

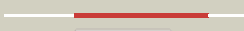


























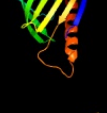



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0088 (-)_96924_97598
Date	Tue Jul 23 14:50:12 BST 2019
Unique Job ID	275e98aafd132349

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xrwA_	 Alignment		99.8	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	c5woxA_	 Alignment		99.7	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
3	c2m47A_	 Alignment		99.7	23	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
4	c4xrtB_	 Alignment		99.7	15	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
5	c2lf2A_	 Alignment		99.7	15	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
6	c3tfzB_	 Alignment		99.7	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
7	c3pu2G_	 Alignment		99.7	16	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.
8	c2l9pA_	 Alignment		99.7	13	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
9	d1xuva_	 Alignment		99.7	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
10	c2kf2A_	 Alignment		99.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: solution nmr structure of of streptomcyes coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365
11	c2l8oA_	 Alignment		99.6	18	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

12	d1z94a1	Alignment		99.6	14	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
13	d2b79a1	Alignment		99.6	12	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
14	c3uidA	Alignment		99.6	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
15	d1xfsa	Alignment		99.6	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
16	d2d4ra1	Alignment		99.6	14	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
17	c2lghA	Alignment		99.6	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.
18	d2rera1	Alignment		99.5	11	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
19	c5z8oA	Alignment		99.5	17	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
20	c2ldkA	Alignment		99.5	16	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
21	c2lcgA	Alignment	not modelled	99.5	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
22	d2pcsa1	Alignment	not modelled	99.4	13	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
23	c3otlA	Alignment	not modelled	99.4	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
24	c2leqA	Alignment	not modelled	99.4	15	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
25	d2ns9a1	Alignment	not modelled	99.4	15	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
26	c3rd6A	Alignment	not modelled	99.4	17	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
27	d1t17a	Alignment	not modelled	99.4	18	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
						PDB header: structural genomics, unknown function

28	c2kczA_	Alignment	not modelled	99.3	16	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
29	c3q64A_	Alignment	not modelled	99.3	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.
30	c3p9vA_	Alignment	not modelled	99.3	14	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
31	c4r7kA_	Alignment	not modelled	99.3	13	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.
32	c2le1A_	Alignment	not modelled	99.3	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
33	d3elia1	Alignment	not modelled	99.2	19	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
34	c3q63F_	Alignment	not modelled	99.2	17	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.
35	d1xn5a_	Alignment	not modelled	99.2	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
36	c4n0gC_	Alignment	not modelled	99.2	13	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
37	c2nn5A_	Alignment	not modelled	99.2	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
38	d3cnwa1	Alignment	not modelled	99.1	6	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
39	d2nn5a1	Alignment	not modelled	99.1	11	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
40	c2m89A_	Alignment	not modelled	99.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
41	c2kewA_	Alignment	not modelled	99.1	13	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
42	d2k5ga1	Alignment	not modelled	99.1	18	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
43	c3p51A_	Alignment	not modelled	99.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein q2y8n9_nitmu from nitrospira2 multiformis, northeast structural genomics consortium target nmr118
44	c5vglA_	Alignment	not modelled	99.0	14	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
45	d1xn6a_	Alignment	not modelled	99.0	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
46	d2il5a1	Alignment	not modelled	99.0	11	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
47	c3q6aH_	Alignment	not modelled	98.9	16	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
48	c2lakA_	Alignment	not modelled	98.9	20	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	c3oh8A_	Alignment	not modelled	98.9	12	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
50	c3oquB_	Alignment	not modelled	98.8	14	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor py9 with aba
51	c2luzA_	Alignment	not modelled	98.8	17	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

52	c3qtjA_	Alignment	not modelled	98.7	13	PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo)
53	d1zxfa1	Alignment	not modelled	98.7	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
54	c3k90C_	Alignment	not modelled	98.7	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
55	c5z4eA_	Alignment	not modelled	98.6	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: txn09; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
56	c2vq5B_	Alignment	not modelled	98.6	13	PDB header: lyase Chain: B: PDB Molecule: s-norococlaurine synthase; PDBTitle: x-ray structure of norococlaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
57	d1x53a1	Alignment	not modelled	98.4	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
58	d2qpva1	Alignment	not modelled	98.4	17	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
59	c4igyB_	Alignment	not modelled	98.4	16	PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
60	c3ni8A_	Alignment	not modelled	98.3	24	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
61	c3klxB_	Alignment	not modelled	98.3	12	PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3
62	c4rejA_	Alignment	not modelled	98.3	11	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)
63	c3kdiA_	Alignment	not modelled	98.2	12	PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2
64	c4oicA_	Alignment	not modelled	98.0	16	PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein
65	c5ujvA_	Alignment	not modelled	98.0	16	PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepyr1 in complex with abscisic acid
66	c3c0vC_	Alignment	not modelled	97.9	12	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
67	c2i9yA_	Alignment	not modelled	97.9	16	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
68	c2k7hA_	Alignment	not modelled	97.7	15	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4
69	c5e4bB_	Alignment	not modelled	97.7	12	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
70	d1icxa_	Alignment	not modelled	97.7	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
71	d1ifva_	Alignment	not modelled	97.5	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
72	d1xdfa1	Alignment	not modelled	97.5	14	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
73	d1fm4a_	Alignment	not modelled	97.3	19	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
74	d2bk0a1	Alignment	not modelled	97.2	14	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
75	d1qmra_	Alignment	not modelled	97.0	19	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
76	c3qsZB_	Alignment	not modelled	96.7	10	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
77	d1e09a_	Alignment	not modelled	96.6	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
						PDB header: plant protein, biosynthetic protein

78	c3ie5A_	Alignment	not modelled	96.2	12	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
79	c6gq9A_	Alignment	not modelled	96.1	16	PDB header: allergen Chain: A; PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
80	d1txca1	Alignment	not modelled	96.0	18	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
81	c3fo5A_	Alignment	not modelled	95.7	16	PDB header: lipid transport Chain: A; PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
82	c3rwsA_	Alignment	not modelled	94.9	13	PDB header: plant protein Chain: A; PDB Molecule: mtn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin
83	c2r55B_	Alignment	not modelled	93.4	13	PDB header: transport protein Chain: B; PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
84	d1ln1a_	Alignment	not modelled	89.1	13	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
85	d2psoa1	Alignment	not modelled	87.1	16	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
86	d2ffsa1	Alignment	not modelled	82.8	17	Fold: TBP-like Superfamily: Bet v1-like Family: PA1206-like
87	c2mouA_	Alignment	not modelled	72.8	8	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)
88	c2lioA_	Alignment	not modelled	68.7	8	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
89	d1em2a_	Alignment	not modelled	65.0	14	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
90	d1vjha_	Alignment	not modelled	61.6	18	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
91	c3p0lC_	Alignment	not modelled	42.5	16	PDB header: transport protein Chain: C; PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein
92	c1jssB_	Alignment	not modelled	40.2	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).
93	d1jssa_	Alignment	not modelled	40.2	9	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
94	c2e3rB_	Alignment	not modelled	37.6	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)
95	c3pmdA_	Alignment	not modelled	23.1	19	PDB header: lipid binding protein Chain: A; PDB Molecule: conserved domain protein; PDBTitle: crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
96	d2g9ga1	Alignment	not modelled	19.5	70	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Extended PAW domain
97	c2g9gA_	Alignment	not modelled	18.4	70	PDB header: hydrolase Chain: A; PDB Molecule: peptide n-glycanase; PDBTitle: crystal structure of his-tagged mouse pngase c-terminal domain
98	c3qrzC_	Alignment	not modelled	17.2	27	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
99	d2jn4a1	Alignment	not modelled	16.8	16	Fold: NifT/FixU barrel-like Superfamily: NifT/FixU-like Family: NifT/FixU