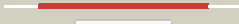



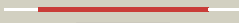






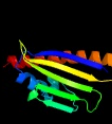














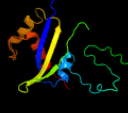
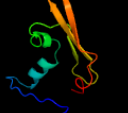





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2186c (-)_2447613_2448002
Date	Mon Aug 5 13:25:31 BST 2019
Unique Job ID	b9c9431ac3c1598b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5woxA	 Alignment		97.8	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
2	c2m47A	 Alignment		97.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein cgl2373; PDBTitle: solution nmr structure of the polyketide_cyc-like protein cgl2372 from2 corynebacterium glutamicum, northeast structural genomics consortium3 target cgr160
3	d2ns9a1	 Alignment		97.6	21	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
4	d2pcsA1	 Alignment		97.5	15	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
5	d2d4ra1	 Alignment		96.8	17	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
6	d2rera1	 Alignment		96.8	17	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
7	d1xn5a	 Alignment		96.7	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
8	d1t17a	 Alignment		96.6	11	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
9	c4xrwA	 Alignment		96.3	18	PDB header: lyase Chain: A: PDB Molecule: bex1; PDBTitle: crystal structure of the di-domain aro/cyc bex1 from the be-7585a2 biosynthetic pathway
10	c2kf2A	 Alignment		96.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365
11	d2b79a1	 Alignment		96.1	12	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like

12	c2lcgA	Alignment		96.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
13	c3tfzB	Alignment		95.7	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
14	d1xn6a	Alignment		95.4	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
15	c2m89A	Alignment		95.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
16	c2kczA	Alignment		94.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein dr_a0006; PDBTitle: solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d
17	c3pu2G	Alignment		94.4	13	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.
18	c5z8oA	Alignment		94.3	20	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
19	c3p9vA	Alignment		93.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197
20	c2le1A	Alignment		93.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a
21	c2kewA	Alignment	not modelled	92.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yndb; PDBTitle: the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy
22	d3cnwa1	Alignment	not modelled	91.9	8	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
23	c3q63F	Alignment	not modelled	91.1	12	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: mll2253 protein; PDBTitle: x-ray crystal structure of protein mll2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404.
24	c2lakA	Alignment	not modelled	89.9	17	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: ahsa1-like protein rhe_ch02687; PDBTitle: solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242
25	c2lghA	Alignment	not modelled	89.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99.
26	c4xrtB	Alignment	not modelled	89.0	21	PDB header: lyase Chain: B: PDB Molecule: stfq aromatase/cyclase; PDBTitle: crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway
27	c3uidA	Alignment	not modelled	88.9	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
28	d1xuva	Alignment	not modelled	88.7	17	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain

29	c2l8oA_	Alignment	not modelled	86.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148
30	c2leqA_	Alignment	not modelled	85.8	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145
31	c2nn5A_	Alignment	not modelled	85.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ef_2215; PDBTitle: structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis
32	c2l9pA_	Alignment	not modelled	83.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147
33	c3rd6A_	Alignment	not modelled	83.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mll3558 protein; PDBTitle: crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
34	c3p51A_	Alignment	not modelled	82.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118
35	c4r7kA_	Alignment	not modelled	81.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein jhp0584; PDBTitle: 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori.
36	c2lf2A_	Alignment	not modelled	81.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152
37	d1xfsa_	Alignment	not modelled	80.9	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
38	d1x53a1	Alignment	not modelled	80.2	5	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
39	c5vglA_	Alignment	not modelled	75.7	8	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
40	c3q64A_	Alignment	not modelled	73.8	27	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: mll3774 protein; PDBTitle: x-ray crystal structure of protein mll3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.
41	c4n0gC_	Alignment	not modelled	72.4	5	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
42	d2nn5a1	Alignment	not modelled	70.6	18	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
43	c3otiA_	Alignment	not modelled	68.5	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261
44	c3q6aH_	Alignment	not modelled	66.0	18	PDB header: structure genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116
45	d1z94a1	Alignment	not modelled	64.7	22	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
46	d2k5ga1	Alignment	not modelled	63.1	23	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
47	c2ldkA_	Alignment	not modelled	62.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein aaur_3427 from arthrobacter2 aurescens, northeast structural genomics consortium target aar96
48	c3ni8A_	Alignment	not modelled	38.2	10	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
49	c6r77B_	Alignment	not modelled	31.6	16	PDB header: lyase Chain: B: PDB Molecule: proline racemase; PDBTitle: crystal structure of trans-3-hydroxy-l-proline dehydratase in complex2 with substrate - closed conformation
50	c2luzA_	Alignment	not modelled	31.3	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: calu16; PDBTitle: solution nmr structure of calu16 from micromonospora echinospora,2 northeast structural genomics consortium (nesg) target mir12
51	c5z4eA_	Alignment	not modelled	23.4	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: txno9; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
52	c3fo5A_	Alignment	not modelled	23.1	19	PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2;

						PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
53	c6gmaA_	Alignment	not modelled	22.7	63	PDB header: protein binding Chain: A: PDB Molecule: rb1-inducible coiled-coil protein 1; PDBTitle: crystal structure of the fip200 c-terminal region
54	d3elia1	Alignment	not modelled	21.0	20	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
55	d1zxfa1	Alignment	not modelled	20.7	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
56	c3p0lC_	Alignment	not modelled	20.1	16	PDB header: transport protein Chain: C: PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein
57	c6d7yA_	Alignment	not modelled	19.8	20	PDB header: toxin Chain: A: PDB Molecule: hemagglutinin; PDBTitle: 1.75 angstrom resolution crystal structure of the toxic c-terminal tip2 of cdia from pseudomonas aeruginosa in complex with immune protein
58	c3k90C_	Alignment	not modelled	18.1	11	PDB header: hormone receptor, hydrolase regulator Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: the abscisic acid receptor pyr1 in complex with abscisic acid
59	c4glwA_	Alignment	not modelled	17.3	26	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
60	c5e4bB_	Alignment	not modelled	17.0	16	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
61	d2psoa1	Alignment	not modelled	16.9	23	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
62	d1nosa_	Alignment	not modelled	15.3	53	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
63	c4lb8A_	Alignment	not modelled	14.1	86	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4848 family protein (bt3222) from2 bacteroides thetaiotaomicron vpi-5482 at 2.49 a resolution
64	c3oquB_	Alignment	not modelled	13.9	14	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
65	c2owoA_	Alignment	not modelled	13.9	28	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
66	c1v9pB_	Alignment	not modelled	13.4	33	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
67	c6j7cA_	Alignment	not modelled	13.1	19	PDB header: isomerase Chain: A: PDB Molecule: proline racemase; PDBTitle: crystal structure of proline racemase-like protein from thermococcus2 litoralis in complex with proline
68	c4kwyB_	Alignment	not modelled	12.3	19	PDB header: transport protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative lipoprotein (cc_3750) from caulobacter2 crescentus cb15 at 2.40 a resolution
69	d1b04a_	Alignment	not modelled	12.1	25	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
70	d1o94c_	Alignment	not modelled	11.6	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
71	d2fug71	Alignment	not modelled	11.0	20	Fold: N domain of copper amine oxidase-like Superfamily: Fratxin/Nqo15-like Family: Nqo15-like
72	c3jlsA_	Alignment	not modelled	10.5	31	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
73	d1em2a_	Alignment	not modelled	10.2	13	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
74	d2il5a1	Alignment	not modelled	9.9	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
75	d3clsc1	Alignment	not modelled	9.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
76	c2m6jA_	Alignment	not modelled	9.6	38	PDB header: toxin Chain: A: PDB Molecule: toxin abtx; PDBTitle: structure of a vertebrate toxin from the badge huntsman spider
77	c2p09A_	Alignment	not modelled	9.6	70	PDB header: de novo protein Chain: A: PDB Molecule: a non-biological atp binding protein with two mutations PDBTitle: structural insights into the evolution of a non-biological protein
78	c2m1hA_	Alignment	not modelled	9.6	35	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor s-ii; PDBTitle: solution structure of a pwwp domain from trypanosoma

						brucei
79	c1zauA_	Alignment	not modelled	9.4	21	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: adenylation domain of nad+ dependent dna ligase from m.tuberculosis
80	d1dgsa3	Alignment	not modelled	9.2	15	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
81	c3pn1A_	Alignment	not modelled	9.1	29	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
82	c2k9mA_	Alignment	not modelled	8.9	25	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
83	c4qglA_	Alignment	not modelled	8.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
84	c4k7gD_	Alignment	not modelled	8.6	29	PDB header: isomerase Chain: D: PDB Molecule: 3-hydroxyproline dehydratse; PDBTitle: crystal structure of a 3-hydroxyproline dehydratse from agrobacterium2 vitis, target efi-506470, with bound pyrrole 2-carboxylate, ordered3 active site
85	d1jssa_	Alignment	not modelled	8.0	15	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
86	c1jssB_	Alignment	not modelled	8.0	15	PDB header: lipid binding protein Chain: B: PDB Molecule: cholesterol-regulated start protein 4; PDBTitle: crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4).
87	c2e76G_	Alignment	not modelled	7.7	50	PDB header: photosynthesis Chain: G: PDB Molecule: cytochrome b6-f complex subunit 5; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
88	c4b8uD_	Alignment	not modelled	7.7	20	PDB header: lyase Chain: D: PDB Molecule: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase; PDBTitle: crystal structure of 3-hydroxydecanoyl-acyl carrier protein2 dehydratase (faba) from pseudomonas aeruginosa in complex with3 n-isobutyl-2-(5-(2-thienyl)-1,2-oxazol-3-yl-methoxy)acetamide
89	d1ta8a_	Alignment	not modelled	7.5	25	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
90	c3qszB_	Alignment	not modelled	7.2	23	PDB header: unknown function Chain: B: PDB Molecule: star-related lipid transfer protein; PDBTitle: crystal structure of the star-related lipid transfer protein (fragment2 25-204) from xanthomonas axonopodis at the resolution 2.4a, northeast3 structural genomics consortium target xar342
91	c5vitC_	Alignment	not modelled	7.2	47	PDB header: transferase Chain: C: PDB Molecule: mdcc; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
92	c3bacA_	Alignment	not modelled	7.1	27	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: structural basis for the inhibition of bacterial nad+2 dependent dna ligase
93	c2aenH_	Alignment	not modelled	6.7	57	PDB header: viral protein Chain: H: PDB Molecule: outer capsid protein vp4, vp8* core; PDBTitle: crystal structure of the rotavirus strain ds-1 vp8* core
94	c2p0xA_	Alignment	not modelled	6.6	60	PDB header: de novo protein Chain: A: PDB Molecule: abiotic atp-binding, folding optimized protein; PDBTitle: solution structure of a non-biological atp-binding protein
95	d1n26a1	Alignment	not modelled	6.6	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
96	d1v9pa3	Alignment	not modelled	6.6	21	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
97	c1dgsB_	Alignment	not modelled	6.5	15	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
98	c3sgIA_	Alignment	not modelled	6.3	29	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: crystal structure of dna ligase a brct domain deleted mutant of2 mycobacterium tuberculosis
99	c5ui5I_	Alignment	not modelled	6.1	25	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna