




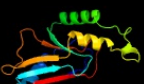


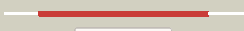
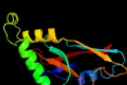











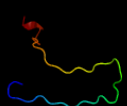
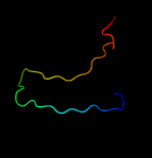


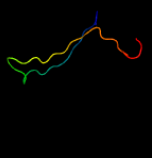
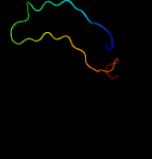
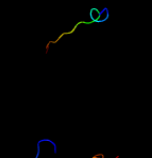
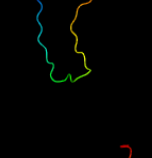
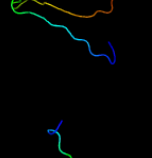



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2556c_(-)_2876586_2876975
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	45627bf60fa85b80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p6cB_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: aq_2013 protein; PDBTitle: crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
2	d1vpha_	 Alignment		100.0	29	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
3	d1vmja_	 Alignment		100.0	22	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
4	c1ve0A_	 Alignment		100.0	28	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein (st2072); PDBTitle: crystal structure of uncharacterized protein st2072 from sulfobolus2 tokodaii
5	c2p6hB_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
6	d1vmha_	 Alignment		100.0	26	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
7	d1vmfa_	 Alignment		100.0	24	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
8	c2cu5C_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved hypothetical protein tt1486; PDBTitle: crystal structure of the conserved hypothetical protein tt1486 from 2 thermus thermophilus hb8
9	d1ojja_	 Alignment		38.1	11	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
10	c2rfyB_	 Alignment		35.6	12	PDB header: hydrolase Chain: B: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: crystal structure of cellobiohydrolase from melanocarpus albomyces2 complexed with cellobiose
11	c4zpb_	 Alignment		34.8	17	PDB header: hydrolase Chain: B: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: dictyostelium purpureum cellobiohydrolase cel7a apo structure

12	d1gpia_	Alignment		34.8	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
13	c2yg1A_	Alignment		34.7	14	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: apo structure of cellobiohydrolase 1 (cel7a) from heterobasidion2 annosum
14	d2v3ia1	Alignment		33.8	14	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
15	c4csiB_	Alignment		33.4	17	PDB header: hydrolase Chain: B: PDB Molecule: cellulase; PDBTitle: crystal structure of the thermostable cellobiohydrolase2 cel7a from the fungus humicola grisea var. thermoidea.
16	d1q9ha_	Alignment		31.3	12	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
17	c2mdaB_	Alignment		31.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
18	d3ovwa_	Alignment		30.2	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
19	c4hapB_	Alignment		30.2	12	PDB header: hydrolase Chain: B: PDB Molecule: gh7 family protein; PDBTitle: crystal structure of a gh7 family cellobiohydrolase from limnoria2 quadripunctata in complex with cellobiose
20	d2qmwa2	Alignment		29.4	7	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
21	c4xnnA_	Alignment	not modelled	28.7	15	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase chbi; PDBTitle: crystal structure of a gh7 family cellobiohydrolase from daphnia pulex
22	c3hi2D_	Alignment	not modelled	25.2	28	PDB header: dna binding protein/toxin Chain: D: PDB Molecule: motility quorum-sensing regulator mqsr; PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqsA2 (ygit/b3021) in complex with the e. coli toxin mqsR (ygiu/b3022)
23	d1eg1a_	Alignment	not modelled	25.2	12	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
24	c5o51A_	Alignment	not modelled	19.3	25	PDB header: protein binding Chain: A: PDB Molecule: rho guanyl nucleotide exchange factor (rom2), putative; PDBTitle: afrom2 cnh domain
25	d1n8ia_	Alignment	not modelled	19.2	21	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
26	c3luyA_	Alignment	not modelled	16.8	21	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
27	d1phza1	Alignment	not modelled	15.8	7	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
28	c3mwbA_	Alignment	not modelled	15.7	7	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a

29	d1i8fa_	Alignment	not modelled	14.4	16	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
30	d2hq2a1	Alignment	not modelled	13.1	20	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/Chus-like
31	c4lubA_	Alignment	not modelled	12.2	7	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
32	c5yvFD_	Alignment	not modelled	12.0	20	PDB header: plant protein Chain: D: PDB Molecule: bfa1; PDBTitle: crystal structure of bfa1
33	c6c6lO_	Alignment	not modelled	11.6	6	PDB header: membrane protein Chain: O: PDB Molecule: v-type proton atpase subunit f; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
34	d1cl1a_	Alignment	not modelled	11.1	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
35	c6cgvW_	Alignment	not modelled	10.9	47	PDB header: virus Chain: W: PDB Molecule: pre-protein vi; PDBTitle: revised crystal structure of human adenovirus
36	d1omwa2	Alignment	not modelled	10.8	31	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
37	d1dq3a2	Alignment	not modelled	10.5	26	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: PI-Pfui intein middle domain
38	c3er0A_	Alignment	not modelled	10.4	18	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5a-2; PDBTitle: crystal structure of the full length eif5a from2 saccharomyces cerevisiae
39	c2qdrA_	Alignment	not modelled	9.9	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
40	d2j0pa1	Alignment	not modelled	9.9	14	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/Chus-like
41	d1ud2a1	Alignment	not modelled	9.6	26	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
42	d2drpa2	Alignment	not modelled	9.6	13	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
43	c3c9pA_	Alignment	not modelled	9.5	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sp1917; PDBTitle: crystal structure of uncharacterized protein sp1917
44	c6dgaA_	Alignment	not modelled	8.3	17	PDB header: unknown function Chain: A: PDB Molecule: rpfr; PDBTitle: cronobacter turicensis rpfr quorum-sensing receptor rpff interaction2 domain
45	d1rutx4	Alignment	not modelled	8.2	0	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
46	c5dx5B_	Alignment	not modelled	8.1	22	PDB header: lyase Chain: B: PDB Molecule: methionine gamma-lyase; PDBTitle: crystal structure of methionine gamma-lyase from clostridium2 sporogenes
47	c2qqnB_	Alignment	not modelled	7.9	22	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-lyase; PDBTitle: cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
48	d1d8ca_	Alignment	not modelled	7.7	22	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
49	c2qmxB_	Alignment	not modelled	7.2	7	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
50	c4mcjC_	Alignment	not modelled	6.9	19	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nucleoside deoxyribosyltransferase2 (bdi_0649) from parabacteroides distasonis atcc 8503 at 2.40 a3 resolution
51	c4ue0A_	Alignment	not modelled	6.8	39	PDB header: viral protein Chain: A: PDB Molecule: fiber; PDBTitle: structure of the bovine atadenovirus type 4 fibre head protein
52	c2i57A_	Alignment	not modelled	6.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an uncharacterized thioredoxin-like protein from2 clostridium perfringens
53	d1mwza_	Alignment	not modelled	6.6	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
54	c5dggB_	Alignment	not modelled	6.3	38	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: central domain of uncharacterized lpg1148 protein from legionella2 pneumophila
						Fold: Immunoglobulin-like beta-sandwich

55	d1xo8a_	Alignment	not modelled	6.3	35	Superfamily: LEA14-like Family: LEA14-like
56	c2ogxB_	Alignment	not modelled	6.3	13	PDB header: metal binding protein Chain: B; PDB Molecule: molybdenum storage protein subunit beta; PDBTitle: the crystal structure of the molybdenum storage protein from <i>azotobacter vinelandii</i> loaded with polyoxotungstates (wsto)
57	c3i38E_	Alignment	not modelled	5.5	33	PDB header: chaperone Chain: E; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from <i>klebsiella2 pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578
58	c3i38C_	Alignment	not modelled	5.5	33	PDB header: chaperone Chain: C; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from <i>klebsiella2 pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578
59	c3i38L_	Alignment	not modelled	5.4	33	PDB header: chaperone Chain: L; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from <i>klebsiella2 pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578
60	c3jb9b_	Alignment	not modelled	5.4	16	PDB header: rna binding protein/rna Chain: B; PDB Molecule: pre-mrna-splicing factor cwf10; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution