













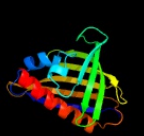



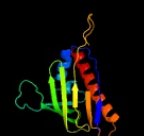



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1919c_(-)_2171068_2171532
Date	Fri Aug 2 13:30:53 BST 2019
Unique Job ID	c479f5b5f826eb33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xrwA_	 Alignment		99.9	18	PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway
2	c2kf2A_	 Alignment		99.9	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
3	c3tfzB_	 Alignment		99.9	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
4	d2rera1	 Alignment		99.9	14	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
5	c4n0gC_	 Alignment		99.9	9	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
6	c5z8oA_	 Alignment		99.9	15	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
7	c4xrtB_	 Alignment		99.9	22	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
8	c2le1A_	 Alignment		99.9	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
9	d1t17a_	 Alignment		99.8	18	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
10	d2d4ra1	 Alignment		99.8	16	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
11	c3qtjA_	 Alignment		99.8	14	PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal strcuture of aba receptor pyl10 (apo)

12	d3cnwa1	Alignment		99.8	14	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
13	d2b79a1	Alignment		99.8	17	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
14	c3oquB_	Alignment		99.8	12	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
15	c5vglA_	Alignment		99.8	11	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
16	c2m47A_	Alignment		99.8	19	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
17	d2pcsa1	Alignment		99.8	8	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
18	c4oicA_	Alignment		99.8	16	PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structrual of a soluble protein
19	c5ujvA_	Alignment		99.8	16	PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepyr1 in complex with abscisic acid
20	c5woxA_	Alignment		99.8	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
21	c5e4bB_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
22	d2ns9a1	Alignment	not modelled	99.8	12	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
23	c3p51A_	Alignment	not modelled	99.7	18	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
24	c3kxB_	Alignment	not modelled	99.7	13	PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3
25	c3p9vA_	Alignment	not modelled	99.7	9	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 mgr197
26	c3k90C_	Alignment	not modelled	99.7	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
27	c3kdiA_	Alignment	not modelled	99.7	15	PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2
28	c2l9pA_	Alignment	not modelled	99.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5hl19 from staphylococcus

					epidermidis,2 northeast structural genomics consortium target ser147
29	d1xuva_	Alignment	not modelled	99.7	13 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
30	d1xfsa_	Alignment	not modelled	99.7	13 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
31	c2kczA_	Alignment	not modelled	99.6	11 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
32	c2leqA_	Alignment	not modelled	99.6	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
33	c2ldkA_	Alignment	not modelled	99.6	11 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein aaur_3427 from arthrobacter2 aureescens, northeast structural genomics consortium target aar96
34	c3pu2G_	Alignment	not modelled	99.6	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.
35	c2lf2A_	Alignment	not modelled	99.6	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
36	c4r7kA_	Alignment	not modelled	99.6	10 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.
37	c3uidA_	Alignment	not modelled	99.6	11 PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
38	c3q64A_	Alignment	not modelled	99.6	14 PDB header: structure genomics, unknown function Chain: A: PDB Molecule: ml13774 protein; PDBTitle: x-ray crystal structure of protein ml13774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.
39	d1lfva_	Alignment	not modelled	99.5	16 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
40	c3otlA_	Alignment	not modelled	99.5	14 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
41	d1z94a1	Alignment	not modelled	99.5	15 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
42	c3rd6A_	Alignment	not modelled	99.5	17 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
43	c4igyB_	Alignment	not modelled	99.5	7 PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
44	d2il5a1	Alignment	not modelled	99.5	9 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
45	c2vq5B_	Alignment	not modelled	99.5	12 PDB header: lyase Chain: B: PDB Molecule: s-noroclaurine synthase; PDBTitle: x-ray structure of noroclaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
46	c2lcgA_	Alignment	not modelled	99.5	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein nh_rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
47	d1zxfa1	Alignment	not modelled	99.5	10 Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
48	c2lghA_	Alignment	not modelled	99.5	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.
49	c4rejA_	Alignment	not modelled	99.5	10 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)
50	d1lcxa_	Alignment	not modelled	99.5	16 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
51	c3q63F_	Alignment	not modelled	99.4	19 PDB header: structural genomics, unknown function Chain: F: PDB Molecule: ml12253 protein; PDBTitle: x-ray crystal structure of protein ml12253 from mesorhizobium loti,2 northeast structural genomics consortium

						target mir404.
52	d2bk0a1	Alignment	not modelled	99.4	16	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
53	d1e09a	Alignment	not modelled	99.4	15	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
54	c2nn5A	Alignment	not modelled	99.4	17	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
55	c3c0vC	Alignment	not modelled	99.4	11	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
56	c2l8oA	Alignment	not modelled	99.4	14	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
57	d1qmrA	Alignment	not modelled	99.4	16	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
58	d1fm4a	Alignment	not modelled	99.4	16	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
59	c3oh8A	Alignment	not modelled	99.4	11	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	d2qpva1	Alignment	not modelled	99.4	16	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
61	c2k7hA	Alignment	not modelled	99.4	18	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4
62	d1xn6a	Alignment	not modelled	99.4	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
63	c2i9yA	Alignment	not modelled	99.4	10	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
64	d2nn5a1	Alignment	not modelled	99.4	17	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
65	c2m89A	Alignment	not modelled	99.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
66	d3elia1	Alignment	not modelled	99.3	9	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
67	d2k5ga1	Alignment	not modelled	99.3	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
68	d1xn5a	Alignment	not modelled	99.3	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
69	c2luzA	Alignment	not modelled	99.3	20	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
70	d1xdfa1	Alignment	not modelled	99.3	19	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
71	c6gq9A	Alignment	not modelled	99.3	15	PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
72	c2lakA	Alignment	not modelled	99.3	21	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
73	d1txca1	Alignment	not modelled	99.3	18	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
74	c3ie5A	Alignment	not modelled	99.2	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
75	c3q6aH	Alignment	not modelled	99.2	11	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
76	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

77	c2kewA	Alignment	not modelled	99.2	16	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
78	c3ni8A	Alignment	not modelled	99.1	18	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
79	c5z4eA	Alignment	not modelled	99.1	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: txn09; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
80	c3qszB	Alignment	not modelled	99.1	12	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
81	d1x53a1	Alignment	not modelled	99.0	16	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
82	c2r55B	Alignment	not modelled	98.8	13	PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
83	c3p0LC	Alignment	not modelled	98.6	17	PDB header: transport protein Chain: C: PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein
84	d1em2a	Alignment	not modelled	98.5	15	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
85	d1ln1a	Alignment	not modelled	98.4	9	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
86	c2mouA	Alignment	not modelled	98.4	11	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)
87	c1jssB	Alignment	not modelled	98.4	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).
88	d1jssa	Alignment	not modelled	98.4	9	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
89	c3fo5A	Alignment	not modelled	98.1	10	PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
90	c2e3rB	Alignment	not modelled	97.5	7	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)
91	d1vjha	Alignment	not modelled	97.3	21	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
92	d2psoa1	Alignment	not modelled	97.0	10	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
93	c3qzrC	Alignment	not modelled	94.3	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
94	d2ffsa1	Alignment	not modelled	91.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: PA1206-like
95	c2lioA	Alignment	not modelled	85.0	9	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
96	c2psoC	Alignment	not modelled	48.1	8	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
97	c2lafA	Alignment	not modelled	47.4	18	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
98	c5yqiA	Alignment	not modelled	36.1	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
99	d1ghoa2	Alignment	not modelled	31.1	15	Fold: Prealbumin-like Superfamily: Starch-binding domain-like Family: Starch-binding domain
100	c2ejxA	Alignment	not modelled	28.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stk_08120; PDBTitle: crystal structure of the hypothetical protein stk_08120 from2 sulfolobus tokodaii
101	c5tpjA	Alignment	not modelled	28.0	38	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
102	c5ys0A	Alignment	not modelled	26.1	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

103	c6bymA_	Alignment	not modelled	22.3	7	complex with2 ergosterol PDB header: lipid transport Chain: A: PDB Molecule: sterol-binding protein; PDBTitle: crystal structure of the sterol-bound second start domain of yeast2 lam4
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