


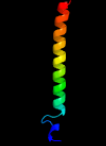





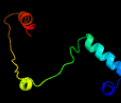
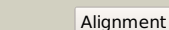
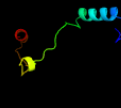

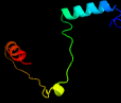
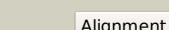

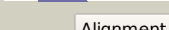







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1588c_(-)_1789175_1789843
Date	Fri Aug 2 13:30:18 BST 2019
Unique Job ID	7bad082843416c48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c4rC_	 Alignment		20.7	18	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein encoded by2 cryptic prophage
2	c2hv8D_	 Alignment		20.2	13	PDB header: protein transport Chain: D; PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
3	c3frwF_	 Alignment		19.0	17	PDB header: structural genomics, unknown function Chain: F; PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
4	c5tw9D_	 Alignment		16.6	25	PDB header: lipid-binding protein Chain: D; PDB Molecule: iron uptake system component efeo; PDBTitle: 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
5	c2dbaA_	 Alignment		15.0	27	PDB header: transcriptional regulator Chain: A; PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
6	cli1gA_	 Alignment		14.9	14	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
7	c2e1cA_	 Alignment		14.4	14	PDB header: transcription/dna Chain: A; PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
8	c3at7B_	 Alignment		13.5	18	PDB header: structural protein Chain: B; PDB Molecule: alginate-binding flagellin; PDBTitle: crystal structure of bacterial cell-surface alginate-binding protein2 alg7
9	c4bgoA_	 Alignment		12.6	14	PDB header: hydrolase Chain: A; PDB Molecule: efem m75 peptidase; PDBTitle: structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
10	c1m8pB_	 Alignment		11.0	28	PDB header: transferase Chain: B; PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
11	c3korD_	 Alignment		10.9	16	PDB header: transcription Chain: D; PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus

12	c2cfxD_	Alignment		10.5	14	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator Irpc; PDBTitle: structure of b.subtilis Irpc
13	c5o8kB_	Alignment		10.0	38	PDB header: replication Chain: B: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of mammalian rev7 in complex with rev3 1875-1895
14	c2a45H_	Alignment		9.7	33	PDB header: hydrolase/hydrolase inhibitor Chain: H: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
15	c4fjoD_	Alignment		9.1	46	PDB header: transferase/dna binding protein Chain: D: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of the rev1 ctd-rev3/7-pol kappa rir complex
16	c2kq5A_	Alignment		8.9	14	PDB header: unknown function Chain: A: PDB Molecule: avirulence protein; PDBTitle: solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
17	c3abdY_	Alignment		8.5	38	PDB header: cell cycle/replication Chain: Y: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
18	c3abdX_	Alignment		8.5	38	PDB header: cell cycle/replication Chain: X: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
19	c4czdD_	Alignment		7.8	14	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the Irp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
20	c4czdA_	Alignment		7.6	14	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the Irp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
21	c5jhfA_	Alignment	not modelled	7.1	33	PDB header: protein transport Chain: A: PDB Molecule: klth0d11660p; PDBTitle: crystal structure of atg13(17br)-atg13(17lr)-atg17-atg29-atg31 complex
22	d1j96a_	Alignment	not modelled	6.9	19	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
23	c3nufB_	Alignment	not modelled	6.4	25	PDB header: transcription regulator Chain: B: PDB Molecule: prd-containing transcription regulator; PDBTitle: crystal structure of a prd-containing transcription regulator2 (Isej_2718) from lactobacillus casei atcc 334 at 1.38 a resolution
24	c3abeZ_	Alignment	not modelled	5.9	38	PDB header: cell cycle/replication Chain: Z: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: structure of human rev7 in complex with a human rev3 fragment in a2 tetragonal crystal
25	c4wghA_	Alignment	not modelled	5.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde reductase; PDBTitle: crystal structure of aldo/keto reductase from klebsiella pneumoniae in2 complex with nadp and acetate at 1.8 a resolution