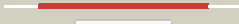



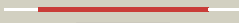




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0910_(-)_1014870_1015304
Date	Fri Jul 26 01:50:50 BST 2019
Unique Job ID	c90cb6b6321ac2a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kf2A_	 Alignment		99.9	9	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
2	d2rera1	 Alignment		99.9	13	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
3	d2d4ra1	 Alignment		99.8	14	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
4	c4xrwA_	 Alignment		99.8	9	PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway
5	d2ns9a1	 Alignment		99.8	18	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
6	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
7	d1t17a_	 Alignment		99.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
8	c3tfzB_	 Alignment		99.8	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
9	c5z8oA_	 Alignment		99.8	14	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeq_0129 from mycobacterium2 smegmatis
10	c2le1A_	 Alignment		99.8	11	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
11	d2b79a1	 Alignment		99.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like

12	c5woxA	Alignment		99.8	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
13	d2pcsA1	Alignment		99.7	16	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
14	c3p9vA	Alignment		99.7	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
15	c4xrtB	Alignment		99.7	10	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
16	c2l9pA	Alignment		99.7	6	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
17	c2lf2A	Alignment		99.6	9	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
18	c3pu2G	Alignment		99.6	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.
19	d3cnwa1	Alignment		99.6	10	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
20	c2ldkA	Alignment		99.6	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
21	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
22	d1xfsa	Alignment	not modelled	99.6	9	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
23	d1z94a1	Alignment	not modelled	99.6	14	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
24	c2kczA	Alignment	not modelled	99.6	12	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
25	c2leqA	Alignment	not modelled	99.5	12	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
26	d2qpva1	Alignment	not modelled	99.5	15	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
27	d1xuva	Alignment	not modelled	99.5	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
28	c4n0gC	Alignment	not modelled	99.5	12	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex

29	c3p51A	Alignment	not modelled	99.5	11	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
30	c2lghA	Alignment	not modelled	99.5	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.
31	c2lcgA	Alignment	not modelled	99.5	9	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
32	c5vglA	Alignment	not modelled	99.4	13	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
33	d2il5a1	Alignment	not modelled	99.4	9	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
34	c2l8oA	Alignment	not modelled	99.4	10	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
35	c3rd6A	Alignment	not modelled	99.4	10	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
36	c3otlA	Alignment	not modelled	99.4	12	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
37	c4r7kA	Alignment	not modelled	99.4	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.
38	c2m89A	Alignment	not modelled	99.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
39	c3q64A	Alignment	not modelled	99.4	10	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.
40	d3elia1	Alignment	not modelled	99.4	14	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
41	c2nn5A	Alignment	not modelled	99.4	10	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
42	d1xn5a	Alignment	not modelled	99.4	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
43	c5e4bB	Alignment	not modelled	99.3	12	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
44	c2luzA	Alignment	not modelled	99.3	16	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
45	c3qtjA	Alignment	not modelled	99.3	10	PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo)
46	c3q63F	Alignment	not modelled	99.3	13	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.
47	d2nn5a1	Alignment	not modelled	99.3	7	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
48	d1xn6a	Alignment	not modelled	99.3	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
49	d2k5ga1	Alignment	not modelled	99.3	17	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
50	c3oquB	Alignment	not modelled	99.3	10	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
51	c2lakA	Alignment	not modelled	99.3	13	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 etii, northeast structural genomics consortium target3 rer242
52	c2kewA	Alignment	not modelled	99.3	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

53	c3oh8A_	Alignment	not modelled	99.2	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
54	c4oicA_	Alignment	not modelled	99.2	9	PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein
55	c3q6aH_	Alignment	not modelled	99.2	14	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
56	c3kixB_	Alignment	not modelled	99.2	11	PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3
57	c3k90C_	Alignment	not modelled	99.2	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
58	c4igyB_	Alignment	not modelled	99.2	11	PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
59	d1zxfa1	Alignment	not modelled	99.1	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
60	c3kdiA_	Alignment	not modelled	99.0	11	PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2
61	c5ujvA_	Alignment	not modelled	99.0	10	PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepyr1 in complex with abscisic acid
62	c5z4eA_	Alignment	not modelled	98.9	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: txn09; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
63	c4reiA_	Alignment	not modelled	98.9	12	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)
64	c2vq5B_	Alignment	not modelled	98.9	9	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
65	d1x53a1	Alignment	not modelled	98.9	7	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
66	c3c0vC_	Alignment	not modelled	98.8	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
67	d1ifva_	Alignment	not modelled	98.8	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
68	d1icxa_	Alignment	not modelled	98.8	9	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
69	c3ni8A_	Alignment	not modelled	98.7	11	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
70	c2k7hA_	Alignment	not modelled	98.7	14	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4
71	c3ie5A_	Alignment	not modelled	98.7	11	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
72	c2i9yA_	Alignment	not modelled	98.7	12	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
73	c3rwsA_	Alignment	not modelled	98.7	13	PDB header: plant protein Chain: A: PDB Molecule: mntn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mntn13) in complex2 with trans-zeatin
74	d2bk0a1	Alignment	not modelled	98.7	9	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
75	d1e09a_	Alignment	not modelled	98.6	13	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
76	c3qszB_	Alignment	not modelled	98.6	9	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	d1qmra_	Alignment	not modelled	98.6	9	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
						Fold: TBP-like

78	d1xdfa1	Alignment	not modelled	98.6	11	Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
79	c6gg9A	Alignment	not modelled	98.5	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
80	d1fm4a	Alignment	not modelled	98.5	9	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
81	d1txca1	Alignment	not modelled	98.4	11	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
82	c3p0lC	Alignment	not modelled	98.0	10	PDB header: transport protein Chain: C: PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein
83	c2r55B	Alignment	not modelled	97.8	12	PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
84	c2mouA	Alignment	not modelled	97.2	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)
85	c1jssB	Alignment	not modelled	97.1	7	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).
86	d1em2a	Alignment	not modelled	97.1	11	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
87	d1jssa	Alignment	not modelled	97.0	9	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
88	c2e3rB	Alignment	not modelled	96.1	13	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)
89	c3fo5A	Alignment	not modelled	96.1	9	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	d2ffsa1	Alignment	not modelled	95.1	13	Fold: TBP-like Superfamily: Bet v1-like Family: PA1206-like
91	d2psoa1	Alignment	not modelled	95.0	15	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
92	d1vjha	Alignment	not modelled	94.2	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
93	d1ln1a	Alignment	not modelled	93.3	9	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
94	c2lioA	Alignment	not modelled	88.9	12	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
95	c5ys0A	Alignment	not modelled	86.5	9	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
96	c2ejxA	Alignment	not modelled	83.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stk_08120; PDBTitle: crystal structure of the hypothetical protein stk_08120 from2 sulfolobus tokodaii
97	c2psoc	Alignment	not modelled	72.0	9	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
98	c5yqiA	Alignment	not modelled	68.8	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	c3qzrC	Alignment	not modelled	53.0	22	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
100	d2bv3a3	Alignment	not modelled	49.1	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
101	c2lafA	Alignment	not modelled	48.4	7	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
102	c6bymA	Alignment	not modelled	45.8	9	PDB header: lipid transport Chain: A: PDB Molecule: sterol-binding protein; PDBTitle: crystal structure of the sterol-bound second start domain of yeast2 lam4
103	c5yqiB	Alignment	not modelled	42.6	11	PDB header: transport protein Chain: B: PDB Molecule: membrane-anchored lipid-binding protein lam4; PDBTitle: crystal structure of the first starkin domain of lam4