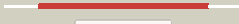



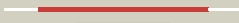
















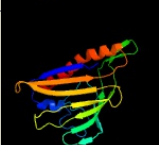


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0481c (-)_569991_570515
Date	Tue Jul 23 14:50:56 BST 2019
Unique Job ID	5b7bece281c3181c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ns9a1	 Alignment		98.7	14	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
2	c3p9vA	 Alignment		98.7	10	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
3	d2rera1	 Alignment		98.5	10	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
4	c2kf2A	 Alignment		98.5	13	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
5	c2le1A	 Alignment		98.2	7	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
6	c5z8oA	 Alignment		98.2	10	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
7	d2d4ra1	 Alignment		98.1	19	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
8	c4xrwA	 Alignment		98.1	14	PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway
9	d2pcsa1	 Alignment		98.1	17	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
10	c4xrtB	 Alignment		98.0	19	PDB header: lyase Chain: B: PDB Molecule: stfq aromataase/cyclase; PDBTitle: crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway
11	d1t17a	 Alignment		98.0	11	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like

12	c3tfzB_	Alignment		97.9	8	PDB header: biosynthetic protein Chain: B; PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromataase/cyclase from streptomcyes sp.2 r1128
13	c4n0gC_	Alignment		97.9	11	PDB header: hydrolase/receptor Chain: C; PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
14	d3cnwa1	Alignment		97.8	17	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
15	c5woxA_	Alignment		97.8	13	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
16	c2vq5B_	Alignment		97.8	15	PDB header: lyase Chain: B; PDB Molecule: s-norcochlorine synthase; PDBTitle: x-ray structure of norcochlorine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
17	c6i3yF_	Alignment		97.6	10	PDB header: lipid transport Chain: F; PDB Molecule: preli domain-containing protein 1, mitochondrial; PDBTitle: crystal structure of the human mitochondrial prelid1k58v-triap12 complex with ps
18	d2b79a1	Alignment		97.6	10	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
19	c6i4yB_	Alignment		97.5	16	PDB header: lipid transport Chain: B; PDB Molecule: preli domain containing protein 3b; PDBTitle: x-ray structure of the human mitochondrial prelid3b-triap1 complex
20	c2i9pA_	Alignment		97.5	7	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
21	c5vglA_	Alignment	not modelled	97.3	11	PDB header: isomerase Chain: A; PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
22	c4xhrB_	Alignment	not modelled	97.2	15	PDB header: lipid transport/oxidoreductase Chain: B; PDB Molecule: protein ups1, mitochondrial; PDBTitle: structure of a phospholipid trafficking complex, native
23	c6gn5A_	Alignment	not modelled	97.2	8	PDB header: lipid transport Chain: A; PDB Molecule: gram domain-containing protein 1c; PDBTitle: crystal structure of human gramd1c start domain
24	c2ldkA_	Alignment	not modelled	97.0	12	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein aaur_3427 from arthrobacter2 aureus, northeast structural genomics consortium target aar96
25	c3qtjA_	Alignment	not modelled	97.0	13	PDB header: hormone receptor Chain: A; PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo)
26	c5yqjB_	Alignment	not modelled	96.8	13	PDB header: transport protein Chain: B; PDB Molecule: membrane-anchored lipid-binding protein lam4; PDBTitle: crystal structure of the first starkin domain of lam4
27	c3rd6A_	Alignment	not modelled	96.8	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: ml13558 protein; PDBTitle: crystal structure of ml13558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
28	d1xuva_	Alignment	not modelled	96.8	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain

29	d1z94a1	Alignment	not modelled	96.8	18	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
30	c3q64A	Alignment	not modelled	96.6	16	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.
31	d1xfsa	Alignment	not modelled	96.5	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
32	c3pu2G	Alignment	not modelled	96.4	11	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.
33	c2lf2A	Alignment	not modelled	96.4	12	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
34	d1lcxa	Alignment	not modelled	96.4	14	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
35	c2lcgA	Alignment	not modelled	96.2	13	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
36	c5jqmB	Alignment	not modelled	96.2	15	PDB header: transport protein Chain: B: PDB Molecule: protein ups1, mitochondrial,mitochondrial distribution and PDBTitle: crystal structure of phosphatidic acid transporter ups1/mdm35 void of2 bound phospholipid from saccharomyces cerevisiae at 1.5 angstroms3 resolution
37	c5yqiA	Alignment	not modelled	96.2	10	PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the first starkin domain of lam2
38	d1ifva	Alignment	not modelled	96.1	15	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
39	c3uidA	Alignment	not modelled	96.0	9	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
40	d1xn5a	Alignment	not modelled	96.0	19	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
41	c3c0vC	Alignment	not modelled	95.9	14	PDB header: plant protein Chain: C: PDB Molecule: cytokinin-specific binding protein; PDBTitle: crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12
42	c2m89A	Alignment	not modelled	95.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
43	d2bk0a1	Alignment	not modelled	95.3	18	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
44	c3k90C	Alignment	not modelled	95.3	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
45	c5ys0A	Alignment	not modelled	95.2	11	PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the second starkin domain of lam2 in complex with2 ergosterol
46	c4igyB	Alignment	not modelled	95.2	8	PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
47	c3ni8A	Alignment	not modelled	94.8	22	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
48	c6bymA	Alignment	not modelled	94.7	10	PDB header: lipid transport Chain: A: PDB Molecule: sterol-binding protein; PDBTitle: crystal structure of the sterol-bound second start domain of yeast2 lam4
49	d3elia1	Alignment	not modelled	94.7	11	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
50	c2m47A	Alignment	not modelled	94.6	16	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
51	d1x53a1	Alignment	not modelled	94.3	21	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
52	c3oquB	Alignment	not modelled	94.2	10	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
53	c4reiA	Alignment	not modelled	94.2	9	PDB header: protein binding Chain: A: PDB Molecule: major latex-like protein;

53	c4lqjA	Alignment	not modelled	94.2	9	PDBTitle: crystal structure of ginseng major latex-like protein 151 (glp) from2 panax ginseng. (crystal-3)
54	c3otlA	Alignment	not modelled	94.1	11	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
55	c3p51A	Alignment	not modelled	93.5	13	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
56	c6ggq9A	Alignment	not modelled	93.5	11	PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
57	d1qmra	Alignment	not modelled	92.3	11	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
58	c2lakA	Alignment	not modelled	92.2	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
59	c2lghA	Alignment	not modelled	92.2	15	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.
60	d1xn6a	Alignment	not modelled	91.8	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
61	c2i9yA	Alignment	not modelled	91.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: major latex protein-like protein 28 or mlp-like PDBTitle: solution structure of arabidopsis thaliana protein2 at1g70830, a member of the major latex protein family
62	c2luzA	Alignment	not modelled	91.4	26	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
63	d2il5a1	Alignment	not modelled	91.4	14	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
64	c2kewA	Alignment	not modelled	91.2	12	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
65	c2leqA	Alignment	not modelled	91.2	17	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
66	d2k5ga1	Alignment	not modelled	91.1	22	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
67	c3q6aH	Alignment	not modelled	91.0	8	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
68	d1e09a	Alignment	not modelled	90.3	14	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
69	c2nn5A	Alignment	not modelled	89.8	23	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
70	c6gqfC	Alignment	not modelled	89.8	12	PDB header: lipid transport Chain: C: PDB Molecule: gram domain-containing protein 1a; PDBTitle: the structure of mouse astera (gramd1a) with 25-hydroxy cholesterol
71	d2nn5a1	Alignment	not modelled	88.0	23	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
72	d1fm4a	Alignment	not modelled	87.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
73	c2l8oA	Alignment	not modelled	86.9	11	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
74	d1xdfa1	Alignment	not modelled	83.4	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
75	c5e4bB	Alignment	not modelled	82.1	11	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
76	d2qpva1	Alignment	not modelled	81.8	18	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
77	c2k7hA	Alignment	not modelled	81.1	16	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4

78	c3q63F_	Alignment	not modelled	78.8	13	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: mlI2253 protein; PDBTitle: x-ray crystal structure of protein mlI2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404.
79	d1zxfa1	Alignment	not modelled	78.5	14	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
80	d2a1la1	Alignment	not modelled	74.9	28	Fold: TBP-like Superfamily: Bet v1-like Family: Phoshatidylinositol transfer protein, PITP
81	c3klxB_	Alignment	not modelled	74.3	15	PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3
82	c3fo5A_	Alignment	not modelled	73.7	14	PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
83	d1t27a_	Alignment	not modelled	71.4	26	Fold: TBP-like Superfamily: Bet v1-like Family: Phoshatidylinositol transfer protein, PITP
84	d1txca1	Alignment	not modelled	70.7	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
85	c4oicA_	Alignment	not modelled	69.7	11	PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein
86	c5z4eA_	Alignment	not modelled	68.1	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: txn09; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
87	c2r55B_	Alignment	not modelled	64.3	8	PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
88	c3rwsA_	Alignment	not modelled	62.6	14	PDB header: plant protein Chain: A: PDB Molecule: mtn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin
89	c2kczA_	Alignment	not modelled	58.0	16	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
90	c3kdiA_	Alignment	not modelled	54.5	13	PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2
91	c3ie5A_	Alignment	not modelled	54.4	13	PDB header: plant protein, biosynthetic protein Chain: A: PDB Molecule: phenolic oxidative coupling protein hyp-1; PDBTitle: crystal structure of hyp-1 protein from hypericum perforatum (st2 john's wort) involved in hypericin biosynthesis
92	c5sydA_	Alignment	not modelled	49.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: azurin, chimeric construct; PDBTitle: circularly permuted azurin (cpaz) based on p. aeruginosa azurin2 sequence
93	c4r7kA_	Alignment	not modelled	46.8	12	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.
94	c3oh8A_	Alignment	not modelled	42.8	14	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
95	c5ujvA_	Alignment	not modelled	29.9	13	PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of feyr1 in complex with abscisic acid
96	d1cuka2	Alignment	not modelled	27.0	17	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
97	c1d8lA_	Alignment	not modelled	25.7	17	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
98	c2kp7A_	Alignment	not modelled	24.7	26	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
99	d2bcqa1	Alignment	not modelled	24.2	33	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
100	d2fmpa1	Alignment	not modelled	22.7	26	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
101	c2wpzA_	Alignment	not modelled	22.5	22	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper mutant with two vxnxmx motifs2 coordinating chloride
102	d1jmsa1	Alignment	not modelled	20.7	26	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
						PDB header: transcription

103	c2wpzB_	Alignment	not modelled	20.7	22	Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
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