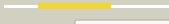
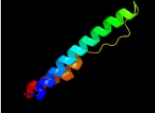
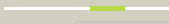
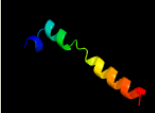

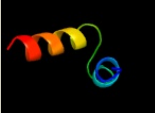

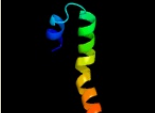


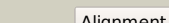

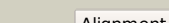

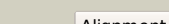








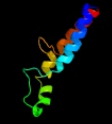


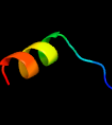


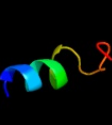



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0475_(hbhA)_565800_566399
 Date Tue Jul 23 14:50:55 BST 2019
 Unique Job ID eb3ef9de5eedcdfb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nfoA_	 Alignment		70.5	22	PDB header: lipid transport Chain: A; PDB Molecule: apolipoprotein e2; PDBTitle: apolipoprotein e2 (apoe2, d154a mutation)
2	c6f7sB_	 Alignment		61.7	25	PDB header: rna binding protein Chain: B; PDB Molecule: serrate rna effector molecule homolog; PDBTitle: crystal structure of human ars2 residues 147-270 + 408-763 with2 deletion of loop b
3	c2julA_	 Alignment		49.2	38	PDB header: dna binding protein Chain: A; PDB Molecule: calsenilin; PDBTitle: nmr structure of dream
4	c6epgD_	 Alignment		29.1	35	PDB header: toxin Chain: D; PDB Molecule: zeta_1 toxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 neisseria gonorrhoeae.
5	d1bjfa_	 Alignment		28.5	36	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
6	c5x1hS_	 Alignment		28.3	19	PDB header: protein transport Chain: S; PDB Molecule: icmj (dotn); PDBTitle: structure of legionella pneumophila dotn
7	c2yomA_	 Alignment		18.4	37	PDB header: signaling protein Chain: A; PDB Molecule: sensory box protein; PDBTitle: solution nmr structure of the c-terminal extension of two bacterial2 light, oxygen, voltage (lov) photoreceptor proteins from3 pseudomonas putida
8	c1gw4A_	 Alignment		17.9	31	PDB header: high density lipoproteins Chain: A; PDB Molecule: apoa-i; PDBTitle: the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
9	c4jo6Y_	 Alignment		16.8	31	PDB header: unknown function Chain: Y; PDB Molecule: sbp-tag; PDBTitle: streptavidin complex with sbp-tag
10	c4jo6Z_	 Alignment		16.8	31	PDB header: unknown function Chain: Z; PDB Molecule: sbp-tag; PDBTitle: streptavidin complex with sbp-tag
11	d1dгна_	 Alignment		16.4	17	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD

12	c5xzoA_	Alignment		16.2	25	PDB header: hydrolase Chain: A; PDB Molecule: beta-xylanase; PDBTitle: crystal structure of gh10 xylanase xyl10c from bispora. sp mey-1
13	c6cc4A_	Alignment		15.9	28	PDB header: transport protein Chain: A; PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
14	c5kwoA_	Alignment		15.3	43	PDB header: de novo protein Chain: A; PDB Molecule: designed peptide nc_ehe_d1; PDBTitle: nmr solution structure of designed peptide nc_ehe_d1
15	c6br8B_	Alignment		14.8	27	PDB header: viral protein Chain: B; PDB Molecule: protein a6 homolog; PDBTitle: structure of a6 reveals a novel lipid transporter
16	d1ae9a_	Alignment		14.6	33	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
17	d1q8ia_	Alignment		14.0	36	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
18	d1ryla_	Alignment		13.3	30	Fold: Hypothetical protein yfbM Superfamily: Hypothetical protein yfbM Family: Hypothetical protein yfbM
19	c6conF_	Alignment		12.6	22	PDB header: hydrolase Chain: F; PDB Molecule: coa-transferase subunit beta; PDBTitle: crystal structure of mycobacterium tuberculosis ipdab
20	c2jo8B_	Alignment		11.9	29	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
21	c6c52D_	Alignment	not modelled	11.9	43	PDB header: de novo protein Chain: D; PDB Molecule: cross-alpha amyloid-like structure alphetat; PDBTitle: cross-alpha amyloid-like structure alphetat
22	c6c52C_	Alignment	not modelled	11.9	43	PDB header: de novo protein Chain: C; PDB Molecule: cross-alpha amyloid-like structure alphetat; PDBTitle: cross-alpha amyloid-like structure alphetat
23	c6c52A_	Alignment	not modelled	11.9	43	PDB header: de novo protein Chain: A; PDB Molecule: cross-alpha amyloid-like structure alphetat; PDBTitle: cross-alpha amyloid-like structure alphetat
24	c6c52B_	Alignment	not modelled	11.9	43	PDB header: de novo protein Chain: B; PDB Molecule: cross-alpha amyloid-like structure alphetat; PDBTitle: cross-alpha amyloid-like structure alphetat
25	c4e1rA_	Alignment	not modelled	11.7	27	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
26	c4e1pA_	Alignment	not modelled	11.7	27	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 2 1 space group
27	c2mwqA_	Alignment	not modelled	11.6	27	PDB header: plant protein Chain: A; PDB Molecule: oxygen-evolving enhancer protein 3, chloroplastic; PDBTitle: solution structure of psbq from spinacia oleracea
28	d1y0na_	Alignment	not modelled	11.5	26	Fold: YehU-like Superfamily: YehU-like Family: YehU-like

29	c6co6B_	Alignment	not modelled	11.2	33	PDB header: hydrolase Chain: B: PDB Molecule: probable coa-transferase beta subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab
30	d1gs9a_	Alignment	not modelled	10.7	25	Fold: Four-helical up-and-down bundle Superfamily: Apolipoprotein Family: Apolipoprotein
31	c6alyA_	Alignment	not modelled	10.7	24	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 15; PDBTitle: solution structure of yeast med15 abd2 residues 277-368
32	c6f1ux_	Alignment	not modelled	10.6	32	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1; PDBTitle: n terminal region of dynein tail domains in complex with dynactin2 filament and bicdr-1
33	c4l0nG_	Alignment	not modelled	10.6	36	PDB header: transferase Chain: G: PDB Molecule: serine/threonine-protein kinase 3; PDBTitle: crystal structure of stk3 (mst2) sarah domain
34	c5wknD_	Alignment	not modelled	10.4	36	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the parainfluenza virus 5 nucleoprotein-2 phosphoprotein complex
35	c5wknC_	Alignment	not modelled	10.2	36	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the parainfluenza virus 5 nucleoprotein-2 phosphoprotein complex
36	c4bl6A_	Alignment	not modelled	9.6	22	PDB header: protein transport Chain: A: PDB Molecule: protein bicaudal d; PDBTitle: bicaudal-d uses a parallel, homodimeric coiled coil with heterotypic2 registry to co-ordinate recruitment of cargos to dynein
37	c3h36A_	Alignment	not modelled	9.6	18	PDB header: transferase Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of an uncharacterized domain in polyribonucleotide2 nucleotidyltransferase from streptococcus mutans ua159
38	c2v8gD_	Alignment	not modelled	9.4	28	PDB header: hydrolase Chain: D: PDB Molecule: beta-alanine synthase; PDBTitle: crystal structure of beta-alanine synthase from2 saccharomyces kluveri in complex with the product beta-3 alanine
39	d2clyb1	Alignment	not modelled	8.8	30	Fold: ATP synthase D chain-like Superfamily: ATP synthase D chain-like Family: ATP synthase D chain-like
40	d1lqsl_	Alignment	not modelled	8.7	40	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
41	d1poia_	Alignment	not modelled	8.6	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
42	c4fqnC_	Alignment	not modelled	8.5	25	PDB header: protein binding Chain: C: PDB Molecule: malcavernin; PDBTitle: crystal structure of the ccm2 c-terminal harmonin homology domain2 (hhd)
43	c2zvWk_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: K: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
44	c2zvWp_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: P: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
45	c2zvWl_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: L: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
46	c2zvVx_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: X: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cellular nuclear antigen2 1 and short peptide from human p21
47	c2zvWn_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: N: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
48	c2zvWo_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: O: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
49	c2zvWj_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: J: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
50	c2zvWl_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: I: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
51	c2zvWm_	Alignment	not modelled	8.5	22	PDB header: dna binding protein Chain: M: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: crystal structure of proliferating cell nuclear antigen 22 and short peptide from human p21
52	d1kx9b_	Alignment	not modelled	8.4	22	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
53	c5jbrA_	Alignment	not modelled	8.4	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bcav_2135; PDBTitle: crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
54	c2gvsA_	Alignment	not modelled	8.3	19	PDB header: lipid binding protein Chain: A: PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
						PDB header: metal binding protein

55	c2ct9A	Alignment	not modelled	8.2	16	Chain: A: PDB Molecule: calcium-binding protein p22; PDBTitle: the crystal structure of calcineurin b homologous proein 1 (chp1)
56	d1o26a	Alignment	not modelled	8.1	24	Fold: Thymidylate synthase-complementing protein Thy1 Superfamily: Thymidylate synthase-complementing protein Thy1 Family: Thymidylate synthase-complementing protein Thy1
57	d1c3ca	Alignment	not modelled	8.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
58	d1p9ba	Alignment	not modelled	8.0	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
59	c5uifC	Alignment	not modelled	8.0	12	PDB header: hydrolase Chain: C: PDB Molecule: ps01740; PDBTitle: crystal structure of native ps01740
60	c5e0uE	Alignment	not modelled	7.9	25	PDB header: dna binding protein Chain: E: PDB Molecule: cyclin-dependent kinase inhibitor 1; PDBTitle: human pcna variant (s228i) complexed with p21 at 1.9 angstroms
61	c3mlcC	Alignment	not modelled	7.7	19	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
62	c6c34A	Alignment	not modelled	7.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
63	c3l0iA	Alignment	not modelled	7.6	44	PDB header: protein binding/protein transport Chain: A: PDB Molecule: drra; PDBTitle: complex structure of sidm/drra with the wild type rab1
64	c2i5gB	Alignment	not modelled	7.4	17	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas aeruginosa
65	d1y0pa3	Alignment	not modelled	7.4	19	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
66	c6bn1A	Alignment	not modelled	7.3	15	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase hippo; PDBTitle: salvador hippo sarah domain complex
67	c5h1nB	Alignment	not modelled	7.3	18	PDB header: unknown function Chain: B: PDB Molecule: upf0253 protein yaep; PDBTitle: crystal structure of sf173 from shigella flexneri
68	c4xdnA	Alignment	not modelled	7.2	17	PDB header: cell cycle Chain: A: PDB Molecule: mau2 chromatid cohesion factor homolog; PDBTitle: crystal structure of scc4 in complex with scc2n
69	d2odgc1	Alignment	not modelled	7.1	21	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
70	c4b1yM	Alignment	not modelled	7.0	41	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-3 bound to g-actin
71	d1r3na1	Alignment	not modelled	7.0	30	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
72	c2l4hA	Alignment	not modelled	7.0	28	PDB header: metal binding protein Chain: A: PDB Molecule: calcium and integrin-binding protein 1; PDBTitle: the solution structure of calcium bound cib1
73	c5b8iB	Alignment	not modelled	6.8	17	PDB header: hydrolase Chain: B: PDB Molecule: calcineurin subunit b, variant; PDBTitle: crystal structure of calcineurin a and calcineurin b in complex with2 fkbp12 and fk506 from coccidioides immitis rs
74	c4uzmA	Alignment	not modelled	6.8	67	PDB header: structural protein Chain: A: PDB Molecule: putative membrane protein igaa homolog; PDBTitle: shotgun proteolysis: a practical application
75	c2mbyA	Alignment	not modelled	6.7	21	PDB header: rna binding protein Chain: A: PDB Molecule: ribosomal rna-processing protein 7; PDBTitle: nmr structure of rrp7 c-terminal domain
76	c3tweA	Alignment	not modelled	6.4	24	PDB header: unknown function Chain: A: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
77	c2zkro	Alignment	not modelled	6.4	20	PDB header: ribosomal protein/rna Chain: O: PDB Molecule: rna expansion segment es30; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
78	c4c9yB	Alignment	not modelled	6.4	17	PDB header: cell cycle Chain: B: PDB Molecule: spindle and kinetochore-associated protein 1; PDBTitle: structural basis for the microtubule binding of the human2 kinetochore ska complex
79	c6idxA	Alignment	not modelled	6.4	21	PDB header: cell adhesion Chain: A: PDB Molecule: engulfment and cell motility protein 2; PDBTitle: crystal structure of bai1/elmo2 complex
80	d1yqfa1	Alignment	not modelled	6.3	33	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like

81	d1n8va_	Alignment	not modelled	6.2	16	Fold: alpha-alpha superhelix Superfamily: Chemiosensory protein Csp2 Family: Chemiosensory protein Csp2
82	d2vqca1	Alignment	not modelled	6.2	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like
83	c2vqcA_	Alignment	not modelled	6.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical 13.2 kda protein; PDBTitle: structure of a dna binding winged-helix protein, f-112, from2 sulfolobus spindle-shaped virus 1.
84	c2c1nA_	Alignment	not modelled	6.1	18	PDB header: signaling protein Chain: A: PDB Molecule: 14-3-3 protein zeta/delta; PDBTitle: molecular basis for the recognition of phosphorylated and2 phosphoacetylated histone h3 by 14-3-3
85	c2pg1E_	Alignment	not modelled	6.1	15	PDB header: structural protein Chain: E: PDB Molecule: dynein light chain tctex-type; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
86	c2p4fA_	Alignment	not modelled	6.0	6	PDB header: chaperone Chain: A: PDB Molecule: similar to sp p32453 saccharomyces cerevisiae ynl315c
87	d1p32a_	Alignment	not modelled	5.9	33	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like
88	c4ycgB_	Alignment	not modelled	5.8	18	PDB header: cytokine Chain: B: PDB Molecule: bone morphogenetic protein 9 growth factor domain; PDBTitle: pro-bone morphogenetic protein 9
89	d2cvoa2	Alignment	not modelled	5.8	25	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
90	c4etvA_	Alignment	not modelled	5.8	33	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor 2 (2699-2904)
91	c3cezA_	Alignment	not modelled	5.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
92	c2ki0A_	Alignment	not modelled	5.7	47	PDB header: de novo protein Chain: A: PDB Molecule: ds119; PDBTitle: nmr structure of a de novo designed beta alpha beta
93	c2vs0B_	Alignment	not modelled	5.7	23	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
94	d2ilkA_	Alignment	not modelled	5.6	35	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
95	c3qv0A_	Alignment	not modelled	5.6	33	PDB header: protein binding Chain: A: PDB Molecule: mitochondrial acidic protein mam33; PDBTitle: crystal structure of saccharomyces cerevisiae mam33
96	c2lycA_	Alignment	not modelled	5.5	10	PDB header: protein binding Chain: A: PDB Molecule: spindle and kinetochore-associated protein 1 homolog; PDBTitle: structure of c-terminal domain of ska1
97	d1go3f_	Alignment	not modelled	5.5	44	Fold: SAM domain-like Superfamily: HRDC-like Family: RNA polymerase II subunit RBP4 (RpoF)
98	c4e1oC_	Alignment	not modelled	5.5	19	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
99	d1rj9b1	Alignment	not modelled	5.4	30	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins