
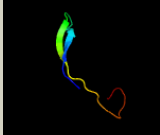

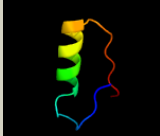

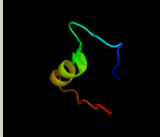



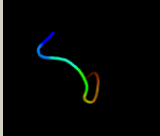

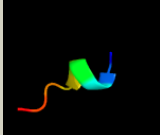



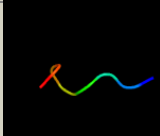



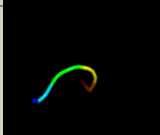

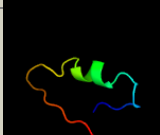

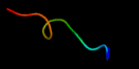



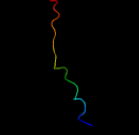
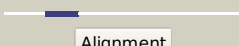

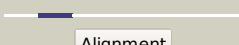
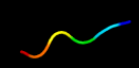
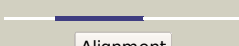


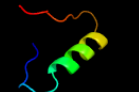



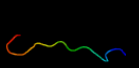
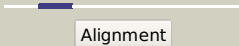
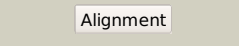

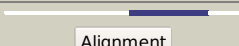
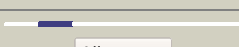


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2274A\_(RVBD2274A)\_2546849\_2547097  
 Date Mon Aug 5 13:25:41 BST 2019  
 Unique Job ID 119a4ebe1e34eedf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1b5sa_</a>	 Alignment		12.4	42	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
2	<a href="#">d1sq5a_</a>	 Alignment		11.9	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
3	<a href="#">c6n39A_</a>	 Alignment		9.7	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dephospho-coa kinase; <b>PDBTitle:</b> crystal structure of an dephospho-coa kinase coae from mycobacterium2 paratuberculosis
4	<a href="#">c3tqcB_</a>	 Alignment		9.2	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii
5	<a href="#">c5m73H_</a>	 Alignment		8.6	63	<b>PDB header:</b> rna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> signal recognition particle subunit srp72; <b>PDBTitle:</b> structure of the human srp s domain with srp72 rna-binding domain
6	<a href="#">c2ndjA_</a>	 Alignment		8.2	78	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3; <b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel
7	<a href="#">c2gesA_</a>	 Alignment		7.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
8	<a href="#">c3n92A_</a>	 Alignment		7.7	88	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase, gh57 family; <b>PDBTitle:</b> crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
9	<a href="#">d1deka_</a>	 Alignment		7.6	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
10	<a href="#">c5m73D_</a>	 Alignment		7.5	83	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> signal recognition particle subunit srp72; <b>PDBTitle:</b> structure of the human srp s domain with srp72 rna-binding domain
11	<a href="#">c5b3fB_</a>	 Alignment		7.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribulokinase/uridine kinase; <b>PDBTitle:</b> crystal structure of phosphoribulokinase from methanospirillum2 hungatei

12	<a href="#">c2jrwA_</a>	 Alignment		7.3	54	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> cyclic extended pep.1; <b>PDBTitle:</b> solution structure of cyclic extended pep1(cyc.ext.pep.1)2 for autoimmune myasthenia gravis
13	<a href="#">c2m1tA_</a>	 Alignment		7.2	54	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> pulmonary surfactant-associated protein b; <b>PDBTitle:</b> sp-b c-terminal (residues 59-80) peptide in dpc micelles
14	<a href="#">c1f8vA_</a>	 Alignment		7.2	45	<b>PDB header:</b> virus/rna <b>Chain:</b> A; <b>PDB Molecule:</b> mature capsid protein beta; <b>PDBTitle:</b> the structure of pariacoto virus reveals a dodecahedral cage of duplex2 rna
15	<a href="#">c4e6kH_</a>	 Alignment		7.1	50	<b>PDB header:</b> metal binding protein/electron transport <b>Chain:</b> H; <b>PDB Molecule:</b> bacterioferritin-associated ferredoxin; <b>PDBTitle:</b> 2.0 a resolution structure of pseudomonas aeruginosa bacterioferritin2 (bfrb) in complex with bacterioferritin associated ferredoxin (bfd)
16	<a href="#">c1ufaA_</a>	 Alignment		7.0	75	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tt1467 protein; <b>PDBTitle:</b> crystal structure of tt1467 from thermus thermophilus hb8
17	<a href="#">c5x90B_</a>	 Alignment		6.9	32	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> icmw; <b>PDBTitle:</b> structure of dotl(656-783)-icms-icmw-lvga derived from legionella2 pneumophila
18	<a href="#">c3tr0A_</a>	 Alignment		6.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> structure of guanylate kinase (gmk) from coxiella burnetii
19	<a href="#">c6h7gB_</a>	 Alignment		6.2	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoribulokinase, chloroplastic; <b>PDBTitle:</b> crystal structure of redox-sensitive phosphoribulokinase (prk) from2 the green algae chlamydomonas reinhardtii
20	<a href="#">c4w5xA_</a>	 Alignment		5.9	57	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> late protein h7; <b>PDBTitle:</b> the structure of vaccina virus h7 protein displays a novel2 phosphoinositide binding fold required for membrane biogenesis
21	<a href="#">d1ufaa2</a>	 Alignment	not modelled	5.9	75	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> AmyC N-terminal domain-like
22	<a href="#">c2aorB_</a>	 Alignment	not modelled	5.8	36	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> dna mismatch repair protein muth; <b>PDBTitle:</b> crystal structure of muth-hemimethylated dna complex
23	<a href="#">c2x43S_</a>	 Alignment	not modelled	5.8	70	<b>PDB header:</b> membrane protein <b>Chain:</b> S; <b>PDB Molecule:</b> sherp; <b>PDBTitle:</b> structural basis of molecular recognition by sherp at membrane2 surfaces
24	<a href="#">c6gveG_</a>	 Alignment	not modelled	5.4	34	<b>PDB header:</b> photosynthesis <b>Chain:</b> G; <b>PDB Molecule:</b> phosphoribulokinase; <b>PDBTitle:</b> gapdh-cp12-prk complex
25	<a href="#">c5wu7A_</a>	 Alignment	not modelled	5.3	88	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii