kdp operon transcriptional regulatory protein kdpe; PDBTitle: the structure of dna-binding domain of response regulator from2 escherichia coli k-12
6	c5ju7A_	 Alignment		99.1	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: dna binding domain of e.coli cadc
7	c2pmuD_	 Alignment		99.1	20	PDB header: transcription regulation Chain: D: PDB Molecule: response regulator phop; PDBTitle: crystal structure of the dna-binding domain of phop
8	c4ixaA_	 Alignment		99.1	20	PDB header: transcription Chain: A: PDB Molecule: response regulator saer; PDBTitle: structure of dna-binding domain of the response regulator saer from2 staphylococcus epidermidis
9	c5dcmB_	 Alignment		99.1	26	PDB header: signaling protein Chain: B: PDB Molecule: phob family transcriptional regulator; PDBTitle: structure of a lantibiotic response regulator: c-terminal domain of2 the nisin resistance regulator nsrr
10	c4uhtA_	 Alignment		99.0	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cpxr; PDBTitle: crystal structure of the dna binding domain of cpxr from e. coli
11	c2k4jA_	 Alignment		99.0	20	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: arsr dna binding domain

12	c2zxB	Alignment		99.0	26	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein walr; PDBTitle: crystal structure of yycf dna-binding domain from staphylococcus2 aureus
13	d1gxqa	Alignment		99.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
14	c2rv8A	Alignment		99.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
15	d1p2fa1	Alignment		99.0	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
16	c2hqnA	Alignment		99.0	21	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
17	c2jzvA	Alignment		99.0	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein pcor; PDBTitle: solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
18	d1opca	Alignment		99.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
19	c3ripA	Alignment		99.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: covr; PDBTitle: crystal structure of the dna binding domain of covr from streptococcus2 pyogenes
20	c3q9vB	Alignment		99.0	27	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
21	d1ys7a1	Alignment	not modelled	98.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
22	c2m87A	Alignment	not modelled	98.9	29	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional regulatory protein basr/pmra; PDBTitle: structural basis of dna recognition by the effector domain of2 klebsiella pneumoniae pmra
23	c2nazA	Alignment	not modelled	98.8	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein rsta; PDBTitle: the solution nmr structure of the c-terminal effector domain of bfmr2 from acinetobacter baumannii
24	d1kgsa1	Alignment	not modelled	98.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
25	c5x5IM	Alignment	not modelled	98.7	18	PDB header: dna binding protein/dna Chain: M: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader dna binding domain in2 complex with an intercistronic region
26	c2m1bA	Alignment	not modelled	98.7	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein, c terminal family PDBTitle: solution structure of the chxr dna-binding domain
27	c4kfcB	Alignment	not modelled	98.7	22	PDB header: transcription regulator/dna Chain: B: PDB Molecule: kdp operon transcriptional regulatory protein kdpe; PDBTitle: crystal structure of a hyperactive mutant of response regulator kdpe2 complexed to its promoter dna
28	c2agrA	Alignment	not modelled	98.7	17	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3;

28	c20q1A	Alignment	not modelled	98.7	17	PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis PDB header: transcription regulator
29	c1ys7B	Alignment	not modelled	98.7	23	Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
30	c2gwrA	Alignment	not modelled	98.4	22	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
31	c2hqrA	Alignment	not modelled	98.4	21	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
32	c5u8mA	Alignment	not modelled	98.2	25	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
33	c1kt0A	Alignment	not modelled	98.2	14	PDB header: isomerase Chain: A: PDB Molecule: 51 kda fk506-binding protein; PDBTitle: structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
34	c4s05B	Alignment	not modelled	98.2	29	PDB header: transcription/dna Chain: B: PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
35	c4i2wA	Alignment	not modelled	98.1	13	PDB header: chaperone/protein binding Chain: A: PDB Molecule: protein unc-45; PDBTitle: crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
36	c5ompA	Alignment	not modelled	98.1	12	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp5; PDBTitle: human fkbp5 protein
37	c1p2fA	Alignment	not modelled	98.0	26	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
38	d2hr2a1	Alignment	not modelled	98.0	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
39	c2if4A	Alignment	not modelled	97.9	12	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
40	c5djsA	Alignment	not modelled	97.9	21	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
41	c4aifA	Alignment	not modelled	97.9	8	PDB header: signaling protein/peptide Chain: A: PDB Molecule: ah receptor-interacting protein; PDBTitle: aip tpr domain in complex with human hsp90 peptide
42	c3r0jA	Alignment	not modelled	97.9	17	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
43	c6n3qF	Alignment	not modelled	97.9	13	PDB header: transport protein Chain: F: PDB Molecule: translocation protein sec72; PDBTitle: cryo-em structure of the yeast sec complex
44	c4b09F	Alignment	not modelled	97.9	24	PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
45	c5wftA	Alignment	not modelled	97.8	11	PDB header: structural protein Chain: A: PDB Molecule: pelb; PDBTitle: pelb 319-436 from pseudomonas aeruginosa pao1
46	c5dseC	Alignment	not modelled	97.8	17	PDB header: protein binding Chain: C: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
47	c3pe3D	Alignment	not modelled	97.8	18	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
48	c3rkvA	Alignment	not modelled	97.8	17	PDB header: isomerase Chain: A: PDB Molecule: putative peptidylprolyl isomerase; PDBTitle: c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans
49	c3qyzB	Alignment	not modelled	97.7	8	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
50	c5dseA	Alignment	not modelled	97.7	18	PDB header: protein binding Chain: A: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
51	c2xpiA	Alignment	not modelled	97.7	16	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
52	c2c2ID	Alignment	not modelled	97.7	19	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
53	c1qz2B	Alignment	not modelled	97.7	13	PDB header: isomerase/chaperone Chain: B: PDB Molecule: fk506-binding protein 4; PDBTitle: crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
54	c4ui9K	Alignment	not modelled	97.6	13	PDB header: cell cycle Chain: K: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: atomic structure of the human anaphase-promoting

						complex
55	c1kgsA_	Alignment	not modelled	97.6	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
56	c5fzqB_	Alignment	not modelled	97.6	17	PDB header: unknown function Chain: B: PDB Molecule: designed tpr protein; PDBTitle: designed tpr protein m4n
57	c1wao4_	Alignment	not modelled	97.6	12	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
58	c4j8dC_	Alignment	not modelled	97.6	15	PDB header: chaperone Chain: C: PDB Molecule: hsc70-interacting protein; PDBTitle: middle domain of hsc70-interacting protein, crystal form ii
59	c4kvmA_	Alignment	not modelled	97.6	15	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
60	c4ui9C_	Alignment	not modelled	97.6	13	PDB header: cell cycle Chain: C: PDB Molecule: cell division cycle protein 23 homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
61	c2y4tA_	Alignment	not modelled	97.5	14	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
62	c2xcbA_	Alignment	not modelled	97.5	9	PDB header: protein binding Chain: A: PDB Molecule: regulatory protein pcrh; PDBTitle: crystal structure of pcrh in complex with the chaperone2 binding region of popd
63	c5jttA_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine-protein phosphatase 5; PDBTitle: crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
64	c1ihgA_	Alignment	not modelled	97.5	10	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
65	c5nnd_	Alignment	not modelled	97.4	14	PDB header: transferase Chain: D: PDB Molecule: n-terminal acetyltransferase-like protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
66	c2katA_	Alignment	not modelled	97.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206
67	c4uqzA_	Alignment	not modelled	97.4	21	PDB header: protein transport Chain: A: PDB Molecule: hsie1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
68	c6hpgA_	Alignment	not modelled	97.4	12	PDB header: plant protein Chain: A: PDB Molecule: outer envelope protein 64, mitochondrial; PDBTitle: arabidopsis om64 tpr domain
69	c2kcvA_	Alignment	not modelled	97.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tetratricopeptide repeat domain protein; PDBTitle: solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
70	c5mgxG_	Alignment	not modelled	97.4	17	PDB header: isomerase Chain: G: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp8; PDBTitle: the structure of fkbp38 in complex with the meevd tetratricopeptide2 binding-motif of hsp90
71	d1hxia_	Alignment	not modelled	97.4	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
72	c5xw7B_	Alignment	not modelled	97.4	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: cellulose synthase subunit c; PDBTitle: crystal structure of the flexible tandem repeat domain of bacterial2 cellulose synthase subunit c
73	c2gw1A_	Alignment	not modelled	97.3	17	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
74	c3k9iA_	Alignment	not modelled	97.3	12	PDB header: protein binding Chain: A: PDB Molecule: bh0479 protein; PDBTitle: crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
75	c6hftA_	Alignment	not modelled	97.3	10	PDB header: chaperone Chain: A: PDB Molecule: hsp70/hsp90 co-chaperone cns1; PDBTitle: hsp90 co-chaperone cns1 from saccharomyces cerevisiae (delta69)
76	d2ooea1	Alignment	not modelled	97.3	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
77	d1w3ba_	Alignment	not modelled	97.3	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
78	c5l0wB_	Alignment	not modelled	97.2	16	PDB header: membrane protein Chain: B: PDB Molecule: sec72; PDBTitle: structure of post-translational translocation sec71/sec72 complex
79	c4rg6B_	Alignment	not modelled	97.2	17	PDB header: protein binding Chain: B: PDB Molecule: cell division cycle protein 27 homolog; PDBTitle: crystal structure of apc3-apc16 complex
						PDB header: transport protein

80	c3fp4A_	Alignment	not modelled	97.2	6	Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
81	c2vsnB_	Alignment	not modelled	97.2	16	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
82	c2avpA_	Alignment	not modelled	97.2	21	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
83	c4nrhB_	Alignment	not modelled	97.2	22	PDB header: chaperone/protein binding Chain: B: PDB Molecule: chaperone sycd; PDBTitle: copn-scc3 complex
84	d2fba1	Alignment	not modelled	97.2	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
85	c2fbaA_	Alignment	not modelled	97.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 70 kda peptidylprolyl isomerase, putative; PDBTitle: plasmodium falciparum putative fk506-binding protein2 pfl2275c, c-terminal tpr-containing domain
86	c4ui9Y_	Alignment	not modelled	97.2	17	PDB header: cell cycle Chain: Y: PDB Molecule: anaphase-promoting complex subunit 7; PDBTitle: atomic structure of the human anaphase-promoting complex
87	c2dbaA_	Alignment	not modelled	97.2	13	PDB header: structural protein Chain: A: PDB Molecule: smooth muscle cell associated protein-1, isoform PDBTitle: the solution structure of the tetratricopeptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
88	c3iegB_	Alignment	not modelled	97.2	13	PDB header: chaperone Chain: B: PDB Molecule: dnaJ homolog subfamily c member 3; PDBTitle: crystal structure of p58(ipk) tpr domain at 2.5 a
89	c3ly8A_	Alignment	not modelled	97.2	16	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
90	c6g70A_	Alignment	not modelled	97.2	11	PDB header: splicing Chain: A: PDB Molecule: pre-mrna-processing factor 39; PDBTitle: structure of murine prpf39
91	c2kckA_	Alignment	not modelled	97.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tpr repeat; PDBTitle: nmr solution structure of the northeast structural genomics consortium2 (nesg) target mrr121a
92	d1p5qa1	Alignment	not modelled	97.1	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
93	c3upvA_	Alignment	not modelled	97.1	15	PDB header: peptide binding protein Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: tpr2b-domain:phsp70-complex of yeast sti1
94	c1na3A_	Alignment	not modelled	97.1	21	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctrp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
95	c3beeB_	Alignment	not modelled	97.1	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
96	c5aioA_	Alignment	not modelled	97.1	13	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 131 kda subunit; PDBTitle: crystal structure of t131 n-terminal tpr array
97	c5m72A_	Alignment	not modelled	97.1	5	PDB header: protein transport Chain: A: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp68-72 protein-binding domain complex
98	c6c95A_	Alignment	not modelled	97.1	19	PDB header: transferase Chain: A: PDB Molecule: n-alpha-acetyltransferase 15, nata auxiliary subunit; PDBTitle: the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
99	c2l6jA_	Alignment	not modelled	97.0	9	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
100	c3hymB_	Alignment	not modelled	97.0	13	PDB header: cell cycle, ligase Chain: B: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
101	c2kc7A_	Alignment	not modelled	97.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bfr218_protein; PDBTitle: solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
102	c4uzuA_	Alignment	not modelled	97.0	18	PDB header: motor protein Chain: A: PDB Molecule: flagellar associated protein; PDBTitle: crystal structure of the chlamydomonas ift70 and ift52 complex
103	c4hnxA_	Alignment	not modelled	97.0	12	PDB header: transferase Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata acetyltransferase complex bound to ppgpp
104	c3n71A_	Alignment	not modelled	97.0	12	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
105	c5ic8A_	Alignment	not modelled	97.0	17	PDB header: structural protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of utp6

106	c4u0zH_	 Alignment	not modelled	97.0	11	PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
107	d1zbpa1	 Alignment	not modelled	96.9	12	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
108	c5jqyA_	 Alignment	not modelled	96.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph) oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
109	d1elwa_	 Alignment	not modelled	96.9	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
110	c3cvpA_	 Alignment	not modelled	96.9	20	PDB header: transport protein Chain: A: PDB Molecule: peroxisome targeting signal 1 receptor pex5; PDBTitle: structure of peroxisomal targeting signal 1 (pts1) binding domain of2 trypanosoma brucei peroxin 5 (tbpex5)complexed to pts1 peptide (10-3 skl)
111	c5jj6A_	 Alignment	not modelled	96.9	13	PDB header: transferase Chain: A: PDB Molecule: adenosine monophosphate-protein transferase ficd homolog; PDBTitle: fic-1 (aa134 - 508) from c. elegans
112	c3q49B_	 Alignment	not modelled	96.9	18	PDB header: ligase/chaperone Chain: B: PDB Molecule: stip1 homology and u box-containing protein 1; PDBTitle: crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
113	c1fchB_	 Alignment	not modelled	96.8	20	PDB header: signaling protein Chain: B: PDB Molecule: peroxisomal targeting signal 1 receptor; PDBTitle: crystal structure of the pts1 complexed to the tpr region2 of human pex5
114	c4ga0A_	 Alignment	not modelled	96.8	13	PDB header: transport protein Chain: A: PDB Molecule: re3 sumo-protein ligase ranbp2; PDBTitle: structure of the n-terminal domain of nup358
115	c3q9sA_	 Alignment	not modelled	96.8	26	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
116	c5l0yE_	 Alignment	not modelled	96.8	15	PDB header: protein transport Chain: E: PDB Molecule: sec72-ssa1 c-terminal peptide fusion protein; PDBTitle: crystal structure of a sec72-ssa1 c-terminal peptide fusion protein
117	d1fcha_	 Alignment	not modelled	96.8	20	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
118	c5xi8A_	 Alignment	not modelled	96.8	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: structure and function of the tpr domain
119	d2c2la1	 Alignment	not modelled	96.7	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
120	c5tqbB_	 Alignment	not modelled	96.7	11	PDB header: ribosomal protein Chain: B: PDB Molecule: assembly chaperone of ribosomal protein l4 (acl4); PDBTitle: crystal structure of assembly chaperone of ribosomal protein l4 (acl4)2 in complex with ribosomal protein l4 (rpl4)