









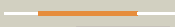





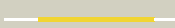


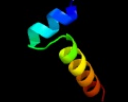


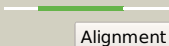

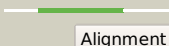

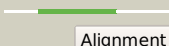

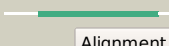
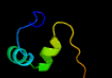
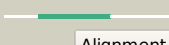

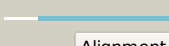






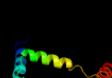
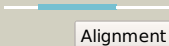
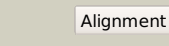
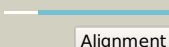
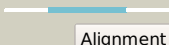
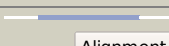
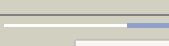
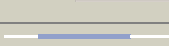
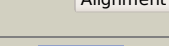


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1398c_(-)_1574516_1574773
Date	Wed Jul 31 22:05:50 BST 2019
Unique Job ID	8c7e9335cb31a0f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	 Alignment		98.0	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	c1q5vB_	 Alignment		93.7	40	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
3	c2ca9B_	 Alignment		92.7	28	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
4	d2bj7a1	 Alignment		92.7	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
5	c2bj3D_	 Alignment		91.7	23	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
6	c5x3tA_	 Alignment		89.4	36	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vappbc from mycobacterium tuberculosis
7	d2hzab1	 Alignment		86.2	38	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
8	d2hzaa1	 Alignment		85.0	38	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	c3kk4B_	 Alignment		75.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
10	c3h87D_	 Alignment		69.9	50	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
11	d2bsqe1	 Alignment		58.1	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like

12	c1ea4K	 Alignment		56.3	34	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
13	d2cpga	 Alignment		56.3	34	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
14	c2mdvB	 Alignment		52.8	35	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
15	c2oviA	 Alignment		45.5	24	PDB header: ligand binding protein, metal transport Chain: A: PDB Molecule: hypothetical protein chux; PDBTitle: structure of the heme binding protein chux
16	c2zp2B	 Alignment		41.1	21	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
17	c2ph0A	 Alignment		39.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
18	c6noyB	 Alignment		38.8	21	PDB header: structural protein Chain: B: PDB Molecule: maintenance of carboxysome positioning b protein, mcsb; PDBTitle: structure of cyanothecce mcdb
19	c6cetM	 Alignment		37.9	32	PDB header: signaling protein Chain: M: PDB Molecule: gator complex protein nprl3; PDBTitle: cryo-em structure of gator1
20	c2h1oH	 Alignment		37.3	27	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
21	d2phcb1	 Alignment	not modelled	35.4	16	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
22	c5dudB	 Alignment	not modelled	33.1	19	PDB header: unknown function Chain: B: PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk
23	c5exvD	 Alignment	not modelled	32.1	15	PDB header: heme-binding protein Chain: D: PDB Molecule: hemin-degrading hems.chux domain protein; PDBTitle: crystal structure of heme binding protein hutx from vibrio cholerae
24	d1kska3	 Alignment	not modelled	30.1	45	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
25	c2k29A	 Alignment	not modelled	26.7	26	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
26	c4ayaA	 Alignment	not modelled	21.9	38	PDB header: cell cycle Chain: A: PDB Molecule: dna-binding protein inhibitor id-2; PDBTitle: crystal structure of id2 hlh homodimer at 2.1a resolution
27	c6g1nB	 Alignment	not modelled	21.7	18	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
28	c1x93B	 Alignment	not modelled	21.6	32	PDB header: transcription Chain: B: PDB Molecule: hypothetical protein hp0222; PDBTitle: nmr structure of helicobacter pylori hp0222
						Fold: Ribbon-helix-helix

29	d1x93a1	Alignment	not modelled	21.6	32	Superfamily: Ribbon-helix-helix Family: CopG-like
30	c2zdgA	Alignment	not modelled	19.5	39	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
31	c2phcB	Alignment	not modelled	19.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
32	c6qeqD	Alignment	not modelled	17.0	15	PDB header: dna binding protein Chain: D: PDB Molecule: pcff; PDBTitle: pcff from enterococcus faecalis pcf10
33	c4me7E	Alignment	not modelled	16.3	33	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
34	c3ebnD	Alignment	not modelled	15.8	26	PDB header: hydrolase Chain: D: PDB Molecule: replicase polyprotein 1ab; PDBTitle: a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping
35	c4cimP	Alignment	not modelled	15.6	50	PDB header: apoptosis Chain: P: PDB Molecule: bcl-2-like protein 2; PDBTitle: complex of a bcl-w bh3 mutant with a bh3 domain
36	c4cimQ	Alignment	not modelled	15.6	50	PDB header: apoptosis Chain: Q: PDB Molecule: bcl-2-like protein 2; PDBTitle: complex of a bcl-w bh3 mutant with a bh3 domain
37	c4q2uM	Alignment	not modelled	14.2	18	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
38	c3se7A	Alignment	not modelled	13.7	30	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
39	c3mkyP	Alignment	not modelled	11.1	29	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
40	c1zgwA	Alignment	not modelled	11.0	36	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
41	c2pn0D	Alignment	not modelled	10.0	13	PDB header: transcription Chain: D: PDB Molecule: prokaryotic transcription elongation factor PDBTitle: prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
42	c2an7A	Alignment	not modelled	9.6	32	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
43	c2a8vA	Alignment	not modelled	9.6	25	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
44	c2ypbB	Alignment	not modelled	9.1	21	PDB header: immune system Chain: B: PDB Molecule: transcription factor e2-alpha; PDBTitle: structure of the scl:e47 complex bound to dna
45	d1bl0a1	Alignment	not modelled	9.1	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
46	d1uklc	Alignment	not modelled	8.8	36	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
47	c4athB	Alignment	not modelled	8.3	33	PDB header: dna binding protein Chain: B: PDB Molecule: microphthalmia-associated transcription factor; PDBTitle: mitf apo structure
48	c5j3nA	Alignment	not modelled	7.4	23	PDB header: hydrolase Chain: A: PDB Molecule: green fluorescent protein,hsdr; PDBTitle: c-terminal domain of ecor124i hsdR subunit fused with the ph-sensitive2 gfp variant ratiometric phluorin
49	c2krxA	Alignment	not modelled	7.4	22	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.
50	c6a7vU	Alignment	not modelled	7.2	39	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
51	d2hq2a1	Alignment	not modelled	7.1	14	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
52	c2o1sC	Alignment	not modelled	7.0	15	PDB header: transferase Chain: C: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
53	d2fi0a1	Alignment	not modelled	6.9	22	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
54	c2lfhA	Alignment	not modelled	6.9	40	PDB header: dna binding protein inhibitor Chain: A: PDB Molecule: dna-binding protein inhibitor id-3; PDBTitle: solution nmr structure of the helix-loop-helix domain of human id32 protein, northeast structural genomics consortium target hr3111a
55	c2jgdA	Alignment	not modelled	6.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-oxoglutarate dehydrogenase e1 component;

						PDBTitle: e. coli 2-oxoglutarate dehydrogenase (e1o)
56	c4fxeB_	Alignment	not modelled	6.8	26	PDB header: toxin/toxin inhibitor Chain: B; PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
57	c5ukhA_	Alignment	not modelled	6.4	45	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of telc from streptococcus intermedius b196
58	c3mkzU_	Alignment	not modelled	6.4	29	PDB header: dna-binding protein/dna Chain: U; PDB Molecule: protein sopb; PDBTitle: structure of sopb(155-272)-18mer complex, p21 form
59	c5gnjI_	Alignment	not modelled	6.2	29	PDB header: dna binding protein/dna Chain: I; PDB Molecule: transcription factor myc2; PDBTitle: structure of a transcription factor and dna complex
60	c5z08C_	Alignment	not modelled	6.1	27	PDB header: cell cycle Chain: C; PDB Molecule: cenp-k; PDBTitle: the crystal structure of kinetochore subunits cenp-h//k triple2 complex
61	c4egjD_	Alignment	not modelled	6.1	29	PDB header: ligase Chain: D; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
62	c5dmxC_	Alignment	not modelled	6.1	29	PDB header: ligase Chain: C; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
63	c5ytpA_	Alignment	not modelled	6.0	39	PDB header: dna binding protein Chain: A; PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 I34a from thermus thermophilus hb8
64	c3u5vA_	Alignment	not modelled	6.0	21	PDB header: transcription Chain: A; PDB Molecule: protein max, transcription factor e2-alpha chimera; PDBTitle: crystal structure of max-e47
65	c4dg7D_	Alignment	not modelled	5.9	28	PDB header: dna binding protein Chain: D; PDB Molecule: gm27569p; PDBTitle: low resolution structure of drosophila translin
66	c3lfb_	Alignment	not modelled	5.9	24	PDB header: transferase Chain: B; PDB Molecule: phosphotransferase system, mannose/fructose/n- PDBTitle: crystal structure of manxb from thermoanaerobacter tengcongensis
67	d2gmga1	Alignment	not modelled	5.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like
68	d1an4a_	Alignment	not modelled	5.6	18	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
69	c3r23B_	Alignment	not modelled	5.5	25	PDB header: ligase Chain: B; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
70	c2wtth_	Alignment	not modelled	5.5	22	PDB header: transcription Chain: H; PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal form ii)
71	d2fnoa2	Alignment	not modelled	5.4	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
72	d1hr6a1	Alignment	not modelled	5.4	18	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
73	c4luqB_	Alignment	not modelled	5.4	40	PDB header: protein binding/toxin inhibitor Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of virulence effector tse3 in complex with2 neutralizer tsi3
74	c5x3hA_	Alignment	not modelled	5.3	26	PDB header: dna binding protein Chain: A; PDB Molecule: uracil-dna glycosylase; PDBTitle: the y81g mutant of the ung crystal structure from nitratifactor2 salsuginis