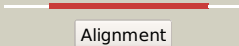
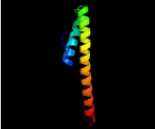

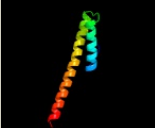
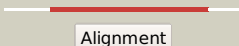

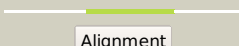

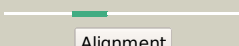

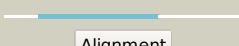

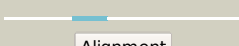
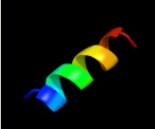
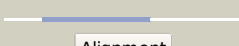



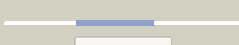



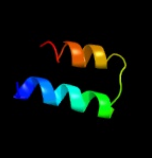
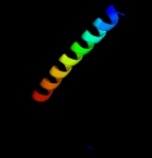
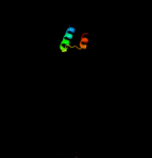

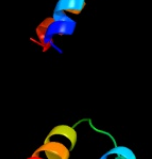
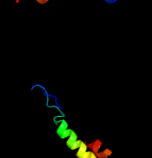

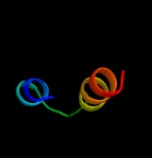
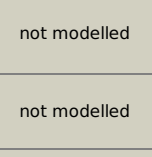


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1107c_(xseB)_1233971_1234228
 Date Wed Jul 31 22:05:18 BST 2019
 Unique Job ID 599eafd779a236fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vp7a_	 Alignment		99.7	30	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
2	d1vp7b_	 Alignment		99.7	29	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
3	c1vp7D_	 Alignment		99.6	30	PDB header: hydrolase Chain: D: PDB Molecule: exodeoxyribonuclease vii small subunit; PDBTitle: crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
4	c3he4A_	 Alignment		66.3	21	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
5	c4lh9A_	 Alignment		42.6	29	PDB header: transcription Chain: A: PDB Molecule: heterocyst differentiation control protein; PDBTitle: crystal structure of the refolded hood domain (asp256-gly295) of hetr
6	d1pina2	 Alignment		35.4	6	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
7	c4ynlB_	 Alignment		31.8	29	PDB header: transcription Chain: B: PDB Molecule: heterocyst differentiation control protein; PDBTitle: crystal structure of the hood domain of anabaena hetr in complex with2 the hexapeptide ergsgr derived from pats
8	c2jzvA_	 Alignment		28.7	5	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: solution structure of s. aureus prsa-ppiase
9	c2y0sQ_	 Alignment		28.6	24	PDB header: transferase Chain: Q: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in p21 space2 group
10	c2y0sj_	 Alignment		28.6	24	PDB header: transferase Chain: J: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in p21 space2 group
11	c3hxxA_	 Alignment		27.6	26	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp

12	c3hkzY_	Alignment		26.8	21	PDB header: transferase Chain: Y; PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
13	c3iv1F_	Alignment		25.4	24	PDB header: hydrolase Chain: F; PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
14	c5knnG_	Alignment		25.0	17	PDB header: ligase Chain: G; PDB Molecule: alanine--trna ligase, cytoplasmic; PDBTitle: evolutionary gain of alanine mischarging to non-cognate trnas with a2 g4:u69 base pair
15	c3hkzZ_	Alignment		22.2	21	PDB header: transferase Chain: Z; PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
16	d1wtya_	Alignment		22.1	14	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Family 1 bi-partite nucleotidyltransferase subunit
17	c2wb1Q_	Alignment		21.9	32	PDB header: transcription Chain: Q; PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
18	c1f8aB_	Alignment		21.5	7	PDB header: isomerase Chain: B; PDB Molecule: peptidyl-prolyl cis-trans isomerase nima-interacting 1; PDBTitle: structural basis for the phosphoserine-proline recognition by group iv2 ww domains
19	c2gl2B_	Alignment		21.3	12	PDB header: cell adhesion Chain: B; PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
20	c2wb1J_	Alignment		21.1	32	PDB header: transcription Chain: J; PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
21	c3ucsB_	Alignment	not modelled	19.9	18	PDB header: chaperone Chain: B; PDB Molecule: chaperone-modulator protein cbpm; PDBTitle: crystal structure of the complex between cbpa j-domain and cbpm
22	c2dl1A_	Alignment	not modelled	17.9	14	PDB header: protein transport Chain: A; PDB Molecule: spartin; PDBTitle: solution structure of the mit domain from human spartin
23	c4h79A_	Alignment	not modelled	17.6	38	PDB header: dna binding protein Chain: A; PDB Molecule: crispr-associated protein, cse2 family; PDBTitle: crystal structure of casb from thermobifida fusca
24	c2lw1A_	Alignment	not modelled	17.3	15	PDB header: dna binding protein Chain: A; PDB Molecule: abc transporter atp-binding protein uup; PDBTitle: the c-terminal domain of the uup protein is a dna-binding coiled coil2 motif
25	c2krxA_	Alignment	not modelled	17.0	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: asl3597 protein; PDBTitle: solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
26	c2r5xA_	Alignment	not modelled	16.1	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein yugn from2 geobacillus kaustophilus hta426
27	c6g6hB_	Alignment	not modelled	16.1	18	PDB header: de novo protein Chain: B; PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
28	c6g6hE_	Alignment	not modelled	16.1	18	PDB header: de novo protein Chain: E; PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l

29	c6g6hD	Alignment	not modelled	16.1	18	PDB header: de novo protein Chain: D: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
30	c6g6hC	Alignment	not modelled	16.1	18	PDB header: de novo protein Chain: C: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
31	c6g6hA	Alignment	not modelled	16.1	18	PDB header: de novo protein Chain: A: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
32	c4ysvA	Alignment	not modelled	15.9	11	PDB header: isomerase Chain: A: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in apo-form
33	c1ic2B	Alignment	not modelled	15.9	16	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
34	c2ehwD	Alignment	not modelled	15.5	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein tthb059; PDBTitle: conserved hypothetical protein (tthb059) from thermo thermophilus hb8
35	c3pu2G	Alignment	not modelled	15.1	24	PDB header: structure genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.
36	c1eqfA	Alignment	not modelled	15.0	7	PDB header: transcription Chain: A: PDB Molecule: rna polymerase ii transcription initiation PDBTitle: crystal structure of the double bromodomain module from2 human tafii250
37	c2waqQ	Alignment	not modelled	13.9	24	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-directed rna2 polymerase
38	c4mjsQ	Alignment	not modelled	13.1	21	PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
39	d1mb6a	Alignment	not modelled	13.0	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
40	c5n9jG	Alignment	not modelled	12.7	13	PDB header: transcription Chain: G: PDB Molecule: mediator of rna polymerase ii transcription subunit 4; PDBTitle: core mediator of transcriptional regulation
41	d1niya	Alignment	not modelled	12.7	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
42	c5u07B	Alignment	not modelled	12.6	17	PDB header: immune system Chain: B: PDB Molecule: cse2; PDBTitle: crispr rna-guided surveillance complex
43	c4iwbA	Alignment	not modelled	12.5	9	PDB header: motor protein Chain: A: PDB Molecule: flic, flis chimera; PDBTitle: novel fold of flic/flis fusion protein
44	c6dmpB	Alignment	not modelled	12.1	22	PDB header: de novo protein Chain: B: PDB Molecule: designed orthogonal protein dhd13_xaaa_b; PDBTitle: de novo design of a protein heterodimer with specificity mediated by2 hydrogen bond networks
45	c2d9eA	Alignment	not modelled	11.8	16	PDB header: transcription Chain: A: PDB Molecule: peregrin; PDBTitle: solution structure of the bromodomain of peregrin
46	c4rodA	Alignment	not modelled	11.5	9	PDB header: transcription Chain: A: PDB Molecule: transcription factor iiib 50 kda subunit; PDBTitle: human tfiib-related factor 2 (brf2) and tpb bound to trnau1 promoter
47	c4b1pj	Alignment	not modelled	11.4	18	PDB header: transferase/dna Chain: J: PDB Molecule: rna polymerase subunit 13; PDBTitle: archaeal rnap-dna binary complex at 4.32ang
48	c4hpqE	Alignment	not modelled	11.4	19	PDB header: protein transport Chain: E: PDB Molecule: atg31; PDBTitle: crystal structure of the atg17-atg31-atg29 complex
49	c3q94B	Alignment	not modelled	11.2	14	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
50	c5we3A	Alignment	not modelled	11.1	33	PDB header: toxin Chain: A: PDB Molecule: beta-theraphotoxin-ps1a; PDBTitle: solution nmr structure of paurtx-3
51	d1m5ya3	Alignment	not modelled	11.1	18	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
52	c2lj4A	Alignment	not modelled	10.9	10	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase/rotamase, putative; PDBTitle: solution structure of the tbpin1
53	c4aybQ	Alignment	not modelled	10.9	18	PDB header: transferase Chain: Q: PDB Molecule: dna-directed rna polymerase; PDBTitle: rnap at 3.2ang
54	c1yw5A	Alignment	not modelled	10.9	10	PDB header: isomerase Chain: A: PDB Molecule: peptidyl prolyl cis/trans isomerase; PDBTitle: peptidyl-prolyl isomerase ess1 from candida albicans

55	c5lxoG	Alignment	not modelled	10.8	15	PDB header: structural protein Chain: G; PDB Molecule: transforming acidic coiled-coil-containing protein 3; PDBTitle: coiled-coil protein
56	c3mxzA	Alignment	not modelled	10.5	19	PDB header: chaperone Chain: A; PDB Molecule: tubulin-specific chaperone a; PDBTitle: crystal structure of tubulin folding cofactor a from arabidopsis2 thaliana
57	c5epmC	Alignment	not modelled	10.4	57	PDB header: toxin/immune system Chain: C; PDB Molecule: beta-theraphotoxin-cm1a; PDBTitle: ceratotoxin variant in complex with specific antibody fab fragment
58	c4eijA	Alignment	not modelled	10.2	24	PDB header: replication Chain: A; PDB Molecule: p protein; PDBTitle: structure of the mumps virus phosphoprotein oligomerization domain
59	c3epyA	Alignment	not modelled	10.0	27	PDB header: lipid binding protein Chain: A; PDB Molecule: acyl-coa-binding domain-containing protein 7; PDBTitle: crystal structure of human acyl-coa binding domain 7 complexed with2 palmitoyl-coa
60	c4merD	Alignment	not modelled	10.0	5	PDB header: unknown function Chain: D; PDB Molecule: streptococcal histidine-rich glycoprotein interacting PDBTitle: crystal structure of the novel protein and virulence factor ship2 (q99xu0) from streptococcus pyogenes
61	c4uotD	Alignment	not modelled	9.8	18	PDB header: de novo protein Chain: D; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
62	c4uotC	Alignment	not modelled	9.8	18	PDB header: de novo protein Chain: C; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
63	c4uotA	Alignment	not modelled	9.8	18	PDB header: de novo protein Chain: A; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
64	c4uotE	Alignment	not modelled	9.8	18	PDB header: de novo protein Chain: E; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
65	c4uotB	Alignment	not modelled	9.8	18	PDB header: de novo protein Chain: B; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
66	d1wwma1	Alignment	not modelled	9.6	20	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: TENA/THI-4
67	d2ftsa2	Alignment	not modelled	9.6	7	Fold: MoeA N-terminal region -like Superfamily: MoeA N-terminal region -like Family: MoeA N-terminal region -like
68	d1uz5a2	Alignment	not modelled	9.5	7	Fold: MoeA N-terminal region -like Superfamily: MoeA N-terminal region -like Family: MoeA N-terminal region -like
69	c4b1oQ	Alignment	not modelled	9.4	18	PDB header: transferase/dna Chain: Q; PDB Molecule: rrna polymerase subunit 13; PDBTitle: archaeal rnap-dna binary complex at 4.32ang
70	c6dmpA	Alignment	not modelled	9.4	21	PDB header: de novo protein Chain: A; PDB Molecule: designed orthogonal protein dhd13_xaaa_a; PDBTitle: de novo design of a protein heterodimer with specificity mediated by2 hydrogen bond networks
71	c5jzB	Alignment	not modelled	9.3	22	PDB header: transferase Chain: B; PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfct in complex with ecfca mutant e28g
72	c5jzF	Alignment	not modelled	9.3	22	PDB header: transferase Chain: F; PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfct in complex with ecfca mutant e28g
73	c3ctwB	Alignment	not modelled	9.0	35	PDB header: protein binding Chain: B; PDB Molecule: rcda; PDBTitle: crystal structure of rcda from caulobacter crescentus cb15
74	d1riqa1	Alignment	not modelled	9.0	20	Fold: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Superfamily: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Family: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
75	c3elfA	Alignment	not modelled	8.5	10	PDB header: lyase Chain: A; PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
76	c4wvmB	Alignment	not modelled	8.5	2	PDB header: toxin Chain: B; PDB Molecule: stonustoxin subunit beta; PDBTitle: stonustoxin structure
77	c5tosB	Alignment	not modelled	8.5	16	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase bik1; PDBTitle: botrytis-induced kinase 1 (bik1) from arabidopsis thaliana
78	c1u2uA	Alignment	not modelled	8.3	23	PDB header: transcription Chain: A; PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
79	c4amqA	Alignment	not modelled	8.3	15	PDB header: transferase Chain: A; PDB Molecule: i544; PDBTitle: a megaviridae orfan gene encodes a new nucleotidyl

						transferase
80	c3cmaG_	Alignment	not modelled	8.2	23	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: the structure of cca and cca-phe-cap-bio bound to the large ribosomal2 subunit of haloarcula marismortui
81	c2iswB_	Alignment	not modelled	8.2	14	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
82	c3u0cA_	Alignment	not modelled	8.0	10	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipab; PDBTitle: crystal structure of n-terminal region of type iii secretion first2 translocator ipab (residues 74-224)
83	d1j6ya_	Alignment	not modelled	8.0	8	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
84	c5jffD_	Alignment	not modelled	7.8	22	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfct mutant g55r in complex with ecfca
85	c5uyvA_	Alignment	not modelled	7.8	25	PDB header: de novo protein Chain: A: PDB Molecule: heeh_rd4_0097; PDBTitle: solution nmr structure of the de novo mini protein heeh_rd4_0097
86	c6btvA_	Alignment	not modelled	7.8	57	PDB header: toxin Chain: A: PDB Molecule: beta-theraphotoxin-cm1b; PDBTitle: solution nmr structures for ccotx-ii
87	c3cd0B_	Alignment	not modelled	7.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxy-3-methylglutaryl-coenzyme a reductase; PDBTitle: thermodynamic and structure guided design of statin hmg-coa reductase2 inhibitors
88	d2cpta1	Alignment	not modelled	7.4	17	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
89	d1dqaa4	Alignment	not modelled	7.4	20	Fold: Substrate-binding domain of HMG-CoA reductase Superfamily: Substrate-binding domain of HMG-CoA reductase Family: Substrate-binding domain of HMG-CoA reductase
90	d1gvfa_	Alignment	not modelled	7.3	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
91	c3l32B_	Alignment	not modelled	7.3	30	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
92	d1dosa_	Alignment	not modelled	7.3	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
93	c3cmeG_	Alignment	not modelled	7.3	24	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: the structure of ca and cca-phe-cap-bio bound to the large ribosomal2 subunit of haloarcula marismortui
94	c6ofuC_	Alignment	not modelled	7.3	17	PDB header: lyase Chain: C: PDB Molecule: ydji aldolase; PDBTitle: x-ray crystal structure of the ydji aldolase from escherichia coli k12
95	c1junB_	Alignment	not modelled	7.2	18	PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
96	c5h3iC_	Alignment	not modelled	7.2	18	PDB header: lipid binding protein Chain: C: PDB Molecule: putative acyl-coa-binding protein; PDBTitle: crystal structure of oryza sativa acyl-coa-binding protein 2
97	c2mt7A_	Alignment	not modelled	7.1	43	PDB header: toxin Chain: A: PDB Molecule: hs1a; PDBTitle: solution structure of spider-venom peptide hs1a
98	c4zmiA_	Alignment	not modelled	7.1	30	PDB header: dna binding protein Chain: A: PDB Molecule: telomere length regulator taz1; PDBTitle: crystal structure of the helical domain of s. pombe taz1
99	c4pn8C_	Alignment	not modelled	7.1	13	PDB header: de novo protein Chain: C: PDB Molecule: cc-pent; PDBTitle: a de novo designed pentameric coiled coil cc-pent.