


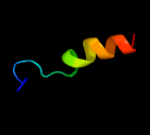

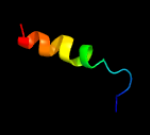





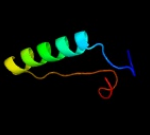

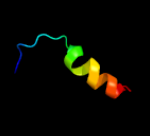

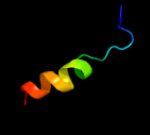

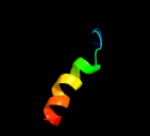



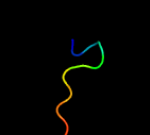


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2826c_(-)_3133719_3134603
Date	Wed Aug 7 12:50:49 BST 2019
Unique Job ID	d6cad19b2ed86d2e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ok0B_	 Alignment		99.5	21	PDB header: transferase Chain: B: PDB Molecule: putative; PDBTitle: crystal structure of putative nucleotidyltransferase from h. pylori
2	d1h9aa2	 Alignment		54.2	48	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
3	d1qkia2	 Alignment		42.8	43	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
4	c1h9aA_	 Alignment		42.7	48	PDB header: oxidoreductase (choh(d) - nad(p)) Chain: A: PDB Molecule: glucose 6-phosphate 1-dehydrogenase; PDBTitle: complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp
5	c4e9iB_	 Alignment		40.8	43	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
6	c5xw4A_	 Alignment		39.6	24	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
7	c4lqvA_	 Alignment		38.5	52	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
8	c2bhlB_	 Alignment		37.7	43	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
9	c1qkiE_	 Alignment		37.0	43	PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
10	c4dzdA_	 Alignment		36.7	45	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygch; PDBTitle: crystal structure of the crispr-associated protein cas6e from2 escherichia coli str. k-12
11	d1wj9a2	 Alignment		35.3	45	Fold: Ferredoxin-like Superfamily: CRISPR-associated protein Family: CRISPR-associated protein

12	c3qrqA_	Alignment		33.7	45	PDB header: rna binding protein/rna Chain: A: PDB Molecule: putative uncharacterized protein tthb192; PDBTitle: structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
13	c1wj9A_	Alignment		32.6	45	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of a crispr-associated protein from2 thermus thermophilus
14	c5u0aA_	Alignment		30.3	43	PDB header: immune system Chain: A: PDB Molecule: crispr-associated protein, cse3 family; PDBTitle: crispr rna-guided surveillance complex
15	d1fpza_	Alignment		27.1	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
16	c1fpzF_	Alignment		21.5	24	PDB header: hydrolase Chain: F: PDB Molecule: cyclin-dependent kinase inhibitor 3; PDBTitle: crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
17	c4nyhB_	Alignment		18.7	30	PDB header: hydrolase Chain: B: PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
18	c1yn9B_	Alignment		15.8	24	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
19	c5z5bA_	Alignment		12.3	32	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase; PDBTitle: crystal structure of tk-ptp in the g95a mutant form
20	d1j2oa2	Alignment		10.8	73	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
21	c2c46B_	Alignment	not modelled	10.1	23	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
22	c4ps2A_	Alignment	not modelled	9.5	36	PDB header: contractile protein Chain: A: PDB Molecule: putative type vi secretion protein; PDBTitle: structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule
23	d1dgsa3	Alignment	not modelled	9.1	45	Fold: ATP-grasp Superfamily: DNA ligase/mrna capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
24	c2ltuA_	Alignment	not modelled	9.1	53	PDB header: transferase Chain: A: PDB Molecule: 5'-amp-activated protein kinase catalytic subunit alpha-2; PDBTitle: solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
25	c6bmnA_	Alignment	not modelled	8.9	36	PDB header: transferase Chain: A: PDB Molecule: human dhhc20 palmitoyltransferase; PDBTitle: structure of human dhhc20 palmitoyltransferase, space group p63
26	c1dvpA_	Alignment	not modelled	8.8	26	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
27	c5lo2A_	Alignment	not modelled	8.7	45	PDB header: structural protein Chain: A: PDB Molecule: ppatyr; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
						PDB header: gene regulation Chain: O: PDB Molecule: inhibitor of trap, regulated by t-box (trp)

28	c3ld0Q_	Alignment	not modelled	8.5	50	sequence rtpa; PDBTitle: crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
29	c1yx5A_	Alignment	not modelled	8.0	46	PDB header: hydrolase Chain: A: PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
30	d1r7aa1	Alignment	not modelled	7.9	70	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
31	c1dgsB_	Alignment	not modelled	7.7	45	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
32	c2ly8A_	Alignment	not modelled	7.2	24	PDB header: chaperone Chain: A: PDB Molecule: budding yeast chaperone scm3; PDBTitle: the budding yeast chaperone scm3 recognizes the partially unfolded2 dimer of the centromere-specific cse4/h4 histone variant
33	c5o60P_	Alignment	not modelled	6.8	40	PDB header: ribosome Chain: P: PDB Molecule: 50s ribosomal protein l18; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
34	c3j3vO_	Alignment	not modelled	6.6	47	PDB header: ribosome Chain: O: PDB Molecule: 50s ribosomal protein l18; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
35	d2oa5a1	Alignment	not modelled	6.4	35	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
36	c3bboQ_	Alignment	not modelled	6.3	47	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l18; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
37	c5lo4A_	Alignment	not modelled	6.2	40	PDB header: structural protein Chain: A: PDB Molecule: ppa-ch3; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
38	c6eonA_	Alignment	not modelled	5.8	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: galactanase bt0290
39	d1d5ra2	Alignment	not modelled	5.7	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
40	d1cixa_	Alignment	not modelled	5.7	71	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
41	c1cixA_	Alignment	not modelled	5.7	71	PDB header: antimicrobial peptide Chain: A: PDB Molecule: protein (tachystatin a); PDBTitle: three-dimensional structure of antimicrobial peptide2 tachystatin a isolated from horseshoe crab
42	d1elka_	Alignment	not modelled	5.6	26	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
43	d2r7da1	Alignment	not modelled	5.5	73	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	c6mv5P_	Alignment	not modelled	5.3	44	PDB header: immune system Chain: P: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: anti-pcsk9 fab 6e2 bound to the n-terminal peptide from pcsk9 (e32k)
45	c5j9hA_	Alignment	not modelled	5.2	29	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)
46	c4a1sE_	Alignment	not modelled	5.2	100	PDB header: cell cycle Chain: E: PDB Molecule: re60102p; PDBTitle: crystallographic structure of the pins:insc complex
47	c1sseA_	Alignment	not modelled	5.1	43	PDB header: transcription activator Chain: A: PDB Molecule: ap-1 like transcription factor yap1; PDBTitle: solution structure of the oxidized form of the yap1 redox2 domain
48	c2bc4C_	Alignment	not modelled	5.1	31	PDB header: immune system Chain: C: PDB Molecule: hla class ii histocompatibility antigen, dm alpha chain; PDBTitle: crystal structure of hla-dm