



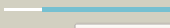
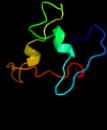

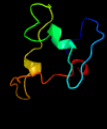



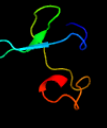







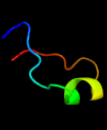

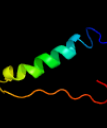


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3612c_(-)_4053697_4054026
Date	Fri Aug 9 18:20:29 BST 2019
Unique Job ID	a6dc6cfc100d97f1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3o5aB_</a>	 Alignment		63.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> diheme cytochrome c napb; <b>PDBTitle:</b> crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids
2	<a href="#">d1ogyb_</a>	 Alignment		46.7	29	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Di-heme elbow motif
3	<a href="#">c1jniA_</a>	 Alignment		38.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diheme cytochrome c napb; <b>PDBTitle:</b> structure of the napb subunit of the periplasmic nitrate2 reductase from haemophilus influenzae.
4	<a href="#">d1jnia_</a>	 Alignment		38.8	28	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Di-heme elbow motif
5	<a href="#">c2ykaB_</a>	 Alignment		23.0	100	<b>PDB header:</b> rna binding protein/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> 52 kda immediate-early phosphoprotein; <b>PDBTitle:</b> rrm domain of mrna export adaptor ref2-i bound to hvs orf572 peptide
6	<a href="#">c3ifuA_</a>	 Alignment		22.3	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein; <b>PDBTitle:</b> the crystal structure of porcine reproductive and respiratory syndrome2 virus (prsv) leader protease nsp1
7	<a href="#">c2c9lZ_</a>	 Alignment		6.9	42	<b>PDB header:</b> viral protein <b>Chain:</b> Z: <b>PDB Molecule:</b> bzlf1 trans-activator protein; <b>PDBTitle:</b> structure of the epstein-barr virus zebra protein
8	<a href="#">d1cf2o2</a>	 Alignment		5.9	37	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
9	<a href="#">c2o6iA_</a>	 Alignment		5.7	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hd domain protein; <b>PDBTitle:</b> structure of an enterococcus faecalis hd domain phosphohydrolase
10	<a href="#">d2o6ia1</a>	 Alignment		5.7	38	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
11	<a href="#">c6dexA_</a>	 Alignment		5.6	33	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of hydroxyurea sensitivity protein 1; <b>PDBTitle:</b> structure of eremothecium gossypii shu1:shu2 complex

12 [c3gqgD\\_](#)

Alignment



5.5

47

**PDB header:** splicing  
**Chain:** D: **PDB Molecule:** protein unc-119 homolog a;  
**PDBTitle:** crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a