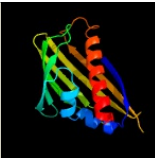



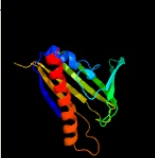


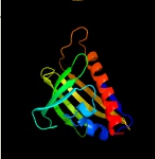



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0164\_(TB18.5)\_193624\_194109  
 Date Tue Jul 23 14:50:21 BST 2019  
 Unique Job ID 0a6ca56e328338fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5z8oA_</a>	Alignment		99.9	60	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cyclase/dehydrase; <b>PDBTitle:</b> structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis
2	<a href="#">d1t17a_</a>	Alignment		99.9	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> oligoketide cyclase/dehydrase-like
3	<a href="#">c2kf2A_</a>	Alignment		99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365
4	<a href="#">d2d4ra1</a>	Alignment		99.9	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> oligoketide cyclase/dehydrase-like
5	<a href="#">d2rera1</a>	Alignment		99.9	16	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> oligoketide cyclase/dehydrase-like
6	<a href="#">c3tfzB_</a>	Alignment		99.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclase; <b>PDBTitle:</b> crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128
7	<a href="#">c2le1A_</a>	Alignment		99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a
8	<a href="#">c4xrwA_</a>	Alignment		99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> bex1; <b>PDBTitle:</b> crystal structure of the di-domain aro/cyc bex1 from the be-7585a2 biosynthetic pathway
9	<a href="#">d2ns9a1</a>	Alignment		99.8	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> CoxG-like
10	<a href="#">d2b79a1</a>	Alignment		99.8	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Smu440-like
11	<a href="#">c5woxA_</a>	Alignment		99.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of kany protein (ms6282) using two 4d-spectra

12	<a href="#">d2pcsa1</a>	Alignment		99.8	9	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> CoxG-like
13	<a href="#">c2m47A_</a>	Alignment		99.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein cgl2373; <b>PDBTitle:</b> solution nmr structure of the polyketide_cyc-like protein cgl2372 from2 corynebacterium glutamicum, northeast structural genomics consortium3 target cgr160
14	<a href="#">c3p9vA_</a>	Alignment		99.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197
15	<a href="#">c4xrtB_</a>	Alignment		99.8	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> stfq aromatase/cyclase; <b>PDBTitle:</b> crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway
16	<a href="#">c4n0gC_</a>	Alignment		99.8	13	<b>PDB header:</b> hydrolase/receptor <b>Chain:</b> C: <b>PDB Molecule:</b> abscisic acid receptor pyl13; <b>PDBTitle:</b> crystal structure of pyl13-pp2ca complex
17	<a href="#">c3oquB_</a>	Alignment		99.7	12	<b>PDB header:</b> hormone receptor <b>Chain:</b> B: <b>PDB Molecule:</b> abscisic acid receptor pyl9; <b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl9 with aba
18	<a href="#">d3cnwa1</a>	Alignment		99.7	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Atu1531-like
19	<a href="#">c5vglA_</a>	Alignment		99.7	6	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> lachrymatory-factor synthase; <b>PDBTitle:</b> crystal structure of lachrymatory factor synthase from allium cepa
20	<a href="#">c3qtjA_</a>	Alignment		99.7	12	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> abscisic acid receptor pyl10; <b>PDBTitle:</b> crystal structure of aba receptor pyl10 (apo)
21	<a href="#">c2kczA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein dr_a0006; <b>PDBTitle:</b> solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d
22	<a href="#">c5e4bB_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxynitrile lyase; <b>PDBTitle:</b> hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde
23	<a href="#">c3p51A_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> three-dimensional structure of protein q2y8n9_nitmu from nitrospira2 multiformis, northeast structural genomics consortium target nmr118
24	<a href="#">c4oicA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> hormone receptor/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bet v i allergen-like; <b>PDBTitle:</b> crystal structural of a soluble protein
25	<a href="#">c3k90C_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hormone receptor, hydrolase regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the abscisic acid receptor pyr1 in complex with abscisic acid
26	<a href="#">d2qpva1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Atu1531-like
27	<a href="#">c3kixB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hormone receptor <b>Chain:</b> B: <b>PDB Molecule:</b> f3n23.20 protein; <b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl3
28	<a href="#">c4r7kA_</a>	Alignment	not modelled	99.5	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein jhp0584; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of hypothetical

						protein2_jhp0584 from helicobacter pylori.
29	<a href="#">c3qszB_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> star-related lipid transfer protein; <b>PDBTitle:</b> 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
30	<a href="#">c3kdiA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein at2g26040; <b>PDBTitle:</b> structure of (+)-aba bound pyl2
31	<a href="#">c2leqA_</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145
32	<a href="#">c2l9pA_</a>	Alignment	not modelled	99.5	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147
33	<a href="#">c2lghA_</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99.
34	<a href="#">c2lf2A_</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152
35	<a href="#">c2lcgA_</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115
36	<a href="#">c5ujvA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> abscisic acid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pyr1; <b>PDBTitle:</b> crystal structure of fepyr1 in complex with abscisic acid
37	<a href="#">d1xfsa_</a>	Alignment	not modelled	99.4	8	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
38	<a href="#">d1xuva_</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
39	<a href="#">c3pu2G_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.
40	<a href="#">c2ldkA_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein aaur_3427 from arthrobacter2 aurescens, northeast structural genomics consortium target aar96
41	<a href="#">c2l8oA_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148
42	<a href="#">c2m89A_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> aha1 domain protein; <b>PDBTitle:</b> solution structure of the aha1 dimer from colwellia psychrerythraea
43	<a href="#">d1ifva_</a>	Alignment	not modelled	99.4	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
44	<a href="#">d1z94a1</a>	Alignment	not modelled	99.4	8	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
45	<a href="#">c3rd6A_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mll3558 protein; <b>PDBTitle:</b> crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403
46	<a href="#">c3q63F_</a>	Alignment	not modelled	99.3	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> mll2253 protein; <b>PDBTitle:</b> x-ray crystal structure of protein mll2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404.
47	<a href="#">c2vq5B_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> s-norcochlorine synthase; <b>PDBTitle:</b> x-ray structure of norcochlorine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
48	<a href="#">c3q64A_</a>	Alignment	not modelled	99.3	8	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mll3774 protein; <b>PDBTitle:</b> x-ray crystal structure of protein mll3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.
49	<a href="#">c3uidA_</a>	Alignment	not modelled	99.3	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein ms6760 from mycobacterium smegmatis
50	<a href="#">c4igyB_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> allergen <b>Chain:</b> B: <b>PDB Molecule:</b> kirola; <b>PDBTitle:</b> crystal structure of kirola (act d 11) - triclinic form
51	<a href="#">d1icxa_</a>	Alignment	not modelled	99.2	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
						<b>PDB header:</b> transport protein

52	<a href="#">c2r55B_</a>	Alignment	not modelled	99.2	13	<b>Chain:</b> B: <b>PDB Molecule:</b> star-related lipid transfer protein 5; <b>PDBTitle:</b> human star-related lipid transfer protein 5
53	<a href="#">c3ot1A_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261
54	<a href="#">c3p01C_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> steroidogenic acute regulatory protein, mitochondrial; <b>PDBTitle:</b> human steroidogenic acute regulatory protein
55	<a href="#">d1xn5a_</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
56	<a href="#">c2mouA_</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> star-related lipid transfer protein 6; <b>PDBTitle:</b> solution structure of star-related lipid transfer domain protein 62 (stard6)
57	<a href="#">c3q6aH_</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116
58	<a href="#">c4rejA_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> major latex-like protein; <b>PDBTitle:</b> crystal structure of cytosol major latex-like protein 151 (glp) from2 panax ginseng. (crystal-3)
59	<a href="#">d1em2a_</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> STAR domain
60	<a href="#">c3c0vC_</a>	Alignment	not modelled	99.1	10	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> cytokinin-specific binding protein; <b>PDBTitle:</b> crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12
61	<a href="#">d1qmra_</a>	Alignment	not modelled	99.1	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
62	<a href="#">c6ggq9A_</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> major allergen cor a 1.0401; <b>PDBTitle:</b> solution structure of the hazel allergen cor a 1.0401
63	<a href="#">c2k7hA_</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> stress-induced protein sam22; <b>PDBTitle:</b> nmr solution structure of soybean allergen gly m 4
64	<a href="#">d1e09a_</a>	Alignment	not modelled	99.1	9	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
65	<a href="#">c2kewA_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yndb; <b>PDBTitle:</b> the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy
66	<a href="#">d1jssa_</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> STAR domain
67	<a href="#">d1xn6a_</a>	Alignment	not modelled	99.1	9	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
68	<a href="#">d2bk0a1</a>	Alignment	not modelled	99.1	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
69	<a href="#">d2il5a1</a>	Alignment	not modelled	99.1	4	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
70	<a href="#">c1jssB_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cholesterol-regulated start protein 4; <b>PDBTitle:</b> crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4).
71	<a href="#">c3ie5A_</a>	Alignment	not modelled	99.1	8	<b>PDB header:</b> plant protein, biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> phenolic oxidative coupling protein hyp-1; <b>PDBTitle:</b> crystal structure of hyp-1 protein from hypericum perforatum (st2 john's wort) involved in hypericin biosynthesis
72	<a href="#">c2i9yA_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> major latex protein-like protein 28 or mlp-like <b>PDBTitle:</b> solution structure of arabidopsis thaliana protein2 at1g70830, a member of the major latex protein family
73	<a href="#">c2lakA_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ahsa1-like protein rhe_ch02687; <b>PDBTitle:</b> solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242
74	<a href="#">d1zxfa1</a>	Alignment	not modelled	99.0	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
75	<a href="#">d1xdfa1</a>	Alignment	not modelled	99.0	12	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
76	<a href="#">c3oh8A_</a>	Alignment	not modelled	99.0	7	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate sugar epimerase (sula family); <b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
						<b>PDB header:</b> plant protein

77	<a href="#">c3rwsA</a>	Alignment	not modelled	99.0	12	<b>Chain:</b> A: <b>PDB Molecule:</b> mtn13 protein; <b>PDBTitle:</b> crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin
78	<a href="#">d1fm4a</a>	Alignment	not modelled	99.0	9	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
79	<a href="#">d3elia1</a>	Alignment	not modelled	98.9	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
80	<a href="#">c2nn5A</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ef_2215; <b>PDBTitle:</b> structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis
81	<a href="#">d1ln1a</a>	Alignment	not modelled	98.9	8	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> STAR domain
82	<a href="#">d2k5ga1</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
83	<a href="#">d2nn5a1</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
84	<a href="#">c2e3rB</a>	Alignment	not modelled	98.9	8	<b>PDB header:</b> lipid transport <b>Chain:</b> B: <b>PDB Molecule:</b> lipid-transfer protein cert; <b>PDBTitle:</b> crystal structure of cert start domain in complex with c18-2 ceramide (p1)
85	<a href="#">d1txca1</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
86	<a href="#">c3fo5A</a>	Alignment	not modelled	98.8	12	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase, adipose associated, isoform bfit2; <b>PDBTitle:</b> human start domain of acyl-coenzyme a thioesterase 11 (acot11)
87	<a href="#">c2luzA</a>	Alignment	not modelled	98.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> calu16; <b>PDBTitle:</b> solution nmr structure of calu16 from micromonospora echinospora,2 northeast structural genomics consortium (nesg) target mir12
88	<a href="#">d1x53a1</a>	Alignment	not modelled	98.6	8	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> AHSA1 domain
89	<a href="#">c3ni8A</a>	Alignment	not modelled	98.5	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pfc0360w protein; <b>PDBTitle:</b> crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum
90	<a href="#">d2psoa1</a>	Alignment	not modelled	98.3	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> STAR domain
91	<a href="#">c5z4eA</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txno9; <b>PDBTitle:</b> an anthrahydroquino-gama-pyrone synthase txn09
92	<a href="#">c2psoc</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> star-related lipid transfer protein 13; <b>PDBTitle:</b> human stard13 (dlc2) lipid transfer and protein localization domain
93	<a href="#">d2ffsa1</a>	Alignment	not modelled	94.8	9	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> PA1206-like
94	<a href="#">d1vjha</a>	Alignment	not modelled	94.1	13	<b>Fold:</b> TBP-like <b>Superfamily:</b> Bet v1-like <b>Family:</b> Pathogenesis-related protein 10 (PR10)-like
95	<a href="#">c2ejxA</a>	Alignment	not modelled	74.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stk_08120; <b>PDBTitle:</b> crystal structure of the hypothetical protein stk_08120 from2 sulfolobus tokodaii
96	<a href="#">c3qrzC</a>	Alignment	not modelled	49.2	24	<b>PDB header:</b> hormone receptor <b>Chain:</b> C: <b>PDB Molecule:</b> abscisic acid receptor pyl5; <b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
97	<a href="#">c2lafA</a>	Alignment	not modelled	48.4	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein 34; <b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
98	<a href="#">c2lioA</a>	Alignment	not modelled	23.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322
99	<a href="#">c3qkbB</a>	Alignment	not modelled	20.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution