
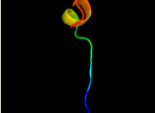

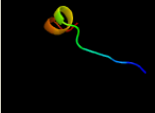





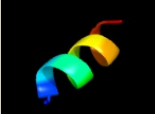



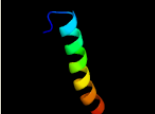

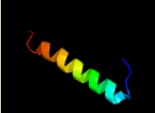





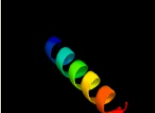
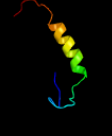
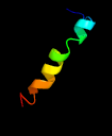
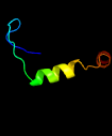


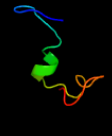
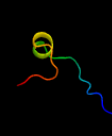

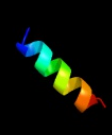


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2237A_(RVBD2237A)_2510359_2510595
 Date Mon Aug 5 13:25:37 BST 2019
 Unique Job ID 4cb2e3c88d77978a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3absD_	 Alignment		59.3	53	PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adenylpentylcobalamin and ethanolamine
2	c3anyB_	 Alignment		59.3	53	PDB header: lyase Chain: B: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
3	c5cofA_	 Alignment		36.3	33	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
4	c2oqgB_	 Alignment		33.5	32	PDB header: transcription Chain: B: PDB Molecule: transcription factor hy5; PDBTitle: crystal structure of hy5 leucine zipper homodimer from arabidopsis2 thaliana
5	c2kitA_	 Alignment		25.3	55	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase tor1; PDBTitle: the solution structure of the reduced yeast tor1 fatc domain bound to2 dpc micelles at 298k
6	c1w1nA_	 Alignment		25.3	55	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 3-kinase tor1; PDBTitle: the solution structure of the fatc domain of the protein kinase tor12 from yeast
7	c6anrA_	 Alignment		21.6	26	PDB header: hydrolase Chain: A: PDB Molecule: colibactin self-protection protein clbs; PDBTitle: crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster
8	c4n6cB_	 Alignment		18.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
9	c2kdpA_	 Alignment		17.2	60	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase complex subunit sap30; PDBTitle: solution structure of the sap30 zinc finger motif
10	c3r10Y_	 Alignment		16.4	30	PDB header: membrane protein/exocytosis Chain: Y: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: truncated snare complex with complexin (p1)
11	c3f1iH_	 Alignment		15.1	35	PDB header: protein binding Chain: H: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: human escrt-0 core complex

12	c3varA_	Alignment		15.1	14	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of dnpep, znzn form
13	c4btgB_	Alignment		14.0	46	PDB header: virus Chain: B: PDB Molecule: major inner protein p1; PDBTitle: coordinates of the bacteriophage phi6 capsid subunits (p1a and p1b)2 fitted into the cryoem reconstruction of the procapsid at 4.4 a3 resolution
14	c4emeB_	Alignment		13.7	19	PDB header: hydrolase Chain: B: PDB Molecule: m18 aspartyl aminopeptidase; PDBTitle: x-ray crystal structure and specificity of the plasmodium falciparum2 malaria aminopeptidase
15	d1t3ta3	Alignment		13.4	43	Fold: PurS-like Superfamily: PurS-like Family: FGAM synthase PurL, PurS-like domain
16	c3c2qA_	Alignment		13.2	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
17	c4i7aD_	Alignment		11.7	42	PDB header: structural protein Chain: D: PDB Molecule: ethanolamine utilization protein eutn/carboxysome PDBTitle: grpn pentameric microcompartment shell protein from rhodospirillum2 rubrum
18	c2d07A_	Alignment		10.8	22	PDB header: hydrolase Chain: A: PDB Molecule: g/t mismatch-specific thymine dna glycosylase; PDBTitle: crystal structure of sumo-3-modified thymine-dna glycosylase
19	c5z08C_	Alignment		10.8	40	PDB header: cell cycle Chain: C: PDB Molecule: cenp-k; PDBTitle: the crystal structure of kinetochore subunits cenp-h/i/k triple2 complex
20	d2o2aa1	Alignment		10.7	38	Fold: SecB-like Superfamily: SecB-like Family: SP1558-like
21	c5wsxA_	Alignment	not modelled	9.8	56	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of sav606
22	d2ywqa1	Alignment	not modelled	9.8	30	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
23	c2na4A_	Alignment	not modelled	9.6	29	PDB header: chaperone, protein transport Chain: A: PDB Molecule: curli production assembly/transport component csge; PDBTitle: curli secretion specificity factor csge w48a/f79a mutant
24	c3vviH_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: H: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
25	c3vviD_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: D: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
26	c3vviG_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: G: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
27	c3vviC_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: C: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
						PDB header: transport protein

28	c3vviB_	Alignment	not modelled	9.4	44	Chain: B: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
29	c3vviE_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: E: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
30	c3vviA_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: A: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
31	c3vviF_	Alignment	not modelled	9.4	44	PDB header: transport protein Chain: F: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
32	d1qmga2	Alignment	not modelled	9.3	41	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
33	c5msjD_	Alignment	not modelled	9.1	11	PDB header: structural protein Chain: D: PDB Molecule: proteasome activator complex subunit 1; PDBTitle: mouse pa28alpha
34	c1yveK_	Alignment	not modelled	8.9	41	PDB header: oxidoreductase Chain: K: PDB Molecule: acetoxyhydroxy acid isomeroeductase; PDBTitle: acetoxyhydroxy acid isomeroeductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropylxamate)
35	d1y7ea2	Alignment	not modelled	8.7	37	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
36	d2hnga1	Alignment	not modelled	8.3	31	Fold: SecB-like Superfamily: SecB-like Family: SP1558-like
37	c2f9uD_	Alignment	not modelled	8.3	86	PDB header: viral protein Chain: D: PDB Molecule: polyprotein; PDBTitle: hcv ns3 protease domain with ns4a peptide and a ketoamide2 inhibitor with a p2 norborane
38	d1ufza_	Alignment	not modelled	8.2	40	Fold: RuvA C-terminal domain-like Superfamily: HBS1-like domain Family: HBS1-like domain
39	d2imra1	Alignment	not modelled	7.9	88	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: DR0824-like
40	c4xlgB_	Alignment	not modelled	7.6	15	PDB header: hydrolase Chain: B: PDB Molecule: structure-specific endonuclease subunit slx4; PDBTitle: c. glabrata slx1 in complex with slx4ccd.
41	c2c2pA_	Alignment	not modelled	7.4	36	PDB header: hydrolase Chain: A: PDB Molecule: g/u mismatch-specific dna glycosylase; PDBTitle: the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
42	c2lseA_	Alignment	not modelled	7.1	48	PDB header: de novo protein Chain: A: PDB Molecule: four helix bundle protein; PDBTitle: solution nmr structure of de novo designed four helix bundle protein,2 northeast structural genomics consortium (nseg) target or188
43	c3di4A_	Alignment	not modelled	6.6	38	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf1989; PDBTitle: crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
44	c1dipA_	Alignment	not modelled	6.5	43	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
45	d1muga_	Alignment	not modelled	6.4	35	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
46	c6k1dB_	Alignment	not modelled	6.1	50	PDB header: hydrolase Chain: B: PDB Molecule: exonuclease 3'-5' domain-containing protein 2; PDBTitle: crystal structure of exd2 exonuclease domain soaked in mn and gmp
47	c2yy0D_	Alignment	not modelled	6.1	16	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
48	c2my1A_	Alignment	not modelled	6.1	13	PDB header: splicing Chain: A: PDB Molecule: pre-mrna-splicing factor bud31; PDBTitle: solution structure of bud31p
49	c5yt6B_	Alignment	not modelled	6.0	60	PDB header: protein binding Chain: B: PDB Molecule: tax1-binding protein 1; PDBTitle: crystal structure of tax1bp1 ubz2 in complex with mono-ubiquitin
50	d2c52b1	Alignment	not modelled	5.8	38	Fold: Nuclear receptor coactivator interlocking domain Superfamily: Nuclear receptor coactivator interlocking domain Family: Nuclear receptor coactivator interlocking domain
51	c2nysA_	Alignment	not modelled	5.5	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: agr_c_3712p; PDBTitle: x-ray crystal structure of protein agr_c_3712 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr88.
						Fold: SspB-like

52	d2nysa1	Alignment	not modelled	5.5	31	Superfamily: SspB-like Family: AGR C 3712p-like
53	c5civA_	Alignment	not modelled	5.4	21	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
54	c6qbzA_	Alignment	not modelled	5.4	27	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome hibernation promoting factor; PDBTitle: solution structure of the n-terminal domain of the staphylococcus2 aureus hibernation promoting factor
55	c6b2zd_	Alignment	not modelled	5.1	36	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
56	c2jnsA_	Alignment	not modelled	5.1	18	PDB header: unknown function Chain: A: PDB Molecule: bromodomain-containing protein 4; PDBTitle: solution structure of the bromodomain-containing protein 42 et domain