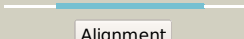

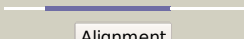
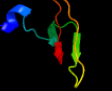
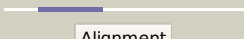
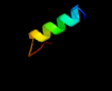

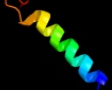
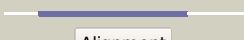




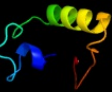










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1545_(-)_1746925_1747152
Date	Fri Aug 2 13:30:13 BST 2019
Unique Job ID	b9fbec2241432602

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3htuE_</a>	 Alignment		32.8	21	<b>PDB header:</b> protein transport <b>Chain:</b> E; <b>PDB Molecule:</b> vacuolar protein-sorting-associated protein 25; <b>PDBTitle:</b> crystal structure of the human vps25-vps20 subcomplex
2	<a href="#">c2wtoB_</a>	 Alignment		18.9	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> orf131 protein; <b>PDBTitle:</b> crystal structure of apo-form czce from c. metallidurans ch34
3	<a href="#">c6j05B_</a>	 Alignment		17.8	23	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
4	<a href="#">d1kxpd3</a>	 Alignment		16.8	31	<b>Fold:</b> Serum albumin-like <b>Superfamily:</b> Serum albumin-like <b>Family:</b> Serum albumin-like
5	<a href="#">d1zj8a2</a>	 Alignment		16.6	20	<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
6	<a href="#">c2va0E_</a>	 Alignment		16.1	34	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> abfs arabinofuranosidase two component system sensor <b>PDBTitle:</b> differential regulation of the xylan degrading apparatus of2 cellvibrio japonicus by a novel two component system
7	<a href="#">c3cuqC_</a>	 Alignment		14.3	21	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> vacuolar protein-sorting-associated protein 25; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
8	<a href="#">c3v2iA_</a>	 Alignment		13.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
9	<a href="#">d2ptha_</a>	 Alignment		12.8	32	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Peptidyl-tRNA hydrolase-like <b>Family:</b> Peptidyl-tRNA hydrolase-like
10	<a href="#">c4ok7A_</a>	 Alignment		11.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> structure of bacteriophage spn1s endolysin from salmonella typhimurium
11	<a href="#">d2akja2</a>	 Alignment		10.8	23	<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

12	<a href="#">c1zj8B_</a>	Alignment		10.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> probable ferredoxin-dependent nitrite reductase nira; <b>PDBTitle:</b> structure of mycobacterium tuberculosis nira protein
13	<a href="#">c2luyA_</a>	Alignment		10.5	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> meiotic chromosome segregation protein p8b7.28c; <b>PDBTitle:</b> solution structure of the tandem zinc finger domain of fission yeast2 stc1
14	<a href="#">c4uqfB_</a>	Alignment		10.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> gtp cyclohydrolase 1; <b>PDBTitle:</b> crystal structure of listeria monocytogenes gtp cyclohydrolase i
15	<a href="#">c2m6oA_</a>	Alignment		9.8	38	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the actinobacterial transcription factor rbpA binds to the principal2 sigma subunit of rna polymerase
16	<a href="#">c5c7eB_</a>	Alignment		8.9	27	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> aspr2 protein; <b>PDBTitle:</b> crystal structure of the rice topless related protein 2 (tpr2) n-2 terminal domain (1-209) in complex with arabidopsis iaa10 peptide
17	<a href="#">d1aopa1</a>	Alignment		8.8	22	<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
18	<a href="#">c4q55B_</a>	Alignment		7.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, streptococcus pyogenes at 2.19a resolution shows the3 closed structure of the substrate binding cleft
19	<a href="#">c4dhwA_</a>	Alignment		7.7	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from pseudomonas2 aeruginosa with adipic acid at 2.4 angstrom resolution
20	<a href="#">d1b8ta1</a>	Alignment		7.7	55	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
21	<a href="#">d1zj8a1</a>	Alignment	not modelled	7.5	17	<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
22	<a href="#">c4fopA_</a>	Alignment	not modelled	7.2	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from acinetobacter2 baumannii at 1.86 a resolution
23	<a href="#">c1m4eA_</a>	Alignment	not modelled	6.0	38	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> solution structure of hepcidin-20
24	<a href="#">c2kefA_</a>	Alignment	not modelled	5.8	60	<b>PDB header:</b> antibiotic, hormone <b>Chain:</b> A; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> solution nmr structures of human hepcidin at 325k
25	<a href="#">c2zkzC_</a>	Alignment	not modelled	5.7	21	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
26	<a href="#">c4qaeT_</a>	Alignment	not modelled	5.7	60	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> T; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> crystal structure of an engineered lipocalin (anticalin) in complex2 with human hepcidin
27	<a href="#">c1m4fA_</a>	Alignment	not modelled	5.6	60	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> solution structure of hepcidin-25
28	<a href="#">c4qaeR_</a>	Alignment	not modelled	5.6	60	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> R; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> crystal structure of an engineered lipocalin (anticalin) in complex2 with human hepcidin
						<b>PDB header:</b> transport protein/signaling protein

29	<a href="#">c4qaeS_</a>	Alignment	not modelled	5.6	60	<b>Chain:</b> S; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> crystal structure of an engineered lipocalin (anticalin) in complex2 with human hepcidin
30	<a href="#">c4qaeQ_</a>	Alignment	not modelled	5.6	60	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> Q; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> crystal structure of an engineered lipocalin (anticalin) in complex2 with human hepcidin
31	<a href="#">c4qaeP_</a>	Alignment	not modelled	5.5	60	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> P; <b>PDB Molecule:</b> hepcidin; <b>PDBTitle:</b> crystal structure of an engineered lipocalin (anticalin) in complex2 with human hepcidin
32	<a href="#">d2csha2</a>	Alignment	not modelled	5.3	57	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
33	<a href="#">c5ijaB_</a>	Alignment	not modelled	5.2	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hydrogenase-specific maturation endopeptidase; <b>PDBTitle:</b> [nife] hydrogenase maturation protease hybd from thermococcus2 kodakarensis
34	<a href="#">c5h92A_</a>	Alignment	not modelled	5.0	17	<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