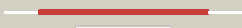



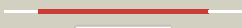






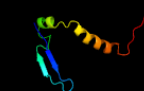
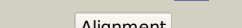
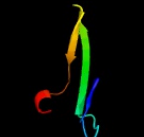

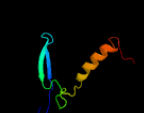
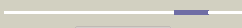
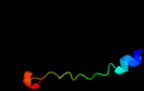

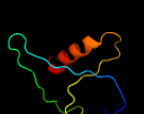

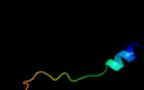
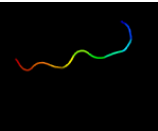
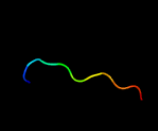
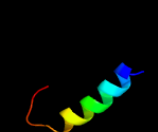
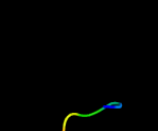

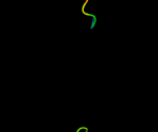


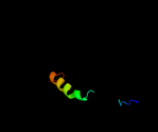


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1794 (- )_2031073_2031975
Date	Fri Aug 2 13:30:40 BST 2019
Unique Job ID	abce7bc38a736141

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4kxrC_</a>	 Alignment		100.0	99	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> espg5; <b>PDBTitle:</b> structure of the mycobacterium tuberculosis type vii secretion system2 chaperone espg5 in complex with pe25-ppe41 dimer
2	<a href="#">c4l4wB_</a>	 Alignment		100.0	21	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> espg3; <b>PDBTitle:</b> structure of espg3 chaperone from the type vii (esx-3) secretion2 system
3	<a href="#">c4w4iA_</a>	 Alignment		100.0	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-3 secretion-associated protein espg3; <b>PDBTitle:</b> crystal structure of espg3 from the esx-3 type vii secretion system of2 m. tuberculosis
4	<a href="#">c4rc1B_</a>	 Alignment		100.0	20	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> espg3; <b>PDBTitle:</b> structure of espg3 chaperone from the type vii (esx-3) secretion2 system, space group p43212
5	<a href="#">c5vbaA_</a>	 Alignment		100.0	26	<b>PDB header:</b> chaperone, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme, esx-1 secretion-associated protein espg1 chimera; <b>PDBTitle:</b> structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
6	<a href="#">d1w79a1</a>	 Alignment		24.6	16	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
7	<a href="#">c4rdkB_</a>	 Alignment		17.6	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
8	<a href="#">c3a3eB_</a>	 Alignment		15.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin binding protein 4 (dacb) from2 haemophilus influenzae, complexed with novel beta-lactam (cmv)
9	<a href="#">d1hynp_</a>	 Alignment		13.8	15	<b>Fold:</b> Phoshotransferase/anion transport protein <b>Superfamily:</b> Phoshotransferase/anion transport protein <b>Family:</b> Anion transport protein, cytoplasmic domain
10	<a href="#">d1ppva_</a>	 Alignment		13.1	12	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> I PP isomerase-like
11	<a href="#">c1hynQ_</a>	 Alignment		11.8	15	<b>PDB header:</b> membrane protein <b>Chain:</b> Q: <b>PDB Molecule:</b> band 3 anion transport protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of human erythrocyte band-2 3 protein

12	<a href="#">d1rk8c</a>	Alignment		11.5	45	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain <b>Family:</b> Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
13	<a href="#">c1rk8C</a>	Alignment		11.5	45	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> within the bgcn gene intron protein; <b>PDBTitle:</b> structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
14	<a href="#">c2ei5B</a>	Alignment		11.2	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ttha0061; <b>PDBTitle:</b> crystal structure of hypothetical protein(ttha0061) from thermus2 thermophilus
15	<a href="#">d1u94a2</a>	Alignment		10.3	25	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
16	<a href="#">d1mo6a2</a>	Alignment		10.2	38	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
17	<a href="#">d2fvva1</a>	Alignment		10.1	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
18	<a href="#">c2fvvA</a>	Alignment		10.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphoinositol polyphosphate phosphohydrolase 1; <b>PDBTitle:</b> human diphosphoinositol polyphosphate phosphohydrolase 1
19	<a href="#">c2v4oB</a>	Alignment		10.0	25	<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
20	<a href="#">d1rrqa2</a>	Alignment		9.7	11	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
21	<a href="#">d1kdga2</a>	Alignment	not modelled	9.4	21	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GMC oxidoreductases
22	<a href="#">d1xp8a2</a>	Alignment	not modelled	9.2	13	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
23	<a href="#">d1ubea2</a>	Alignment	not modelled	9.1	38	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
24	<a href="#">c2ly2A</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tudor domain-containing protein 7; <b>PDBTitle:</b> nmr structure of the second and third lotus domains of tudor domain-2 containing protein 7 (nmr ensemble overlay for lotus #3)
25	<a href="#">d2ex2a1</a>	Alignment	not modelled	8.6	17	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
26	<a href="#">d1w5da1</a>	Alignment	not modelled	8.3	9	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> Dac-like
27	<a href="#">d1v7ba2</a>	Alignment	not modelled	8.1	15	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
28	<a href="#">c4dibF</a>	Alignment	not modelled	7.5	33	<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 <b>PDB header:</b> oxidoreductase

29	<a href="#">c2x5kO_</a>	Alignment	not modelled	7.4	33	<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
30	<a href="#">c5fgoA_</a>	Alignment	not modelled	7.3	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cg1507-pb, isoform b; <b>PDBTitle:</b> crystal structure of d. melanogaster pur-alpha repeat iii.
31	<a href="#">c2eh6A_</a>	Alignment	not modelled	7.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
32	<a href="#">c2o1cB_</a>	Alignment	not modelled	7.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> datp pyrophosphohydrolase; <b>PDBTitle:</b> structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase
33	<a href="#">c4zyeA_</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
34	<a href="#">c2i5pO_</a>	Alignment	not modelled	7.0	22	<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
35	<a href="#">c5jyfB_</a>	Alignment	not modelled	6.9	22	<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
36	<a href="#">c4qx6A_</a>	Alignment	not modelled	6.7	22	<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
37	<a href="#">c1obfO_</a>	Alignment	not modelled	6.5	33	<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.
38	<a href="#">c5ur0B_</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> oxidoreductase <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
39	<a href="#">c3h9eO_</a>	Alignment	not modelled	6.4	33	<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
40	<a href="#">c5j9gB_</a>	Alignment	not modelled	6.4	11	<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
41	<a href="#">c1s7cA_</a>	Alignment	not modelled	6.4	33	<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
42	<a href="#">c2b4rO_</a>	Alignment	not modelled	6.3	33	<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
43	<a href="#">c3hq4R_</a>	Alignment	not modelled	6.3	11	<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
44	<a href="#">d1v8ya_</a>	Alignment	not modelled	6.3	13	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
45	<a href="#">d1g26a_</a>	Alignment	not modelled	6.2	50	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat
46	<a href="#">c2d2iO_</a>	Alignment	not modelled	6.2	22	<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+
47	<a href="#">c3cieC_</a>	Alignment	not modelled	6.2	33	<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
48	<a href="#">c5ld5C_</a>	Alignment	not modelled	6.2	22	<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
49	<a href="#">c3nx3A_</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
50	<a href="#">c3h20B_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R; <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase (nadp+);

50	<a href="#">c3uzvN</a>	Alignment	not modelled	6.1	22	<b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadfrom synechococcus elongatus"
51	<a href="#">c2ep7B</a>	Alignment	not modelled	6.0	22	<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
52	<a href="#">c1ihxD</a>	Alignment	not modelled	6.0	33	<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
53	<a href="#">c1hdgO</a>	Alignment	not modelled	6.0	33	<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
54	<a href="#">d1qbea</a>	Alignment	not modelled	6.0	20	<b>Fold:</b> RNA bacteriophage capsid protein <b>Superfamily:</b> RNA bacteriophage capsid protein <b>Family:</b> RNA bacteriophage capsid protein
55	<a href="#">c4o9lA</a>	Alignment	not modelled	5.9	17	<b>PDB header:</b> antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial antiviral signaling protein (mavs); <b>PDBTitle:</b> crystal structure of horse mavs card domain mutant e26r
56	<a href="#">c3docD</a>	Alignment	not modelled	5.9	44	<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
57	<a href="#">c3hjaB</a>	Alignment	not modelled	5.9	44	<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
58	<a href="#">c2pkrl</a>	Alignment	not modelled	5.8	22	<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
59	<a href="#">c1cerC</a>	Alignment	not modelled	5.8	22	<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
60	<a href="#">c6ok4A</a>	Alignment	not modelled	5.8	22	<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
61	<a href="#">c1rm4O</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
62	<a href="#">d1mgta1</a>	Alignment	not modelled	5.7	11	<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
63	<a href="#">c3sthA</a>	Alignment	not modelled	5.7	33	<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
64	<a href="#">d1vhza</a>	Alignment	not modelled	5.6	2	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
65	<a href="#">c1i32D</a>	Alignment	not modelled	5.6	22	<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
66	<a href="#">c3u5gK</a>	Alignment	not modelled	5.4	21	<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
67	<a href="#">c3i4jC</a>	Alignment	not modelled	5.2	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