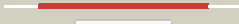



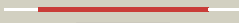



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2035_(-) _2281622_2282110
Date	Mon Aug 5 13:25:14 BST 2019
Unique Job ID	fc1ded1cf281a1a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5z4eA_	 Alignment		100.0	34	PDB header: biosynthetic protein Chain: A: PDB Molecule: txno9; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
2	d1zxfa1	 Alignment		100.0	25	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
3	d2il5a1	 Alignment		100.0	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
4	c2ldkA_	 Alignment		99.9	14	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
5	d2k5ga1	 Alignment		99.9	24	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
6	d3elia1	 Alignment		99.9	23	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
7	c2l9pA_	 Alignment		99.9	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
8	c2lf2A_	 Alignment		99.9	13	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
9	d1xfsa_	 Alignment		99.9	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
10	c3uidA_	 Alignment		99.9	13	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
11	d1xuva_	 Alignment		99.9	16	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain

12	c3otlA_	Alignment		99.9	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
13	c2l8oA_	Alignment		99.9	15	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
14	c2lakA_	Alignment		99.9	24	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
15	c3pu2G_	Alignment		99.9	19	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.
16	c3q63F_	Alignment		99.9	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.
17	c2kewA_	Alignment		99.9	19	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
18	c3q64A_	Alignment		99.9	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.
19	c2luzA_	Alignment		99.9	24	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
20	c3q6aH_	Alignment		99.9	21	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
21	c2leqA_	Alignment	not modelled	99.9	16	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
22	d1xn6a_	Alignment	not modelled	99.9	20	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
23	c2nn5A_	Alignment	not modelled	99.9	18	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
24	c3rd6A_	Alignment	not modelled	99.9	19	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
25	c2m89A_	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
26	d1xn5a_	Alignment	not modelled	99.9	26	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
27	c3ni8A_	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
28	d1x53a1	Alignment	not modelled	99.9	18	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain

29	d1z94a1	Alignment	not modelled	99.9	20	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
30	d2nn5a1	Alignment	not modelled	99.9	18	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
31	c2lghA_	Alignment	not modelled	99.9	17	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.
32	c2lcgA_	Alignment	not modelled	99.9	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
33	c5woxA_	Alignment	not modelled	99.4	9	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
34	c2m47A_	Alignment	not modelled	99.4	17	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
35	d2b79a1	Alignment	not modelled	99.3	12	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
36	c4xrwA_	Alignment	not modelled	99.2	13	PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway
37	d2ns9a1	Alignment	not modelled	99.0	12	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
38	d3cnwa1	Alignment	not modelled	99.0	9	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
39	d2d4ra1	Alignment	not modelled	99.0	13	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
40	c2le1A_	Alignment	not modelled	99.0	12	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
41	c2kf2A_	Alignment	not modelled	98.9	8	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
42	c3p51A_	Alignment	not modelled	98.9	11	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
43	c4xrtB_	Alignment	not modelled	98.9	17	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
44	d2rera1	Alignment	not modelled	98.9	12	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
45	c3tfzB_	Alignment	not modelled	98.9	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
46	d2pcsA1	Alignment	not modelled	98.9	12	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
47	c4n0gC_	Alignment	not modelled	98.9	10	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
48	c2kczA_	Alignment	not modelled	98.8	17	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
49	d1t17a_	Alignment	not modelled	98.7	11	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
50	c5z8oA_	Alignment	not modelled	98.7	11	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
51	c3p9vA_	Alignment	not modelled	98.6	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
52	c5vglA_	Alignment	not modelled	98.4	10	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
53	c4r7kA_	Alignment	not modelled	98.3	11	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.
54	c2vq5B	Alignment	not modelled	98.0	10	PDB header: lyase Chain: B: PDB Molecule: s-norocloaurine synthase; PDBTitle: x-ray structure of norocloaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
55	c5e4bB	Alignment	not modelled	98.0	8	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
56	c3rwsA	Alignment	not modelled	98.0	7	PDB header: plant protein Chain: A: PDB Molecule: mntn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mnt13) in complex2 with trans-zeatin
57	d2bk0a1	Alignment	not modelled	97.9	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
58	d2qpva1	Alignment	not modelled	97.9	13	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
59	c4oicA	Alignment	not modelled	97.8	14	PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein
60	c3k90C	Alignment	not modelled	97.8	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
61	c3qtjA	Alignment	not modelled	97.8	9	PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo)
62	d1ifva	Alignment	not modelled	97.8	7	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
63	c2k7hA	Alignment	not modelled	97.7	7	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4
64	d1qmrA	Alignment	not modelled	97.7	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
65	d1fm4a	Alignment	not modelled	97.7	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
66	d1e09a	Alignment	not modelled	97.6	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
67	c3kdiA	Alignment	not modelled	97.5	10	PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2
68	c3kixB	Alignment	not modelled	97.4	12	PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3
69	c2lioA	Alignment	not modelled	97.4	11	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
70	d1xdfa1	Alignment	not modelled	97.4	8	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
71	d1icxa	Alignment	not modelled	97.3	11	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
72	c4rejA	Alignment	not modelled	97.1	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)
73	c3c0vC	Alignment	not modelled	97.1	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
74	c3oh8A	Alignment	not modelled	97.1	15	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
75	c3oquB	Alignment	not modelled	97.0	11	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
76	c4igyB	Alignment	not modelled	97.0	15	PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
77	c3ie5A	Alignment	not modelled	97.0	9	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
78	c6gq9A	Alignment	not modelled	96.9	9	PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
79	c2i9yA	Alignment	not modelled	96.7	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
80	c5ujvA_	Alignment	not modelled	96.2	16	PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepr1 in complex with abscisic acid
81	d1txca1	Alignment	not modelled	95.8	13	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
82	d3d3ra1	Alignment	not modelled	38.5	13	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
83	c3qszB_	Alignment	not modelled	35.7	8	PDB header: unknown function Chain: B: PDB Molecule: star-related lipid transfer protein; (fragment2 25-204) from xanthomonas axonopodis at the resolution 2.4a, northeast3 structural genomics consortium target xar342
84	c3d3rA_	Alignment	not modelled	34.3	13	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
85	d2psoa1	Alignment	not modelled	33.0	8	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
86	d1vjha_	Alignment	not modelled	30.6	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
87	c5ys0A_	Alignment	not modelled	29.4	7	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
88	c2r55B_	Alignment	not modelled	28.2	7	PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
89	d2z1ca1	Alignment	not modelled	25.2	12	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
90	c5yqiA_	Alignment	not modelled	17.1	18	PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the first starkin domain of lam2
91	c2psoC_	Alignment	not modelled	16.8	16	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
92	d2ot2a1	Alignment	not modelled	13.3	9	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
93	c3fo5A_	Alignment	not modelled	9.2	8	PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11)
94	d1pgl11	Alignment	not modelled	8.3	17	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
95	d1ny711	Alignment	not modelled	7.5	11	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
96	c3qrzC_	Alignment	not modelled	7.3	33	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
97	c3nn8B_	Alignment	not modelled	6.0	17	PDB header: immune system Chain: B: PDB Molecule: engineered scfv, light chain; PDBTitle: crystal structure of engineered antibody fragment based on 3d5
98	c5yqiB_	Alignment	not modelled	5.5	7	PDB header: transport protein Chain: B: PDB Molecule: membrane-anchored lipid-binding protein lam4; PDBTitle: crystal structure of the first starkin domain of lam4
99	c4ca3A_	Alignment	not modelled	5.4	14	PDB header: ribosomal protein Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: solution structure of streptomyces virginiae vira acp5b