
























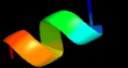







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2620c (- )_2947472_2947897
Date	Wed Aug 7 12:50:26 BST 2019
Unique Job ID	0ea2b2b9550430ad

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1vc2a1</a>	 Alignment		30.0	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
2	<a href="#">d2g82a1</a>	 Alignment		26.3	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
3	<a href="#">c5kzoA_</a>	 Alignment		25.5	23	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> notch1 transmembrane and associated juxtamembrane segment
4	<a href="#">c2muxA_</a>	 Alignment		25.4	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 25; <b>PDBTitle:</b> sumo2 non-covalently interacts with usp25 and downregulates its2 activity
5	<a href="#">d1k3ta1</a>	 Alignment		24.6	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
6	<a href="#">d1ggaa1</a>	 Alignment		24.1	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
7	<a href="#">d1u8fo1</a>	 Alignment		22.1	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
8	<a href="#">d1i32a1</a>	 Alignment		21.8	67	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
9	<a href="#">d3gpdg1</a>	 Alignment		21.0	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
10	<a href="#">d1j0xo1</a>	 Alignment		20.8	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
11	<a href="#">d1hdgo1</a>	 Alignment		20.2	67	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

12	<a href="#">d2b4ro1</a>	Alignment		19.9	89	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
13	<a href="#">d1rm4a1</a>	Alignment		19.7	44	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	<a href="#">d1obfo1</a>	Alignment		19.5	56	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
15	<a href="#">d1gado1</a>	Alignment		19.5	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
16	<a href="#">d2pkqo1</a>	Alignment		18.2	44	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
17	<a href="#">c1q90L_</a>	Alignment		16.6	53	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> cytochrome b6f complex subunit pet1; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
18	<a href="#">d1q90L_</a>	Alignment		16.6	53	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetL subunit of the cytochrome b6f complex <b>Family:</b> PetL subunit of the cytochrome b6f complex
19	<a href="#">d3cmco1</a>	Alignment		15.9	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
20	<a href="#">d1dssg1</a>	Alignment		15.1	78	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
21	<a href="#">d1uf2c1</a>	Alignment	not modelled	13.9	36	<b>Fold:</b> A virus capsid protein alpha-helical domain <b>Superfamily:</b> A virus capsid protein alpha-helical domain <b>Family:</b> Phytoreovirus capsid
22	<a href="#">c1jb0X_</a>	Alignment	not modelled	12.7	43	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem i subunit psax; <b>PDBTitle:</b> crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
23	<a href="#">d1jb0x_</a>	Alignment	not modelled	12.7	43	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit Psax of photosystem I reaction centre <b>Family:</b> Subunit Psax of photosystem I reaction centre
24	<a href="#">c4fe1X_</a>	Alignment	not modelled	12.7	43	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem i 4.8k protein; <b>PDBTitle:</b> improving the accuracy of macromolecular structure refinement at 7 a2 resolution
25	<a href="#">c1uf2F_</a>	Alignment	not modelled	11.8	42	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> outer capsid protein p8; <b>PDBTitle:</b> the atomic structure of rice dwarf virus (rdv)
26	<a href="#">c1i32D_</a>	Alignment	not modelled	11.7	67	<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
27	<a href="#">c5jyFB_</a>	Alignment	not modelled	9.6	67	<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
28	<a href="#">c5ld5C_</a>	Alignment	not modelled	8.8	67	<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
29	<a href="#">c1nw3A_</a>	Alignment	not modelled	8.6	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone methyltransferase dot11; <b>PDBTitle:</b> structure of the catalytic domain of human dot11, a non-set domain2 nucleosomal histone methyltransferase
30	<a href="#">d1nw3a_</a>	Alignment	not modelled	8.6	33	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Catalytic, N-terminal domain of histone methyltransferase Dot11
31	<a href="#">c1u2zC_</a>	Alignment	not modelled	8.2	42	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 <b>PDBTitle:</b> crystal structure of histone k79 methyltransferase dot1p2 from yeast
32	<a href="#">c3thgA_</a>	Alignment	not modelled	7.6	30	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> crystal structure of the creosote rubisco activase c-domain
33	<a href="#">c1obfO_</a>	Alignment	not modelled	7.4	56	<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.
34	<a href="#">d3b7sa1</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> Leukotriene A4 hydrolase C-terminal domain
35	<a href="#">c4er3A_</a>	Alignment	not modelled	6.8	33	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 specific; <b>PDBTitle:</b> crystal structure of human dot11 in complex with inhibitor epz004777
36	<a href="#">c3pcqX_</a>	Alignment	not modelled	6.5	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem i 4.8k protein; <b>PDBTitle:</b> femtosecond x-ray protein nanocrystallography
37	<a href="#">c6iz0A_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> trimeric intracellular cation channel type a; <b>PDBTitle:</b> crystal structure analysis of a eukaryotic membrane protein
38	<a href="#">c6adqP_</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
39	<a href="#">c2jsnA_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> trafficking protein particle complex subunit 4; <b>PDBTitle:</b> solution structure of the atypical pdz-like domain of2 synbindin
40	<a href="#">c3h9eO_</a>	Alignment	not modelled	6.0	78	<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
41	<a href="#">c6m97A_</a>	Alignment	not modelled	6.0	33	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1 <b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1
42	<a href="#">d1u2za_</a>	Alignment	not modelled	5.9	42	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Catalytic, N-terminal domain of histone methyltransferase Dot11
43	<a href="#">c4dwnB_</a>	Alignment	not modelled	5.4	33	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl10-interacting card protein; <b>PDBTitle:</b> crystal structure of human bincard card
44	<a href="#">c2y69W_</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> electron transport <b>Chain:</b> W: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 7a1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
45	<a href="#">d1v54j_</a>	Alignment	not modelled	5.2	18	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIa <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIa
46	<a href="#">c3hjaB_</a>	Alignment	not modelled	5.2	56	<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