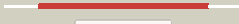



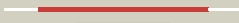


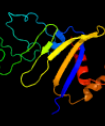













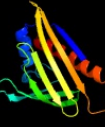


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3718c_(-)_4161993_4162436
Date	Fri Aug 9 18:20:41 BST 2019
Unique Job ID	912e6babaea0a779

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5woxA	 Alignment		100.0	79	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
2	d2d4ra1	 Alignment		99.9	13	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
3	d2ns9a1	 Alignment		99.9	16	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
4	c2kczA	 Alignment		99.9	15	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
5	c2kf2A	 Alignment		99.9	12	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
6	c4xrwA	 Alignment		99.8	13	PDB header: lyase Chain: A: PDB Molecule: bex1; PDBTitle: crystal structure of the di-domain aro/cyc bex1 from the be-7585a2 biosynthetic pathway
7	c3tfzB	 Alignment		99.8	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomyces sp.2 r1128
8	d2rera1	 Alignment		99.8	14	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
9	c3pu2G	 Alignment		99.8	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.
10	d2pcsA1	 Alignment		99.8	9	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
11	c5z8oA	 Alignment		99.8	13	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeG_0129 from mycobacterium2 smegmatis

12	d1t17a_	Alignment		99.8	9	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
13	c2le1A_	Alignment		99.8	10	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
14	c2m47A_	Alignment		99.8	13	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
15	c3p9vA_	Alignment		99.8	13	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
16	d2b79a1	Alignment		99.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
17	d1xfsa_	Alignment		99.8	11	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
18	c2lghA_	Alignment		99.8	11	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.
19	c2l9pA_	Alignment		99.8	14	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
20	d3cnwa1	Alignment		99.8	12	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
21	c3rd6A_	Alignment	not modelled	99.8	18	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
22	c2lf2A_	Alignment	not modelled	99.8	10	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
23	c2ldkA_	Alignment	not modelled	99.8	13	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
24	c3uidA_	Alignment	not modelled	99.8	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
25	c4n0gC_	Alignment	not modelled	99.8	11	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
26	c4xrtB_	Alignment	not modelled	99.8	10	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
27	c3p51A_	Alignment	not modelled	99.8	15	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
						PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;

28	c2leqA_	Alignment	not modelled	99.8	15	PDBTitle: chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145
29	d1z94a1	Alignment	not modelled	99.8	16	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
30	c3q64A_	Alignment	not modelled	99.7	13	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	d2qpva1	Alignment	not modelled	99.7	16	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
32	c2lcgA_	Alignment	not modelled	99.7	12	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
33	c2l8oA_	Alignment	not modelled	99.7	9	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
34	d1xuva_	Alignment	not modelled	99.7	11	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
35	c3otlA_	Alignment	not modelled	99.7	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
36	c5vglA_	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
37	c5e4bB_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
38	c2m89A_	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
39	d2il5a1	Alignment	not modelled	99.7	9	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
40	d1xn5a_	Alignment	not modelled	99.7	14	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
41	c3q6aH_	Alignment	not modelled	99.6	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
42	c3qtjA_	Alignment	not modelled	99.6	12	PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo)
43	c3q63F_	Alignment	not modelled	99.6	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.
44	d2k5ga1	Alignment	not modelled	99.6	17	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
45	c2nn5A_	Alignment	not modelled	99.6	12	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
46	d2nn5a1	Alignment	not modelled	99.6	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
47	d3elia1	Alignment	not modelled	99.6	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
48	c2lakA_	Alignment	not modelled	99.6	16	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
49	c4r7kA_	Alignment	not modelled	99.6	7	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.
50	c2luzA_	Alignment	not modelled	99.6	13	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	c3oquB_	Alignment	not modelled	99.6	14	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
52	d1xn6a_	Alignment	not modelled	99.5	13	Fold: TBP-like Superfamily: Bet v1-like

				Family:AHSA1 domain		
53	c4oicA	Alignment	not modelled	99.5	13	PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein
54	c2kewA	Alignment	not modelled	99.5	10	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
55	d1zxf1	Alignment	not modelled	99.5	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
56	c3klxB	Alignment	not modelled	99.5	11	PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3
57	d1x53a1	Alignment	not modelled	99.4	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
58	c3k90C	Alignment	not modelled	99.4	12	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	c3oh8A	Alignment	not modelled	99.4	10	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
60	c5z4eA	Alignment	not modelled	99.3	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: txno9; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
61	c3ie5A	Alignment	not modelled	99.3	19	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
62	c6gq9A	Alignment	not modelled	99.3	17	PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
63	c2vq5B	Alignment	not modelled	99.3	11	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
64	d1ifva	Alignment	not modelled	99.3	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
65	c3ni8A	Alignment	not modelled	99.3	13	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
66	c5ujvA	Alignment	not modelled	99.3	16	PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepyr1 in complex with abscisic acid
67	c3kdiA	Alignment	not modelled	99.3	13	PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2
68	c4igyB	Alignment	not modelled	99.3	17	PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
69	d1qmra	Alignment	not modelled	99.3	20	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
70	d1fm4a	Alignment	not modelled	99.2	19	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
71	c3rwsA	Alignment	not modelled	99.2	15	PDB header: plant protein Chain: A: PDB Molecule: mtn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin
72	d1e09a	Alignment	not modelled	99.2	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
73	d2bk0a1	Alignment	not modelled	99.2	15	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
74	c2k7hA	Alignment	not modelled	99.2	15	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4
75	d1icxa	Alignment	not modelled	99.1	16	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
76	c4rejA	Alignment	not modelled	99.1	17	PDB header: protein binding Chain: A: PDB Molecule: major latex-like protein; PDBTitle: crystal structure of ginseng major latex-like protein 151 (glp) from2 panax ginseng. (crystal-3)
77	c3c0vC	Alignment	not modelled	99.1	16	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
78	c2i9yA	Alignment	not modelled	99.1	18	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
79	c3qszB_	Alignment	not modelled	99.0	14	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
80	d1xdfa1	Alignment	not modelled	99.0	16	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
81	d1txca1	Alignment	not modelled	98.9	20	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
82	c3p0lC_	Alignment	not modelled	98.5	13	PDB header: transport protein Chain: C: PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein
83	c3fo5A_	Alignment	not modelled	98.3	7	PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
84	c1jssB_	Alignment	not modelled	98.3	9	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).
85	d1jssa_	Alignment	not modelled	98.2	9	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
86	c2r55B_	Alignment	not modelled	98.2	8	PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
87	d1em2a_	Alignment	not modelled	98.0	6	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
88	d1ln1a_	Alignment	not modelled	97.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
89	c2mouA_	Alignment	not modelled	97.8	9	PDB header: transport protein Chain: A: PDB Molecule: star-related lipid transfer protein 6; PDBTitle: solution structure of star-related lipid transfer domain protein 62 (stard6)
90	d1vjha_	Alignment	not modelled	96.7	13	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
91	c2e3rB_	Alignment	not modelled	96.2	9	PDB header: lipid transport Chain: B: PDB Molecule: lipid-transfer protein cert; PDBTitle: crystal structure of cert start domain in complex with c18-2 ceramide (p1)
92	d2psoa1	Alignment	not modelled	96.1	13	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
93	c2lioA_	Alignment	not modelled	87.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322
94	c5yqiA_	Alignment	not modelled	70.4	14	PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the first starkin domain of lam2
95	c3qzrC_	Alignment	not modelled	54.2	17	PDB header: hormone receptor Chain: C: PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
96	c2lafA_	Alignment	not modelled	53.8	14	PDB header: membrane protein Chain: A: PDB Molecule: lipoprotein 34; PDBTitle: nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
97	c5ys0A_	Alignment	not modelled	53.0	13	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
98	c2psoC_	Alignment	not modelled	51.6	10	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: star-related lipid transfer protein 13; PDBTitle: human stard13 (dlc2) lipid transfer and protein localization domain
99	c5yqiB_	Alignment	not modelled	35.8	12	PDB header: transport protein Chain: B: PDB Molecule: membrane-anchored lipid-binding protein lam4; PDBTitle: crystal structure of the first starkin domain of lam4