







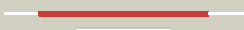




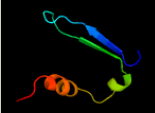








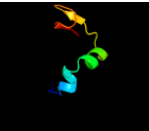

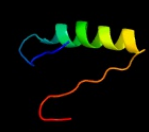

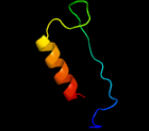
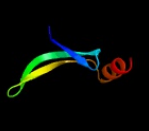





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3735 (-)_4186267_4186755
Date	Fri Aug 9 18:20:43 BST 2019
Unique Job ID	13cea117bf89a3b9

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ekmC_	 Alignment		100.0	58	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein st1511; PDBTitle: structure of st1219 protein from sulfolobus tokodaii
2	c2gl0A_	 Alignment		100.0	55	PDB header: transferase Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: structure of pae2307 in complex with adenosine
3	d1vgga_	 Alignment		100.0	58	Fold: Ta1353-like Superfamily: Ta1353-like Family: Ta1353-like
4	c2d16B_	 Alignment		100.0	45	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ph1918; PDBTitle: crystal structure of ph1918 protein from pyrococcus horikoshii ot3
5	d1rlha_	 Alignment		100.0	46	Fold: Ta1353-like Superfamily: Ta1353-like Family: Ta1353-like
6	c4eacC_	 Alignment		69.5	26	PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12
7	c4lj2A_	 Alignment		49.2	27	PDB header: lyase Chain: A: PDB Molecule: chorismate synthase; PDBTitle: crystal structure of chorismate synthase from acinetobacter baumannii2 at 3.15a resolution
8	c1ypxA_	 Alignment		46.7	30	PDB header: transferase Chain: A: PDB Molecule: putative vitamin-b12 independent methionine synthase family PDBTitle: crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
9	c3bdkB_	 Alignment		41.3	21	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
10	c4h9kA_	 Alignment		32.9	56	PDB header: hydrolase Chain: A: PDB Molecule: hog cholera virus; PDBTitle: crystal structure of cleavage site mutant of npro of classical swine2 fever virus.
11	c5o6uB_	 Alignment		31.0	29	PDB header: antiviral protein Chain: B: PDB Molecule: crispr-associated protein, csy4 family; PDBTitle: structure of the cascade-i-fv r-loop complex from shewanella2 putrefaciens

12	c2ly2A_	Alignment		30.7	24	PDB header: rna binding protein Chain: A: PDB Molecule: tudor domain-containing protein 7; PDBTitle: nmr structure of the second and third lotus domains of tudor domain-2 containing protein 7 (nmr ensemble overlay for lotus #3)
13	c2xlkB_	Alignment		28.2	33	PDB header: hydrolase/rna Chain: B: PDB Molecule: csy4 endoribonuclease; PDBTitle: crystal structure of the csy4-crrna complex, orthorhombic form
14	c3fpnA_	Alignment		27.9	31	PDB header: dna binding protein Chain: A: PDB Molecule: geobacillus stearothermophilus uvra interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains
15	c3zfnA_	Alignment		27.7	50	PDB header: hydrolase Chain: A: PDB Molecule: n-terminal protease npro; PDBTitle: crystal structure of product-like, processed n-terminal protease npro
16	c5ofbB_	Alignment		27.5	36	PDB header: nuclear protein Chain: B: PDB Molecule: morc family cw-type zinc finger protein 2; PDBTitle: crystal structure of human morc2 (residues 1-603) with spinal muscular2 atrophy mutation s87l
17	d1o6aa_	Alignment		26.3	28	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
18	c1t7IA_	Alignment		25.9	29	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of cobalamin-independent methionine synthase from t.2 maritima
19	c3l7sA_	Alignment		24.5	29	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of mete coordinated with zinc from streptococcus2 mutans
20	d1u1ha2	Alignment		23.6	33	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
21	c5xrwA_	Alignment	not modelled	23.4	21	PDB header: motor protein Chain: A: PDB Molecule: flii; PDBTitle: crystal structure of flagellar motor switch complex from h. pylori
22	d1zja1	Alignment	not modelled	21.2	18	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
23	c3mx7A_	Alignment	not modelled	19.5	45	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: crystal structure analysis of human faim-ntd
24	d1u1ha1	Alignment	not modelled	15.1	23	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
25	c2nq5A_	Alignment	not modelled	14.4	29	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of methyltransferase from streptococcus mutans
26	d1tz9a_	Alignment	not modelled	13.7	22	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
27	c2mmtA_	Alignment	not modelled	13.5	44	PDB header: antibiotic Chain: A: PDB Molecule: microcin j25 rgdf mutant; PDBTitle: lasso peptide-based integrin inhibitor: microcin j25 variant with rgdf2 substitution of gly12-ile13-gly14-thr15
28	c1y96C_	Alignment	not modelled	12.8	25	PDB header: rna binding protein Chain: C: PDB Molecule: gem-associated protein 6; PDBTitle: crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
						PDB header: hydrolase Chain: B: PDB Molecule: cleavage and polyadenylation specificity

29	c2xr1B_	Alignment	not modelled	11.4	24	factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
30	c2xdqB_	Alignment	not modelled	11.1	27	PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: dark operative protochlorophyllide oxidoreductase (chlnc-hlb)2 complex
31	c3cxjB_	Alignment	not modelled	11.0	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
32	c3af5A_	Alignment	not modelled	10.0	29	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
33	c2xr1A_	Alignment	not modelled	9.6	24	PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
34	c2ycbA_	Alignment	not modelled	9.6	18	PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor; PDBTitle: structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
35	c3rpdB_	Alignment	not modelled	9.2	27	PDB header: transferase Chain: B: PDB Molecule: methionine synthase (b12-independent); PDBTitle: the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
36	c4v02C_	Alignment	not modelled	9.2	18	PDB header: cell cycle Chain: C: PDB Molecule: probable septum site-determining protein minc; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
37	c2yqrA_	Alignment	not modelled	9.1	20	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0907 protein; PDBTitle: solution structure of the kh domain in kiaa0907 protein
38	c3ievA_	Alignment	not modelled	9.0	36	PDB header: nucleotide binding protein/rna Chain: A: PDB Molecule: gtp-binding protein era; PDBTitle: crystal structure of era in complex with mggpn and the 3' end of 16s2 rrna
39	c3r89A_	Alignment	not modelled	7.6	14	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
40	c3fioB_	Alignment	not modelled	7.5	36	PDB header: nucleotide binding protein, metal bindin Chain: B: PDB Molecule: a cystathionine beta-synthase domain protein PDBTitle: crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
41	c3rv1B_	Alignment	not modelled	7.5	22	PDB header: rna binding protein Chain: B: PDB Molecule: k. polysporus dcr1; PDBTitle: crystal structure of the n-terminal and rnase iii domains of k.2 polysporus dcr1 e224q mutant
42	d1ec6a_	Alignment	not modelled	7.3	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
43	d1dt4a_	Alignment	not modelled	7.3	21	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
44	d1gsoa2	Alignment	not modelled	7.1	28	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
45	c3h0gH_	Alignment	not modelled	6.8	21	PDB header: transcription Chain: H: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc3; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
46	d1fc4a_	Alignment	not modelled	6.7	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
47	c5g5rA_	Alignment	not modelled	6.7	20	PDB header: hydrolase Chain: A: PDB Molecule: site-2 protease; PDBTitle: cbs domain tandem of site-2 protease from archaeoglobus fulgidus in2 complex with llama nanobody - apo form
48	d1kwga1	Alignment	not modelled	6.5	13	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
49	c4zfb_	Alignment	not modelled	6.4	15	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase egtc; PDBTitle: ergothioneine-biosynthetic ntn hydrolase egtc, apo form
50	c2n5jA_	Alignment	not modelled	6.4	25	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 n-terminal domain
51	d1x87a_	Alignment	not modelled	6.2	41	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
52	c3uepB_	Alignment	not modelled	6.2	17	PDB header: protein transport Chain: B: PDB Molecule: yscq-c, type iii secretion protein; PDBTitle: crystal structure of ysqc-c from yersinia pseudotuberculosis
53	c3mtgA_	Alignment	not modelled	6.0	15	PDB header: transferase Chain: A: PDB Molecule: putative phosphoenolpyruvate-dependent sugar PDBTitle: crystal structure of a putative phosphoenolpyruvate-

						dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
54	d2ffca1	Alignment	not modelled	5.8	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
55	c5lj3G	Alignment	not modelled	5.7	17	PDB header: splicing Chain: G: PDB Molecule: isy1; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
56	c2ipcB	Alignment	not modelled	5.7	29	PDB header: transport protein Chain: B: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
57	d1viga	Alignment	not modelled	5.7	24	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
58	c3lyvF	Alignment	not modelled	5.7	58	PDB header: chaperone Chain: F: PDB Molecule: ribosome-associated factor y; PDBTitle: crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
59	d1twfh	Alignment	not modelled	5.6	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNA polymerase subunit RBP8
60	d2q66a2	Alignment	not modelled	5.6	29	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly(A) polymerase, PAP, N-terminal domain
61	c5z9aB	Alignment	not modelled	5.5	31	PDB header: lyase Chain: B: PDB Molecule: chorismate synthase; PDBTitle: crystal structure of chorismate synthase from pseudomonas aeruginosa
62	c4lvpA	Alignment	not modelled	5.5	32	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 81; PDBTitle: crystal structure of ift81 n-terminal domain
63	c1yrlD	Alignment	not modelled	5.4	16	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
64	c4yxaB	Alignment	not modelled	5.4	14	PDB header: protein transport Chain: B: PDB Molecule: surface presentation of antigens protein spao; PDBTitle: complex of spao(spao1,2 semet) and orgb(apar)::t4lysozyme fusion2 protein
65	c3rv0C	Alignment	not modelled	5.4	42	PDB header: rna binding protein Chain: C: PDB Molecule: k. polysporus dcr1; PDBTitle: crystal structure of k. polysporus dcr1 without the c-terminal dsrbd
66	c5ix1A	Alignment	not modelled	5.3	28	PDB header: transcription Chain: A: PDB Molecule: morc family cw-type zinc finger protein 3; PDBTitle: crystal structure of mouse morc3 atpase-cw cassette in complex with2 amppnp and h3k4me3 peptide
67	c3q91D	Alignment	not modelled	5.3	33	PDB header: hydrolase Chain: D: PDB Molecule: uridine diphosphate glucose pyrophosphatase; PDBTitle: crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
68	c3aerB	Alignment	not modelled	5.3	36	PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
69	c4dfcB	Alignment	not modelled	5.2	24	PDB header: hydrolase/dna binding protein Chain: B: PDB Molecule: uvrabc system protein a; PDBTitle: core uvra/trcf complex
70	c5lahA	Alignment	not modelled	5.2	63	PDB header: toxin Chain: A: PDB Molecule: tau-anmtx ueq 12-1; PDBTitle: nmr structure of the sea anemone peptide tau-anmtx ueq 12-1 with an2 uncommon fold
71	c3auyB	Alignment	not modelled	5.2	25	PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
72	c2hh3A	Alignment	not modelled	5.1	21	PDB header: rna binding protein Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the third kh domain of ksrp