
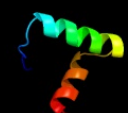



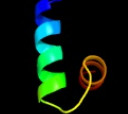






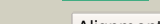







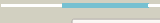



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0662c_(-)_755772_756026
Date	Fri Jul 26 01:50:23 BST 2019
Unique Job ID	7b8aabc26ab57889

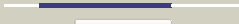


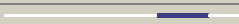
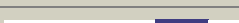

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	 Alignment		93.5	29	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	c5x3tA_	 Alignment		91.7	43	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis
3	c4hv0B_	 Alignment		62.1	26	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
4	c6a6xC_	 Alignment		59.4	40	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
5	c1efaA_	 Alignment		48.0	34	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
6	d1p94a_	 Alignment		46.1	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	d1lcda_	 Alignment		43.9	34	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
8	c2rbfB_	 Alignment		41.7	29	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
9	c2lcvA_	 Alignment		40.3	34	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
10	c1bdhA_	 Alignment		39.6	25	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
11	d2bjca1	 Alignment		37.2	41	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator

12	c6iyaD_	Alignment		36.4	32	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
13	c3h5tA_	Alignment		36.3	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
14	c1zvva_	Alignment		30.4	44	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
15	c1ea4K_	Alignment		27.6	26	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
16	d2cpga_	Alignment		27.6	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
17	c2an7A_	Alignment		27.5	22	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
18	c2l8nA_	Alignment		26.2	34	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
19	c2elhA_	Alignment		26.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
20	c6qeqD_	Alignment		26.1	15	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcf from enterococcus faecalis pcf10
21	d1jhga_	Alignment	not modelled	25.0	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
22	c1lbgB_	Alignment	not modelled	24.7	34	PDB header: PDB COMPND:
23	c4i98C_	Alignment	not modelled	24.6	25	PDB header: cell cycle Chain: C: PDB Molecule: segregation and condensation protein b; PDBTitle: crystal structure of the complex between scpa(residues 1-160)-2 scpb(residues 1-183)
24	d2hsga1	Alignment	not modelled	24.5	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
25	c2zi0B_	Alignment	not modelled	24.2	21	PDB header: gene regulation/rna Chain: B: PDB Molecule: protein 2b; PDBTitle: crystal structure of tav2b/sirna complex
26	d1qpza1	Alignment	not modelled	23.8	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
27	c3kxD_	Alignment	not modelled	23.1	38	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
28	c3w6jC_	Alignment	not modelled	22.6	31	PDB header: cell cycle Chain: C: PDB Molecule: scpb; PDBTitle: crystal structure of scpab core complex
29	c3cz3B_	Alignment	not modelled	22.1	21	PDB header: viral protein/rna Chain: B: PDB Molecule: protein 2b;

29	c0c2jB_	Alignment	not modelled	22.1	41	PDBTitle: crystal structure of tomato aspermy virus 2b in complex with sirna
30	d1efaa1	Alignment	not modelled	21.9	34	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
31	d1qw2a_	Alignment	not modelled	20.8	27	Fold: Hypothetical protein Ta1206 Superfamily: Hypothetical protein Ta1206 Family: Hypothetical protein Ta1206
32	d2ezha_	Alignment	not modelled	20.2	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
33	d1t6sa2	Alignment	not modelled	19.6	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ScpB/YpuH-like
34	c3t2dA_	Alignment	not modelled	19.6	29	PDB header: lyase, hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphate aldolase/phosphatase; PDBTitle: fructose-1,6-bisphosphate aldolase/phosphatase from thermoproteus2 neutrophilus, fbp-bound form
35	c5syszA_	Alignment	not modelled	19.5	38	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
36	c2h1oH_	Alignment	not modelled	19.2	28	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
37	d2bsqe1	Alignment	not modelled	18.6	28	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
38	c5ytpA_	Alignment	not modelled	16.4	40	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 I34a from thermus thermophilus hb8
39	c6bwqB_	Alignment	not modelled	15.3	22	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
40	c1t6sB_	Alignment	not modelled	14.7	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
41	c3frwF_	Alignment	not modelled	13.8	26	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
42	c3t97B_	Alignment	not modelled	13.7	50	PDB header: protein transport Chain: B: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
43	c2dg6A_	Alignment	not modelled	13.6	29	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
44	d2ezia_	Alignment	not modelled	12.9	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
45	c2z99A_	Alignment	not modelled	12.5	42	PDB header: cell cycle Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of scpb from mycobacterium tuberculosis
46	c2bj3D_	Alignment	not modelled	11.4	18	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
47	d1hlva1	Alignment	not modelled	11.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
48	c3c19A_	Alignment	not modelled	10.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
49	d1q9ja2	Alignment	not modelled	10.3	29	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
50	c5y6iB_	Alignment	not modelled	10.2	30	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
51	c3oiqB_	Alignment	not modelled	10.0	54	PDB header: protein binding Chain: B: PDB Molecule: dna polymerase alpha catalytic subunit a; PDBTitle: crystal structure of yeast telomere protein cdc13 ob1 and the2 catalytic subunit of dna polymerase alpha pol1
52	c2yomA_	Alignment	not modelled	9.5	67	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
53	d1o8ba2	Alignment	not modelled	9.5	15	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
54	c5oooA_	Alignment	not modelled	9.2	38	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein ns-s; PDBTitle: structure of the rift valley fever virus nss protein core domain PDB header: transcription

55	c4qpoB	Alignment	not modelled	8.6	14	Chain: B; PDB Molecule: relaxosome protein tram; PDBTitle: mechanistic basis of plasmid-specific dna binding of the f plasmid2 regulatory protein, tram
56	c4g7xB	Alignment	not modelled	8.5	12	PDB header: protein binding/protein binding Chain: B; PDB Molecule: tola protein; PDBTitle: crystal structure of a complex between the ctxphi piii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
57	d1j5ya1	Alignment	not modelled	8.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
58	c3sr2A	Alignment	not modelled	8.2	42	PDB header: dna binding protein/protein binding Chain: A; PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of human xlf-xrcc4 complex
59	d2pnwa1	Alignment	not modelled	8.1	23	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
60	d1uxda	Alignment	not modelled	8.0	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
61	d2ay0a1	Alignment	not modelled	7.9	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
62	d1lk5a2	Alignment	not modelled	7.9	25	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
63	d1gz0f2	Alignment	not modelled	7.7	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
64	c6j07B	Alignment	not modelled	7.6	44	PDB header: dna binding protein Chain: B; PDB Molecule: telomere repeats-binding bouquet formation protein 1; PDBTitle: crystal structure of human terb2 and terb1
65	d1rh5c	Alignment	not modelled	7.5	67	Fold: Single transmembrane helix Superfamily: Sec-beta subunit Family: Sec-beta subunit
66	c1rh5C	Alignment	not modelled	7.5	67	PDB header: protein transport Chain: C; PDB Molecule: secbeta; PDBTitle: the structure of a protein conducting channel
67	d2bj7a1	Alignment	not modelled	7.4	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
68	c1q5vB	Alignment	not modelled	7.2	24	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
69	c3omyB	Alignment	not modelled	6.4	19	PDB header: dna binding protein Chain: B; PDB Molecule: protein tram; PDBTitle: crystal structure of the ped208 tram n-terminal domain
70	d1z6ra1	Alignment	not modelled	6.4	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
71	d1qd1a2	Alignment	not modelled	6.3	27	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
72	c5kwpA	Alignment	not modelled	6.2	45	PDB header: de novo protein Chain: A; PDB Molecule: designed peptide nc_eeh_d2; PDBTitle: nmr solution structure of designed peptide nc_eeh_d2
73	c5mrwG	Alignment	not modelled	6.2	29	PDB header: hydrolase Chain: G; PDB Molecule: potassium-transporting atpase kdpcc subunit; PDBTitle: structure of the kdpfabc complex
74	d1uj4a2	Alignment	not modelled	6.0	20	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
75	d2iqha1	Alignment	not modelled	6.0	39	Fold: Flu NP-like Superfamily: flu NP-like Family: Flu NP-like
76	c2ctoA	Alignment	not modelled	5.9	54	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein fj14904
77	d1jr3a1	Alignment	not modelled	5.9	38	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
78	c2jrwA	Alignment	not modelled	5.8	50	PDB header: immune system Chain: A; PDB Molecule: cyclic extended pep.1; PDBTitle: solution structure of cyclic extended pep1(cyc.ext.pep.1)2 for autoimmune myasthenia gravis
79	c2vt1B	Alignment	not modelled	5.8	28	PDB header: membrane protein Chain: B; PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structure of the cytoplasmic domain of spa40, the specificity2 switch for the shigella flexneri type iii secretion system
80	c3kk4B	Alignment	not modelled	5.7	14	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
81	d1gz0a2	Alignment	not modelled	5.7	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain

82	c2ymnE_	 Alignment	not modelled	5.6	39	PDB header: viral protein Chain: E: PDB Molecule: nucleoprotein; PDBTitle: organization of the influenza virus replication machinery
83	d1pjqa1	 Alignment	not modelled	5.6	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
84	d1trra_	 Alignment	not modelled	5.6	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
85	d1m0sa2	 Alignment	not modelled	5.2	35	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
86	c6eepA_	 Alignment	not modelled	5.1	29	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
87	c3korD_	 Alignment	not modelled	5.1	26	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus