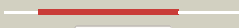
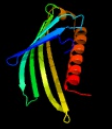



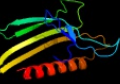
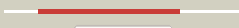
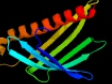

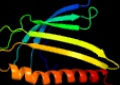



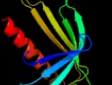



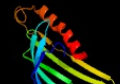



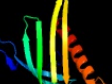


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0369c_(-)_446532_447047
Date	Tue Jul 23 14:50:44 BST 2019
Unique Job ID	894a57030a7ca679

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ns9a1	 Alignment		99.6	16	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
2	d2pcsa1	 Alignment		99.6	20	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
3	c3p9vA_	 Alignment		99.4	16	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
4	d2d4ra1	 Alignment		98.2	14	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
5	d1t17a_	 Alignment		97.9	13	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
6	c5woxA_	 Alignment		97.9	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra
7	d3cnwa1	 Alignment		97.5	7	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
8	c2kf2A_	 Alignment		97.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: solution nmr structure of of streptomycetes coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365
9	c3tfzB_	 Alignment		97.4	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomycetes sp.2 r1128
10	c2le1A_	 Alignment		97.3	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
11	c5z8oA_	 Alignment		97.2	12	PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeq_0129 from mycobacterium2 smegmatis

12	c4n0gC_	Alignment		96.1	11	PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex
13	d1xfsa_	Alignment		96.0	16	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
14	c3pu2G_	Alignment		95.9	15	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.
15	c2ldkA_	Alignment		95.9	15	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
16	c2luzA_	Alignment		95.2	18	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
17	c3uidA_	Alignment		95.0	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis
18	d2rera1	Alignment		94.9	10	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
19	c2lghA_	Alignment		94.7	19	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 rh rdcs, northeast structural3 genomics consortium target ahr99.
20	c4xrwA_	Alignment		94.6	10	PDB header: lyase Chain: A: PDB Molecule: bex1; PDBTitle: crystal structure of the di-domain aro/cyc bex1 from the be-7585a2 biosynthetic pathway
21	c2m47A_	Alignment	not modelled	94.4	12	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
22	d2b79a1	Alignment	not modelled	94.3	17	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
23	c2l9pA_	Alignment	not modelled	94.3	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
24	c5vglA_	Alignment	not modelled	94.3	18	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
25	c2vq5B_	Alignment	not modelled	93.6	12	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
26	d1ifva_	Alignment	not modelled	93.4	8	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
27	c5e4bB_	Alignment	not modelled	93.3	13	PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
28	c3rd6A_	Alignment	not modelled	93.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ml13558 protein;

28	c1u0a_	Alignment	not modelled	93.2	29	PDBTitle: crystal structure of ml3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;
29	c3p51a_	Alignment	not modelled	93.0	11	PDBTitle: three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118
30	d2k5ga1	Alignment	not modelled	92.6	13	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
31	c2lcgA_	Alignment	not modelled	91.3	16	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	c2kczA_	Alignment	not modelled	90.7	14	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
33	c2l8oA_	Alignment	not modelled	89.6	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
34	c2leqA_	Alignment	not modelled	88.7	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
35	c3q64A_	Alignment	not modelled	88.4	20	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: ml3774 protein; PDBTitle: x-ray crystal structure of protein ml3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.
36	c3ie5A_	Alignment	not modelled	88.3	14	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
37	d1icxa_	Alignment	not modelled	88.3	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
38	c2lf2A_	Alignment	not modelled	88.2	14	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
39	c2i9yA_	Alignment	not modelled	88.2	11	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
40	c2lakA_	Alignment	not modelled	86.9	15	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
41	c3oquB_	Alignment	not modelled	86.7	14	PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba
42	d1z94a1	Alignment	not modelled	86.5	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
43	d3elia1	Alignment	not modelled	86.4	15	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
44	c3qszB_	Alignment	not modelled	85.5	16	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
45	c3otIA_	Alignment	not modelled	85.4	15	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
46	d1fm4a_	Alignment	not modelled	84.1	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
47	c6gq9A_	Alignment	not modelled	81.6	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
48	c3c0vC_	Alignment	not modelled	81.4	15	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
49	d1qmra_	Alignment	not modelled	80.1	10	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
50	d1zxfa1	Alignment	not modelled	78.6	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
51	c3rwsA_	Alignment	not modelled	76.7	16	PDB header: plant protein Chain: A: PDB Molecule: mtn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin

52	d1xuva_	Alignment	not modelled	75.7	12	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
53	c3q63F_	Alignment	not modelled	72.9	11	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 mlr404.
54	c4xrtB_	Alignment	not modelled	72.8	14	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
55	d1xdfa1	Alignment	not modelled	72.4	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
56	c2kewA_	Alignment	not modelled	71.0	21	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
57	d1ln1a_	Alignment	not modelled	70.5	10	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
58	c2r55B_	Alignment	not modelled	70.1	10	PDB header: transport protein Chain: B; PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5
59	c5z4eA_	Alignment	not modelled	69.4	16	PDB header: biosynthetic protein Chain: A; PDB Molecule: txn09; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09
60	c2m89A_	Alignment	not modelled	68.4	15	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
61	c4rejA_	Alignment	not modelled	68.0	15	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)
62	d1x53a1	Alignment	not modelled	67.9	10	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
63	c2k7hA_	Alignment	not modelled	66.7	15	PDB header: allergen Chain: A; PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4
64	d1vjha_	Alignment	not modelled	65.2	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
65	d1xn5a_	Alignment	not modelled	62.4	16	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
66	c1jssB_	Alignment	not modelled	60.3	12	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).
67	d1e09a_	Alignment	not modelled	59.6	11	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
68	c4igyB_	Alignment	not modelled	59.3	9	PDB header: allergen Chain: B; PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form
69	c6gn5A_	Alignment	not modelled	57.1	13	PDB header: lipid transport Chain: A; PDB Molecule: gram domain-containing protein 1c; PDBTitle: crystal structure of human gramd1c start domain
70	c3qtjA_	Alignment	not modelled	52.2	14	PDB header: hormone receptor Chain: A; PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal strcuture of aba receptor pyl10 (apo)
71	d2qpva1	Alignment	not modelled	48.4	15	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
72	d1em2a_	Alignment	not modelled	44.2	12	Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain
73	d2il5a1	Alignment	not modelled	40.8	6	Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain
74	d2bk0a1	Alignment	not modelled	40.4	8	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
75	c3oh8A_	Alignment	not modelled	37.9	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
76	c3ni8A_	Alignment	not modelled	37.3	16	PDB header: unknown function Chain: A; PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
77	c2momB_	Alignment	not modelled	35.0	27	PDB header: membrane protein Chain: B; PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles

78	c2momC_	Alignment	not modelled	34.7	27	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
79	c5ys0A_	Alignment	not modelled	32.4	15	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
80	c5f2kA_	Alignment	not modelled	30.6	21	PDB header: transferase Chain: A: PDB Molecule: fatty acid o-methyltransferase; PDBTitle: crystal structure of mycobacterial fatty acid o-methyltransferase in2 complex with sah and octanoate
81	c6bymA_	Alignment	not modelled	25.5	23	PDB header: lipid transport Chain: A: PDB Molecule: sterol-binding protein; PDBTitle: crystal structure of the sterol-bound second start domain of yeast2 lam4
82	c2nn5A_	Alignment	not modelled	25.5	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
83	c2mouA_	Alignment	not modelled	21.9	15	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)
84	d1h6ta1	Alignment	not modelled	20.2	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
85	d2omza1	Alignment	not modelled	17.4	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
86	c2e3rB_	Alignment	not modelled	16.9	11	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)
87	d1h6ua1	Alignment	not modelled	16.5	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Internalin Ig-like domain
88	d1pbya5	Alignment	not modelled	16.1	7	Fold: Streptavidin-like Superfamily: Quinohemoprotein amine dehydrogenase A chain, domain 3 Family: Quinohemoprotein amine dehydrogenase A chain, domain 3
89	c3pbpF_	Alignment	not modelled	15.7	31	PDB header: transport protein,structural protein Chain: F: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
90	c3pbpC_	Alignment	not modelled	15.7	31	PDB header: transport protein,structural protein Chain: C: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
91	c3pbpL_	Alignment	not modelled	15.6	31	PDB header: transport protein,structural protein Chain: L: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
92	d1txca1	Alignment	not modelled	15.3	17	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
93	c3pbpl_	Alignment	not modelled	14.2	31	PDB header: transport protein,structural protein Chain: I: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
94	c6i4yB_	Alignment	not modelled	13.7	8	PDB header: lipid transport Chain: B: PDB Molecule: preli domain containing protein 3b; PDBTitle: x-ray structure of the human mitochondrial prelid3b-triap1 complex
95	c4r7kA_	Alignment	not modelled	13.7	14	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.
96	c3tknB_	Alignment	not modelled	13.4	29	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the nup82-nup159-nup98 heterotrimer
97	c3tknH_	Alignment	not modelled	13.4	29	PDB header: protein transport Chain: H: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the nup82-nup159-nup98 heterotrimer
98	c3tknE_	Alignment	not modelled	13.4	29	PDB header: protein transport Chain: E: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the nup82-nup159-nup98 heterotrimer
99	c3q6aH_	Alignment	not modelled	12.6	20	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