










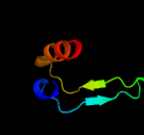





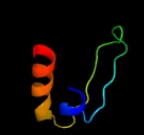



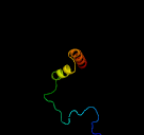
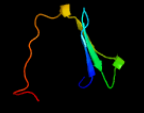

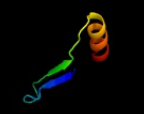


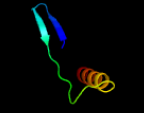


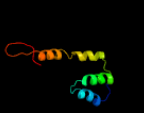


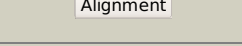
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1227c_(-)_1370298_1370831
Date	Wed Jul 31 22:05:31 BST 2019
Unique Job ID	8b2b13f83f69bb4e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2gcla1</a>	 Alignment		74.2	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> SSRP1-like
2	<a href="#">c3fssA</a>	 Alignment		51.4	8	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> histone chaperone rtt106; <b>PDBTitle:</b> structure of the tandem ph domains of rtt106
3	<a href="#">c6c4vA</a>	 Alignment		49.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1350-1461) of polyketide synthase pks13 from3 mycobacterium tuberculosis
4	<a href="#">c4tyzB</a>	 Alignment		49.4	11	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of an unknown protein from2 leishmania infantum
5	<a href="#">d2hthb1</a>	 Alignment		48.8	7	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> VPS36 N-terminal domain-like
6	<a href="#">d1zj8a1</a>	 Alignment		39.9	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
7	<a href="#">c3gypA</a>	 Alignment		29.5	8	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> histone chaperone rtt106; <b>PDBTitle:</b> rtt106p
8	<a href="#">d1j8ba</a>	 Alignment		29.4	18	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
9	<a href="#">d3c7bb2</a>	 Alignment		28.2	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
10	<a href="#">d2v4jb2</a>	 Alignment		22.8	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
11	<a href="#">d2ebfx3</a>	 Alignment		21.9	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> PMT C-terminal domain like

12	<a href="#">d2caya1</a>	Alignment		20.3	11	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> VPS36 N-terminal domain-like
13	<a href="#">c1ybxA</a>	Alignment		19.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> conserved hypothetical protein cth-383 from clostridium thermocellum
14	<a href="#">c5nocA</a>	Alignment		17.3	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> stage 0 sporulation protein j; <b>PDBTitle:</b> solution nmr structure of the c-terminal domain of parb (spo0j)
15	<a href="#">d3dcxa1</a>	Alignment		16.1	5	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> BPHL domain
16	<a href="#">d1aopa2</a>	Alignment		15.0	6	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
17	<a href="#">c4n7rD</a>	Alignment		12.0	13	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> genomic dna, chromosome 3, p1 clone: mx18; <b>PDBTitle:</b> crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
18	<a href="#">c2fwvA</a>	Alignment		12.0	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mtubf_01000852; <b>PDBTitle:</b> crystal structure of rv0813
19	<a href="#">d1zj8a2</a>	Alignment		11.1	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
20	<a href="#">c5x3xq</a>	Alignment		10.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> Q: <b>PDB Molecule:</b> uncharacterized protein cbiq; <b>PDBTitle:</b> 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
21	<a href="#">c5bncB</a>	Alignment	not modelled	10.2	15	<b>PDB header:</b> heme binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeq_6519; <b>PDBTitle:</b> structure of heme binding protein msmeq_6519 from mycobacterium2 smegmatis
22	<a href="#">d1puga</a>	Alignment	not modelled	10.1	20	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
23	<a href="#">c2d7dB</a>	Alignment	not modelled	10.1	32	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> 40-mer from uvrabc system protein b; <b>PDBTitle:</b> structural insights into the cryptic dna dependent atpase2 activity of uvrb
24	<a href="#">c2v4jE</a>	Alignment	not modelled	10.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
25	<a href="#">c3c7bE</a>	Alignment	not modelled	9.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
26	<a href="#">d2akja1</a>	Alignment	not modelled	8.6	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
27	<a href="#">c2v4jA</a>	Alignment	not modelled	8.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration

28	<a href="#">c3c7bA_</a>		Alignment	not modelled	7.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
29	<a href="#">d1iioa_</a>		Alignment	not modelled	7.3	22	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> Hypothetical protein MTH865 <b>Family:</b> Hypothetical protein MTH865
30	<a href="#">c2kw0A_</a>		Alignment	not modelled	6.6	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
31	<a href="#">c6eznH_</a>		Alignment	not modelled	6.6	17	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
32	<a href="#">c2kl8A_</a>		Alignment	not modelled	6.3	16	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> or15; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
33	<a href="#">d2dx5a1</a>		Alignment	not modelled	6.2	13	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> VPS36 N-terminal domain-like
34	<a href="#">c4e1pA_</a>		Alignment	not modelled	6.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
35	<a href="#">c4e1rA_</a>		Alignment	not modelled	6.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
36	<a href="#">c2n2aA_</a>		Alignment	not modelled	6.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erb2-2; <b>PDBTitle:</b> spatial structure of her2/erb2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
37	<a href="#">c4ev6E_</a>		Alignment	not modelled	5.7	13	<b>PDB header:</b> metal transport <b>Chain:</b> E: <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
38	<a href="#">c2hl7A_</a>		Alignment	not modelled	5.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
39	<a href="#">c5h92A_</a>		Alignment	not modelled	5.5	14	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [ferredoxin], chloroplastic; <b>PDBTitle:</b> crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal