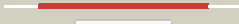

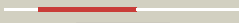









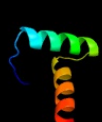





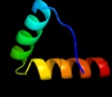









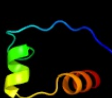

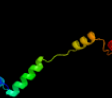
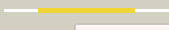


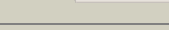
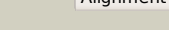


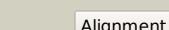



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2547 (-)_2868616_2868873
Date	Wed Aug 7 12:50:18 BST 2019
Unique Job ID	36ac629c11c745e6

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	 Alignment		99.9	25	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	c2bj3D_	 Alignment		97.7	27	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nkr-apo
3	d2bj7a1	 Alignment		97.7	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	c2ca9B_	 Alignment		97.6	34	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
5	c1q5vB_	 Alignment		97.6	34	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
6	c4me7E_	 Alignment		97.3	20	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
7	d2hzaa1	 Alignment		97.0	33	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
8	d2hzab1	 Alignment		96.5	36	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	c5x3tA_	 Alignment		95.6	34	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vappbc from mycobacterium tuberculosis
10	c1ea4K_	 Alignment		94.9	30	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
11	d2cpga_	 Alignment		94.9	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

12	c2k9iB_	 Alignment		93.2	25	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from <i>sulfolobus2 islandicus</i>
13	c6iyaD_	 Alignment		93.1	18	PDB header: antitoxin Chain: D: PDB Molecule: transcriptional regulator copg family; PDBTitle: structure of the dna binding domain of antitoxin copaso
14	c2rbfB_	 Alignment		92.0	24	PDB header: oxidoreductase/dna Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of the ribbon-helix-helix domain of <i>escherichia coli</i> puta2 (puta52) complexed with operator dna (o2)
15	c6g1nB_	 Alignment		89.4	24	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
16	c4p7dA_	 Alignment		88.7	16	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
17	c6qeqD_	 Alignment		84.6	21	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcff from <i>enterococcus faecalis</i> pcf10
18	c5cegC_	 Alignment		84.3	21	PDB header: toxin Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from <i>mesorhizobium2 opportunistum</i>
19	c5yrzC_	 Alignment		83.1	19	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from <i>streptococcus pneumoniae</i>
20	c3h87D_	 Alignment		81.9	28	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from <i>mycobacterium tuberculosis</i>
21	c2kelB_	 Alignment	not modelled	79.2	13	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
22	d2bsqe1	 Alignment	not modelled	76.6	14	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
23	c2an7A_	 Alignment	not modelled	74.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
24	c2mdvB_	 Alignment	not modelled	71.3	33	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
25	c3kk4B_	 Alignment	not modelled	64.5	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from <i>bordetella pertussis</i> tohama i
26	c2h1oH_	 Alignment	not modelled	64.2	15	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
27	d2ay0a1	 Alignment	not modelled	62.0	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
28	c3kxeD_	 Alignment	not modelled	54.5	29	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
29	c4f1dA_	 Alignment	not modelled	42.5	13	PDB header: protein binding Chain: A: PDB Molecule: regulation of nuclear pre-mrna domain-

29	c4nuA	Alignment	not modelled	42.5	13	containing protein PDBTitle: cid of human rprd1b
30	c6gtsC	Alignment	not modelled	41.8	20	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
31	d1p94a	Alignment	not modelled	41.1	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
32	c6a7vU	Alignment	not modelled	37.2	18	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
33	c1kcfB	Alignment	not modelled	36.3	46	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
34	c6ajnF	Alignment	not modelled	35.3	21	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
35	c4uj3B	Alignment	not modelled	34.9	20	PDB header: transport protein Chain: B: PDB Molecule: rab-3a-interacting protein; PDBTitle: crystal structure of human rab11-rabin8-fip3
36	c2xv9A	Alignment	not modelled	33.5	22	PDB header: lipid binding protein Chain: A: PDB Molecule: aba-1a1 repeat unit; PDBTitle: the solution structure of aba-1a saturated with oleic acid
37	c4flbA	Alignment	not modelled	32.4	11	PDB header: protein binding Chain: A: PDB Molecule: regulation of nuclear pre-mrna domain-containing protein 2; PDBTitle: cid of human rprd2
38	d1y9ba1	Alignment	not modelled	20.9	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
39	c2q2kA	Alignment	not modelled	20.0	19	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
40	c2q2kB	Alignment	not modelled	19.8	19	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
41	c3cliA	Alignment	not modelled	19.1	16	PDB header: rna binding protein Chain: A: PDB Molecule: protein nrd1; PDBTitle: structure of the rna polymerase ii ctd-interacting domain of nrd1
42	c5ce7A	Alignment	not modelled	18.7	3	PDB header: transcription Chain: A: PDB Molecule: ctd kinase subunit gamma; PDBTitle: structure of a non-canonical cid of ctk3
43	c4xvzB	Alignment	not modelled	17.9	28	PDB header: transferase Chain: B: PDB Molecule: mycinamicin iii 3''-o-methyltransferase; PDBTitle: mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
44	c6gygA	Alignment	not modelled	16.1	14	PDB header: transcription Chain: A: PDB Molecule: transcription regulator reg576; PDBTitle: x-ray structure of the apo form of the establishment gene regulator2 reg576 of the g+ plasmid p576
45	d1omha	Alignment	not modelled	15.5	15	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain
46	c4hv0B	Alignment	not modelled	15.1	34	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
47	c6a6xC	Alignment	not modelled	14.7	21	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
48	c2mc0A	Alignment	not modelled	14.3	18	PDB header: transcription activator/antibiotic Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: structural basis of a thiopeptide antibiotic multidrug resistance2 system from streptomyces lividans:nosiheptide in complex with tipas
49	c5mdtA	Alignment	not modelled	14.2	12	PDB header: transcription Chain: A: PDB Molecule: rpb7-binding protein seb1; PDBTitle: structure of the ctd-interacting domain (cid) of seb1 from s. pombe.
50	c1jqoA	Alignment	not modelled	13.7	35	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
51	d1jqoa	Alignment	not modelled	13.7	35	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
52	d1jqna	Alignment	not modelled	12.8	36	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
53	c5ytpA	Alignment	not modelled	12.8	46	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 l34a from thermus thermophilus hb8
54	d1q9ja2	Alignment	not modelled	12.2	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
55	d2fm9a1	Alignment	not modelled	11.4	21	Fold: SipA N-terminal domain-like Superfamily: SipA N-terminal domain-like Family: SipA N-terminal domain-like

56	c5nygF_	Alignment	not modelled	10.3	15	PDB header: hydrolase Chain: F: PDB Molecule: anbu; PDBTitle: anbu (gly-1) mutant from hyphomicrobium sp. strain mc1 - sg p2(1)2(1)2 2(1)
57	c2qhoB_	Alignment	not modelled	9.9	55	PDB header: protein binding/ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase edd1; PDBTitle: crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
58	c4errB_	Alignment	not modelled	9.8	17	PDB header: protein binding Chain: B: PDB Molecule: autotransporter adhesin; PDBTitle: 1.55 angstrom crystal structure of the four helical bundle membrane2 localization domain (4hbm) of the vibrio vulnificus marx effector3 domain duf5
59	c1m46B_	Alignment	not modelled	9.7	36	PDB header: cell cycle protein Chain: B: PDB Molecule: iq4 motif from myo2p, a class v myosin; PDBTitle: crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
60	d2ebfx1	Alignment	not modelled	9.7	27	Fold: PMT central region-like Superfamily: PMT central region-like Family: PMT central region-like
61	c1r8jB_	Alignment	not modelled	9.7	23	PDB header: circadian clock protein Chain: B: PDB Molecule: kaia; PDBTitle: crystal structure of circadian clock protein kaia from2 synechococcus elongatus
62	d2fm8c1	Alignment	not modelled	9.5	21	Fold: SipA N-terminal domain-like Superfamily: SipA N-terminal domain-like Family: SipA N-terminal domain-like
63	c2qhoF_	Alignment	not modelled	9.5	55	PDB header: protein binding/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase edd1; PDBTitle: crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
64	c2wk1A_	Alignment	not modelled	9.0	31	PDB header: transferase Chain: A: PDB Molecule: novp; PDBTitle: structure of the o-methyltransferase novp
65	c2kkeA_	Alignment	not modelled	8.6	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
66	c2kkeB_	Alignment	not modelled	8.6	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
67	c3eabK_	Alignment	not modelled	8.5	47	PDB header: cell cycle Chain: K: PDB Molecule: chmp1b; PDBTitle: crystal structure of spastin mit in complex with escrt iii
68	c2lkyA_	Alignment	not modelled	8.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
69	c3f4mA_	Alignment	not modelled	8.3	12	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor, alpha-induced protein 8- PDBTitle: crystal structure of tipe2
70	d2proc1	Alignment	not modelled	8.2	38	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
71	c1ny9A_	Alignment	not modelled	8.1	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator tipa-s; PDBTitle: antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator
72	d1ny9a_	Alignment	not modelled	8.1	17	Fold: Antibiotic binding domain of TipA-like multidrug resistance regulators Superfamily: Antibiotic binding domain of TipA-like multidrug resistance regulators Family: Antibiotic binding domain of TipA-like multidrug resistance regulators
73	c5us5B_	Alignment	not modelled	7.9	11	PDB header: structural genomics Chain: B: PDB Molecule: upf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
74	c3g5oC_	Alignment	not modelled	7.7	6	PDB header: toxin/antitoxin Chain: C: PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
75	d2g6ta1	Alignment	not modelled	7.7	27	Fold: CAC2185-like Superfamily: CAC2185-like Family: CAC2185-like
76	c2kvcA_	Alignment	not modelled	7.6	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
77	d1cuka1	Alignment	not modelled	7.5	28	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
78	c5b7jA_	Alignment	not modelled	7.3	29	PDB header: dna binding protein/dna Chain: A: PDB Molecule: switch-activating protein 1; PDBTitle: structure model of sap1-dna complex
79	d2je6b2	Alignment	not modelled	7.2	19	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
						PDB header: transcription regulator

80	c2km4A_	Alignment	not modelled	7.1	13	Chain: A: PDB Molecule: regulator of ty1 transposition protein 103; PDBTitle: solution structure of rtt103 ctd interacting domain
81	c2kp6A_	Alignment	not modelled	6.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein cv0237 from chromobacterium2 violaceum. northeast structural genomics consortium (nesg) target3 cvt1
82	c3bbnl_	Alignment	not modelled	6.3	17	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein s9; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
83	c3p3vB_	Alignment	not modelled	6.1	15	PDB header: transferase Chain: B: PDB Molecule: pts system, n-acetylgalactosamine-specific iib component; PDBTitle: crystal structure of a pts dependent n-acetyl-galactosamine-iib2 component (agav, spy_0631) from streptococcus pyogenes at 1.65 a3 resolution
84	d2vqei1	Alignment	not modelled	6.0	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
85	d1hh1a_	Alignment	not modelled	6.0	26	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
86	c3jc6E_	Alignment	not modelled	6.0	27	PDB header: replication Chain: E: PDB Molecule: cell division control protein 45; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
87	d1g0wa1	Alignment	not modelled	5.9	20	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
88	c2k29A_	Alignment	not modelled	5.7	15	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
89	c4zvdA_	Alignment	not modelled	5.7	15	PDB header: signaling protein Chain: A: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of mid domain of the e. coli dosc - form ii
90	d1ulva1	Alignment	not modelled	5.6	8	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
91	c5cdjA_	Alignment	not modelled	5.5	45	PDB header: chaperone Chain: A: PDB Molecule: rubisco large subunit-binding protein subunit alpha, PDBTitle: apical domain of chloroplast chaperonin 60a
92	d1qh4a1	Alignment	not modelled	5.5	17	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
93	c4rv0H_	Alignment	not modelled	5.4	27	PDB header: protein binding, transport protein Chain: H: PDB Molecule: nuclear protein localization protein 4 homolog; PDBTitle: crystal structure of tn complex
94	c4zriD_	Alignment	not modelled	5.4	38	PDB header: signaling protein/transferase Chain: D: PDB Molecule: serine/threonine-protein kinase lats2; PDBTitle: crystal structure of merlin-ferm and lats2
95	c4wbeB_	Alignment	not modelled	5.3	31	PDB header: rna binding protein Chain: B: PDB Molecule: caprin-1; PDBTitle: crystal structure of the hr-1 domain of human caprin-1 in the c1212 space group
96	c4zriC_	Alignment	not modelled	5.3	38	PDB header: signaling protein/transferase Chain: C: PDB Molecule: serine/threonine-protein kinase lats2; PDBTitle: crystal structure of merlin-ferm and lats2
97	d1nrza_	Alignment	not modelled	5.2	18	Fold: PTS Iib component Superfamily: PTS Iib component Family: PTS Iib component
98	d1sjpa2	Alignment	not modelled	5.2	64	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
99	d2fug11	Alignment	not modelled	5.1	12	Fold: Bromodomain-like Superfamily: Nqo1C-terminal domain-like Family: Nqo1C-terminal domain-like