
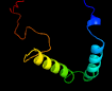
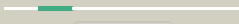
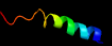

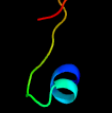

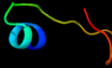











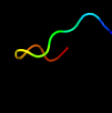

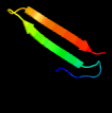

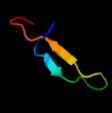

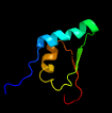

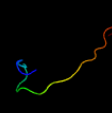
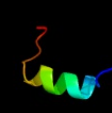

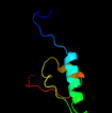


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3882c_(-)_4362210_4363598
Date	Sat Aug 10 22:05:06 BST 2019
Unique Job ID	b997c9dc9702a6db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4k2bA_	 Alignment		53.3	25	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
2	c1z65A_	 Alignment		41.1	29	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: mouse doppel 1-30 peptide
3	c5zkxA_	 Alignment		32.9	27	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: the postfusion structure of human-infecting bourbon virus envelope2 glycoprotein
4	c3duzA_	 Alignment		31.6	32	PDB header: viral protein Chain: A: PDB Molecule: major envelope glycoprotein; PDBTitle: crystal structure of the postfusion form of baculovirus2 fusion protein gp64
5	c4px7A_	 Alignment		31.2	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pggp
6	c5xebC_	 Alignment		30.0	32	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein; PDBTitle: structure of the envelope glycoprotein of dhori virus
7	c5zl6A_	 Alignment		29.8	15	PDB header: isomerase Chain: A: PDB Molecule: histidine racemase; PDBTitle: histidine racemase from leuconostoc mesenteroides subsp. sake nbrc2 102480
8	c5xeaB_	 Alignment		28.2	32	PDB header: viral protein Chain: B: PDB Molecule: envelope glycoprotein; PDBTitle: structure of thogoto virus envelope glycoprotein
9	c4eclA_	 Alignment		21.5	10	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
10	c5xcoB_	 Alignment		18.8	55	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asp-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide
11	d1dmla1	 Alignment		16.7	29	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor

12	c2k42B_	Alignment		15.5	38	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
13	c3mlqH_	Alignment		15.1	17	PDB header: transferase/transcription Chain: H: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
14	d1x4ka1	Alignment		12.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
15	c3co8B_	Alignment		11.7	12	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
16	c5gy6A_	Alignment		11.7	57	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease t1; PDBTitle: ribonuclease from hericium erinaceus (rnase he1)
17	d1w0da_	Alignment		11.7	36	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
18	c2daeA_	Alignment		11.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa0733 protein; PDBTitle: solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting protein 2 (map3k7ip2)
19	c3mb2J_	Alignment		10.8	39	PDB header: isomerase Chain: J: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
20	c4y2wA_	Alignment		10.8	17	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 1; PDBTitle: crystal structure of a thermostable alanine racemase from2 thermoanaerobacter tengcongensis mb4
21	d2rdea1	Alignment	not modelled	10.7	19	Fold: Split barrel-like Superfamily: PilZ domain-like Family: PilZ domain
22	c1dmlG_	Alignment	not modelled	10.0	29	PDB header: dna binding protein/transferase Chain: G: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
23	c2lnhC_	Alignment	not modelled	9.7	38	PDB header: signaling protein/protein binding Chain: C: PDB Molecule: secreted effector protein espf(u); PDBTitle: enterohaemorrhagic e. coli (ehc) exploits a tryptophan switch to2 hijack host f-actin assembly
24	d1fnja_	Alignment	not modelled	8.8	16	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
25	c3e2vA_	Alignment	not modelled	7.9	30	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
26	c3mlqE_	Alignment	not modelled	7.8	18	PDB header: transferase/transcription Chain: E: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
27	c5hk1A_	Alignment	not modelled	7.5	39	PDB header: membrane protein Chain: A: PDB Molecule: sigma non-opioid intracellular receptor 1; PDBTitle: human sigma-1 receptor bound to pd144418
28	c3h87D_	Alignment	not modelled	7.5	25	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

29	d1dbfa_	Alignment	not modelled	7.4	16	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
30	d2icsa1	Alignment	not modelled	7.3	42	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Adenine deaminase
31	c2ej9A_	Alignment	not modelled	7.2	16	PDB header: ligase Chain: A: PDB Molecule: putative biotin ligase; PDBTitle: crystal structure of biotin protein ligase from2 methanococcus jannaschii
32	c3e6eC_	Alignment	not modelled	7.1	14	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
33	d1rdsa_	Alignment	not modelled	7.1	40	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Fungal ribonucleases
34	d1mlaa2	Alignment	not modelled	6.9	26	Fold: Ferredoxin-like Superfamily: Probable ACP-binding domain of malonyl-CoA ACP transacylase Family: Probable ACP-binding domain of malonyl-CoA ACP transacylase
35	c5i8iD_	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
36	c2n5uA_	Alignment	not modelled	6.8	44	PDB header: photosynthesis Chain: A: PDB Molecule: tsr0524 protein; PDBTitle: solution structure of the cyanobacterial cytochrome b6f complex2 subunit petp
37	c3kw3B_	Alignment	not modelled	6.8	9	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
38	c2vy8A_	Alignment	not modelled	6.8	60	PDB header: transcription Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
39	c4bf5A_	Alignment	not modelled	6.7	12	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: structure of broad spectrum racemase from aeromonas hydrophila
40	c5yeeA_	Alignment	not modelled	6.7	50	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of lokipofilin1/rabbit actin complex
41	d1xhoa_	Alignment	not modelled	6.5	17	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
42	c1xhoB_	Alignment	not modelled	6.5	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682
43	c2na1A_	Alignment	not modelled	6.5	16	PDB header: transcription Chain: A: PDB Molecule: polycomb complex protein bmi-1, polyhomeotic-like 2; PDBTitle: uld complex
44	c4i0kC_	Alignment	not modelled	6.3	60	PDB header: hydrolase Chain: C: PDB Molecule: draiii; PDBTitle: crystal structure of a type ii restriction endonuclease
45	c4q6uA_	Alignment	not modelled	6.2	28	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
46	c2axoA_	Alignment	not modelled	5.8	13	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein atu2684; PDBTitle: x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
47	c5irpA_	Alignment	not modelled	5.7	21	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 2; PDBTitle: crystal structure of the alanine racemase bsu17640 from bacillus2 subtilis
48	d1pbya2	Alignment	not modelled	5.7	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
49	c4ag5A_	Alignment	not modelled	5.6	13	PDB header: hydrolase Chain: A: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
50	c2i6hA_	Alignment	not modelled	5.4	41	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0120; PDBTitle: structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
51	d2i6ha1	Alignment	not modelled	5.4	41	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Atu0120-like
52	c2vofB_	Alignment	not modelled	5.3	64	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-binding component 3; PDBTitle: structure of mouse a1 bound to the puma bh3-domain
53	d1i0va_	Alignment	not modelled	5.3	40	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Fungal ribonucleases
54	c1y96C_	Alignment	not modelled	5.3	32	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
55	c6apjA_	Alignment	not modelled	5.2	20 PDB header: transferase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminide alpha-2,6-sialyltransferase PDBTitle: crystal structure of human st6galnac2
56	c2wwaj_	Alignment	not modelled	5.2	15 PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l19; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
57	d1jmx2	Alignment	not modelled	5.1	38 Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
58	c1niuA_	Alignment	not modelled	5.1	17 PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: alanine racemase with bound inhibitor derived from l-2 cycloserine