








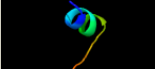




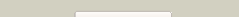
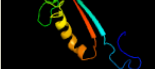



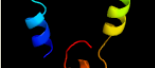

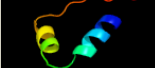
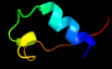










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2336 (-) _2610847_2611815
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	8eff3933f5cca657

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f5zK_	 Alignment		41.6	73	PDB header: oxidoreductase/protein binding Chain: K: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
2	c1zy8M_	 Alignment		40.6	73	PDB header: oxidoreductase Chain: M: PDB Molecule: pyruvate dehydrogenase protein x component, PDBTitle: the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.
3	c2f60K_	 Alignment		31.3	64	PDB header: protein binding Chain: K: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: crystal structure of the dihydrolipoamide dehydrogenase (e3)-binding2 domain of human e3-binding protein
4	c5h0jA_	 Alignment		25.6	47	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of wt pedobacter heparinus smug2
5	c3kwwF_	 Alignment		23.4	38	PDB header: toxin/protein transport Chain: F: PDB Molecule: lethal factor; PDBTitle: structural basis for the unfolding of anthrax lethal factor by2 protective antigen oligomers
6	c3ah5E_	 Alignment		21.6	17	PDB header: transferase Chain: E: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump
7	d1j7na1	 Alignment		21.4	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains
8	c4pugA_	 Alignment		19.6	20	PDB header: dna binding protein Chain: A: PDB Molecule: bola like protein; PDBTitle: bola1 from arabidopsis thaliana
9	c5x42B_	 Alignment		17.7	54	PDB header: protein transport Chain: B: PDB Molecule: icmo (dotl); PDBTitle: structure of dotl(590-659)-dotn derived from legionella pneumophila
10	d1oe4a_	 Alignment		16.2	31	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
11	c3o2eA_	 Alignment		16.0	29	PDB header: unknown function Chain: A: PDB Molecule: bola-like protein; PDBTitle: crystal structure of a bol-like protein from babesia bovis

12	c5nfmA_	Alignment		14.7	24	PDB header: ligase Chain: A: PDB Molecule: yrba; PDBTitle: crystal structure of yrba from sinorhizobium melliloti in complex with2 copper.
13	c5h93C_	Alignment		14.3	53	PDB header: hydrolase Chain: C: PDB Molecule: geobacter metallireducens smug1; PDBTitle: crystal structure of geobacter metallireducens smug1
14	c2hacA_	Alignment		14.1	63	PDB header: membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
15	c2hacB_	Alignment		14.1	63	PDB header: membrane protein Chain: B: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
16	c5w6yB_	Alignment		14.0	64	PDB header: biosynthetic protein,isomerase Chain: B: PDB Molecule: chorismate mutase; PDBTitle: physcomitrella patens chorismate mutase
17	c2q2kB_	Alignment		13.9	48	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
18	c2q2kA_	Alignment		12.8	48	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
19	c6h3pB_	Alignment		12.1	55	PDB header: plant protein Chain: B: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of the cytoplasmic chorismate mutase from zea mays
20	d5csma_	Alignment		12.1	27	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Allosteric chorismate mutase
21	c2af6G_	Alignment	not modelled	12.1	33	PDB header: transferase Chain: G: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of mycobacterium tuberculosis flavin dependent2 thymidylate synthase (mtb thyx) in the presence of co-factor fad and3 substrate analog 5-bromo-2'-deoxyuridine-5'-monophosphate (brdump)
22	c4ppuA_	Alignment	not modelled	12.0	55	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase 1, chloroplastic; PDBTitle: crystal structure of atcm1 with tyrosine bound in allosteric site
23	c5w8cA_	Alignment	not modelled	11.4	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: autoinducer synthase; PDBTitle: the structure of a coa-dependent acyl-homoserine lactone synthase,2 bjai, with mta and isovaleryl-coa
24	d1pv8a_	Alignment	not modelled	11.0	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinat dehydratase, ALAD (porphobilinogen synthase)
25	c5uebA_	Alignment	not modelled	10.3	22	PDB header: unknown function Chain: A: PDB Molecule: negoa.19184.a; PDBTitle: novel crystal structure of a hypothetical protein from neisseria2 gonorrhoeae
26	c2dhmA_	Alignment	not modelled	9.1	17	PDB header: protein binding Chain: A: PDB Molecule: protein bola; PDBTitle: solution structure of the bola protein from escherichia coli
27	c3tr3A_	Alignment	not modelled	9.0	31	PDB header: unknown function Chain: A: PDB Molecule: bola; PDBTitle: structure of a bola protein homologue from coxiella burnetii
28	c1v60A_	Alianment	not modelled	8.9	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: riken cdna 1810037g04;

						PDBTitle: solution structure of bola1 protein from mus musculus
29	c3fnnA_	Alignment	not modelled	8.7	27	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase thyx; PDBTitle: biochemical and structural analysis of an atypical thyx:2 corynebacterium glutamicum nchu 87078 depends on thya for3 thymidine biosynthesis
30	c3obkH_	Alignment	not modelled	8.3	23	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
31	d2c1ha1	Alignment	not modelled	7.9	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
32	c4k59A_	Alignment	not modelled	7.8	43	PDB header: rna binding protein Chain: A: PDB Molecule: rna binding protein rsmf; PDBTitle: crystal structure of pseudomonas aeruginosa rsmf
33	c1xs3A_	Alignment	not modelled	7.5	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein xc975; PDBTitle: solution structure analysis of the xc975 protein
34	c1xfzA_	Alignment	not modelled	7.2	31	PDB header: lyase/metal binding protein Chain: A: PDB Molecule: calmodulin-sensitive adenylate cyclase; PDBTitle: crystal structure of anthrax edema factor (ef) in complex with2 calmodulin in the presence of 1 millimolar exogenously added calcium3 chloride
35	c1xfuE_	Alignment	not modelled	7.2	31	PDB header: lyase/metal binding protein Chain: E: PDB Molecule: calmodulin-sensitive adenylate cyclase; PDBTitle: crystal structure of anthrax edema factor (ef) truncation mutant, ef-2 delta 64 in complex with calmodulin
36	d1h7na_	Alignment	not modelled	7.2	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
37	c4puiA_	Alignment	not modelled	6.7	34	PDB header: protein binding Chain: A: PDB Molecule: sufe-like protein, chloroplastic; PDBTitle: bola domain of sufe1 from arabidopsis thaliana
38	c6fpgG_	Alignment	not modelled	6.4	29	PDB header: cell invasion Chain: G: PDB Molecule: chromosome 16, whole genome shotgun sequence; PDBTitle: structure of the ustilago maydis chorismate mutase 1 in complex with a2 zea mays kiwellin
39	d2csua1	Alignment	not modelled	6.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
40	c2mm9A_	Alignment	not modelled	6.2	43	PDB header: transcription Chain: A: PDB Molecule: bola2; PDBTitle: solution structure of reduced bola2 from arabidopsis thaliana
41	c2nclA_	Alignment	not modelled	5.7	14	PDB header: protein binding Chain: A: PDB Molecule: bola-like protein 3; PDBTitle: solution structure of bola3 from homo sapiens
42	d1gzga_	Alignment	not modelled	5.7	28	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
43	c3gmvX_	Alignment	not modelled	5.6	40	PDB header: protein binding Chain: X: PDB Molecule: beta-lactamase inhibitory protein blip-i; PDBTitle: crystal structure of beta-lactamase inhibitory protein-i (blip-i) in2 apo form
44	d1coka_	Alignment	not modelled	5.6	11	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
45	c3gmxB_	Alignment	not modelled	5.5	53	PDB header: protein binding Chain: B: PDB Molecule: blp; PDBTitle: crystal structure of beta-lactamase inhibitory protein-like protein2 (blp) at 1.05 angstrom resolution
46	c1pwqA_	Alignment	not modelled	5.4	38	PDB header: hydrolase Chain: A: PDB Molecule: lethal factor; PDBTitle: crystal structure of anthrax lethal factor complexed with2 thioacetyl-tyr-pro-met-amide, a metal-chelating peptidyl3 small molecule inhibitor
47	d2py5a2	Alignment	not modelled	5.3	41	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
48	d1l6sa_	Alignment	not modelled	5.2	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
49	c5lzlH_	Alignment	not modelled	5.1	32	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: pyrobaculum caldifontis 5-aminolaevulinic acid dehydratase
50	c3pmkR_	Alignment	not modelled	5.1	53	PDB header: viral protein Chain: R: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex
51	c3pmkP_	Alignment	not modelled	5.1	53	PDB header: viral protein Chain: P: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex
52	c5dcaA_	Alignment	not modelled	5.0	23	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
53	c5oooA_	Alignment	not modelled	5.0	34	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein ns-s; PDBTitle: structure of the rift valley fever virus nss protein core

54	c3pmkN_	Alignment	not modelled	5.0	53	domain PDB header: viral protein Chain: N: PDB Molecule: phosphoprotein; PDBTitle: crystal structure of the vesicular stomatitis virus rna free2 nucleoprotein/phosphoprotein complex
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