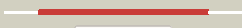



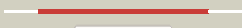










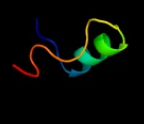

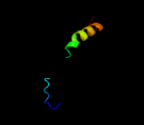







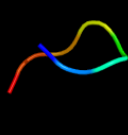
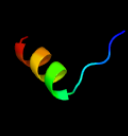
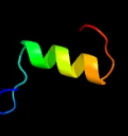
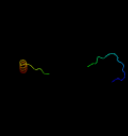

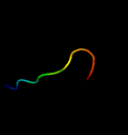


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3866_(- )_4342058_4342909
Date	Sat Aug 10 22:05:05 BST 2019
Unique Job ID	f096195a68ebc5bb

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5vbaA_</a>	 Alignment		100.0	80	<b>PDB header:</b> chaperone, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme, esx-1 secretion-associated protein esp31 chimera; <b>PDBTitle:</b> structure of esp31 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
2	<a href="#">c4l4wB_</a>	 Alignment		100.0	27	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> esp33; <b>PDBTitle:</b> structure of esp33 chaperone from the type vii (esx-3) secretion2 system
3	<a href="#">c4w4iA_</a>	 Alignment		100.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-3 secretion-associated protein esp33; <b>PDBTitle:</b> crystal structure of esp33 from the esx-3 type vii secretion system of2 m. tuberculosis
4	<a href="#">c4kxrC_</a>	 Alignment		100.0	23	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> esp35; <b>PDBTitle:</b> structure of the mycobacterium tuberculosis type vii secretion system2 chaperone esp35 in complex with pe25-ppe41 dimer
5	<a href="#">c4rc1B_</a>	 Alignment		100.0	28	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> esp33; <b>PDBTitle:</b> structure of esp33 chaperone from the type vii (esx-3) secretion2 system, space group p43212
6	<a href="#">c2l3aA_</a>	 Alignment		19.6	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
7	<a href="#">c5w4zA_</a>	 Alignment		16.1	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin lyase; <b>PDBTitle:</b> crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
8	<a href="#">c3u5gK_</a>	 Alignment		15.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 40s ribosomal protein s10-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
9	<a href="#">c2v4oB_</a>	 Alignment		14.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> multifunctional protein sur e; <b>PDBTitle:</b> crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
10	<a href="#">d1qnta1</a>	 Alignment		13.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain
11	<a href="#">c3pm7A_</a>	 Alignment		12.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184

12	<a href="#">c4u5pA</a>	Alignment		12.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> rhcc; <b>PDBTitle:</b> crystal structure of native rhcc (yp_702633.1) from rhodococcus jostii2 rha1 at 1.78 angstrom
13	<a href="#">c2ltdA</a>	Alignment		11.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ydbc; <b>PDBTitle:</b> solution nmr structure of apo ydbc from lactococcus lactis, northeast2 structural genomics consortium (nesg) target kr150
14	<a href="#">c2vxhF</a>	Alignment		10.0	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> chlorite dismutase; <b>PDBTitle:</b> the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
15	<a href="#">d1g26a</a>	Alignment		9.2	63	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat
16	<a href="#">c3obhA</a>	Alignment		8.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
17	<a href="#">c5craB</a>	Alignment		8.7	43	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> sdea; <b>PDBTitle:</b> structure of the sdea dub domain
18	<a href="#">c3jcmK</a>	Alignment		8.5	17	<b>PDB header:</b> transcription <b>Chain:</b> K; <b>PDB Molecule:</b> u4/u6 small nuclear ribonucleoprotein prp3; <b>PDBTitle:</b> cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp
19	<a href="#">c2x5kO</a>	Alignment		8.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O; <b>PDB Molecule:</b> d-erythrose-4-phosphate dehydrogenase; <b>PDBTitle:</b> structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
20	<a href="#">c4dibF</a>	Alignment		8.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 bacillus anthracis str. sterne
21	<a href="#">c5iyfB</a>	Alignment	not modelled	8.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structures of streptococcus agalactiae gbs gapdh in different2 enzymatic states
22	<a href="#">c5a13J</a>	Alignment	not modelled	8.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> chlorite dismutase; <b>PDBTitle:</b> crystal structure of chlorite dismutase from2 magnetospirillum sp. in complex with thiocyanate
23	<a href="#">c2kimA</a>	Alignment	not modelled	8.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o6-methylguanine-dna methyltransferase; <b>PDBTitle:</b> 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.
24	<a href="#">c2i5pO</a>	Alignment	not modelled	7.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O; <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
25	<a href="#">c4qx6A</a>	Alignment	not modelled	7.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 streptococcus agalactiae nem316 at 2.46 angstrom resolution
26	<a href="#">c1obfO</a>	Alignment	not modelled	7.6	18	<b>PDB header:</b> glycolytic pathway <b>Chain:</b> O; <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylooxidans at 1.7 a3 resolution. <b>PDB header:</b> oxidoreductase

27	<a href="#">c5ur0B_</a>	Alignment	not modelled	7.5	18	<b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
28	<a href="#">c3hq4R_</a>	Alignment	not modelled	7.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
29	<a href="#">c1s7cA_</a>	Alignment	not modelled	7.4	18	<b>PDB header:</b> structural genomics, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
30	<a href="#">c5ld5C_</a>	Alignment	not modelled	7.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of a bacterial dehydrogenase at 2.19 angstroms2 resolution
31	<a href="#">c2b4rO_</a>	Alignment	not modelled	7.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
32	<a href="#">c3c6vB_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable tautomerase/dehalogenase au4130; <b>PDBTitle:</b> crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
33	<a href="#">c3h9eO_</a>	Alignment	not modelled	7.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase, testis-specific; <b>PDBTitle:</b> crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
34	<a href="#">c2ep7B_</a>	Alignment	not modelled	7.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structural study of project id aq_1065 from aquifex aeolicus vf5
35	<a href="#">c3cieC_</a>	Alignment	not modelled	7.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
36	<a href="#">c1hdgO_</a>	Alignment	not modelled	7.2	27	<b>PDB header:</b> oxidoreductase (aldehy(d)-nad(a)) <b>Chain:</b> O: <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution
37	<a href="#">c2d2iO_</a>	Alignment	not modelled	7.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
38	<a href="#">c1cerC_</a>	Alignment	not modelled	7.0	18	<b>PDB header:</b> oxidoreductase (aldehyde(d)-nad(a)) <b>Chain:</b> C: <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
39	<a href="#">c5j9gB_</a>	Alignment	not modelled	7.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-p dehydrogenase; <b>PDBTitle:</b> structure of lactobacillus acidophilus glyceraldehyde-3-phosphate2 dehydrogenase at 2.21 angstrom resolution
40	<a href="#">c3docD_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of trka glyceraldehyde-3-phosphate dehydrogenase2 from brucella melitensis
41	<a href="#">c2pkrl_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase aor; <b>PDBTitle:</b> crystal structure of (a+cte)4 chimeric form of photosynthetic2 glyceraldehyde-3-phosphate dehydrogenase, complexed with nadp
42	<a href="#">d1ea0a3</a>	Alignment	not modelled	6.9	18	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
43	<a href="#">c3b20R_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadfrom synechococcus elongatus"
44	<a href="#">c1ihxD_</a>	Alignment	not modelled	6.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
45	<a href="#">c6ok4A_</a>	Alignment	not modelled	6.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase (gapdh)2 from chlamydia trachomatis with bound nad
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate

46	<a href="#">c1rm4Q_</a>	Alignment	not modelled	6.7	18	dehydrogenase a; <b>PDBTitle:</b> crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
47	<a href="#">c2gfgC_</a>	Alignment	not modelled	6.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> upf0204 protein ph0006; <b>PDBTitle:</b> structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
48	<a href="#">c1i32D_</a>	Alignment	not modelled	6.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
49	<a href="#">c3hjaB_</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 borrelia burgdorferi
50	<a href="#">c4rdkB_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> capsid; <b>PDBTitle:</b> crystal structure of norovirus boxer p domain in complex with lewis b2 tetrasaccharide
51	<a href="#">c3i4jC_</a>	Alignment	not modelled	6.3	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
52	<a href="#">c3sthA_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
53	<a href="#">d1l3ac_</a>	Alignment	not modelled	6.2	26	<b>Fold:</b> ssDNA-binding transcriptional regulator domain <b>Superfamily:</b> ssDNA-binding transcriptional regulator domain <b>Family:</b> Plant transcriptional regulator PBF-2
54	<a href="#">d2qlia4</a>	Alignment	not modelled	6.2	31	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
55	<a href="#">c4qyjD_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
56	<a href="#">c3gx4X_</a>	Alignment	not modelled	5.9	10	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> X: <b>PDB Molecule:</b> alkyltransferase-like protein 1; <b>PDBTitle:</b> crystal structure analysis of s. pombe atl in complex with dna
57	<a href="#">d1mgtal</a>	Alignment	not modelled	5.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain
58	<a href="#">c3h8dC_</a>	Alignment	not modelled	5.2	24	<b>PDB header:</b> motor protein/signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin-vi; <b>PDBTitle:</b> crystal structure of myosin vi in complex with dab2 peptide
59	<a href="#">c4r8aF_</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of pafan1 - 5' flap dna complex