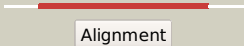

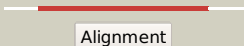

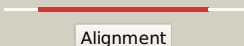







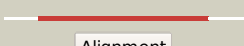












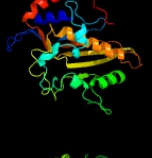


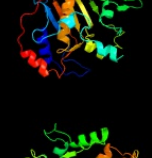
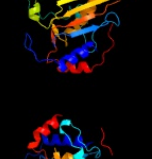
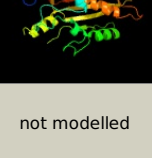


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2492_(-)_2807288_2808040
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	2e0022f3a518a786

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3clbA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhfr-ts; <b>PDBTitle:</b> structure of bifunctional tcdhfr-ts in complex with tmq
2	<a href="#">d2g8oa1</a>	 Alignment		100.0	19	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
3	<a href="#">d1f28a_</a>	 Alignment		100.0	16	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
4	<a href="#">d1seja2</a>	 Alignment		100.0	20	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
5	<a href="#">c2oipE_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> chain a, crystal structure of dhfr; <b>PDBTitle:</b> crystal structure of the s290g active site mutant of ts-dhfr from2 cryptosporidium hominis
6	<a href="#">c2aazG_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> cryptococcus neoformans thymidylate synthase complexed with substrate2 and an antifolate
7	<a href="#">c3jsuA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump
8	<a href="#">c3qj7D_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis thymidylate2 synthase (thya) bound to dump
9	<a href="#">c4eckB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> crystal structure of the toxoplasma gondii ts-dhfr
10	<a href="#">d1qzfa2</a>	 Alignment		100.0	19	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
11	<a href="#">c3k2hA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrofolate reductase/thymidylate synthase; <b>PDBTitle:</b> co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp

12	<a href="#">c6aujC_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of thymidylate synthase from elizabethkingia2 anophelis nuhp1
13	<a href="#">c4g9uD_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of trichinella spiralis thymidylate synthase2 complexed with dump
14	<a href="#">d1j3kc_</a>	Alignment		100.0	15	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
15	<a href="#">d1bkpa_</a>	Alignment		100.0	15	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
16	<a href="#">c4iswB_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of phosphorylated c.elegans thymidylate synthase in2 complex with dump
17	<a href="#">c4dq1A_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> thymidylate synthase from staphylococcus aureus.
18	<a href="#">d1tswa_</a>	Alignment		100.0	25	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
19	<a href="#">d2tsra_</a>	Alignment		100.0	17	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
20	<a href="#">c5b6dB_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cmp 5-hydroxymethylase; <b>PDBTitle:</b> crystal structure of cytidine monophosphate hydroxymethylase mila with2 cmp
21	<a href="#">c3ix6B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of thymidylate synthase thya from brucella2 melitensis
22	<a href="#">c3v8hB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of thymidylate synthase from burkholderia2 thailandensis
23	<a href="#">d1hvya_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
24	<a href="#">d1tisa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
25	<a href="#">c3kqbA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate synthase 1/2; <b>PDBTitle:</b> crystal structure of thymidylate synthase 1/2 from encephalitozoon2 cuciculi at 2.2 a resolution
26	<a href="#">c1hw4A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> structure of thymidylate synthase suggests advantages of chemotherapy2 with noncompetitive inhibitors
27	<a href="#">c1hw3A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> structure of human thymidylate synthase suggests advantages of2 chemotherapy with noncompetitive inhibitors
28	<a href="#">c3egyX_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of human thymidylate synthase a191k with loop 181-2 197 stabilized in the inactive conformation
						<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase

29	<a href="#">d1b5ea_</a>	Alignment	not modelled	100.0	13	<b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
30	<a href="#">c2bn5A_</a>	Alignment	not modelled	33.5	15	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> psi; <b>PDBTitle:</b> p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
31	<a href="#">c2bn6A_</a>	Alignment	not modelled	26.1	15	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> psi; <b>PDBTitle:</b> p-element somatic inhibitor protein
32	<a href="#">d2gnoa2</a>	Alignment	not modelled	25.4	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
33	<a href="#">c2gnoA_</a>	Alignment	not modelled	16.2	16	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii, gamma subunit-related protein; <b>PDBTitle:</b> crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution
34	<a href="#">c4je3B_</a>	Alignment	not modelled	11.5	13	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> central kinetochore subunit chl4; <b>PDBTitle:</b> an iml3-chl4 heterodimer links the core centromere to factors required2 for accurate chromosome segregation
35	<a href="#">c2vsvB_</a>	Alignment	not modelled	10.9	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rhophilin-2; <b>PDBTitle:</b> crystal structure of the pdz domain of human rhophilin-2
36	<a href="#">c4tkzA_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein gbs1890; <b>PDBTitle:</b> crystal structure of phosphotransferase system component eiaa from2 streptococcus agalactiae
37	<a href="#">c3fgrA_</a>	Alignment	not modelled	10.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phospholipase b-like 2 28 kda form; <b>PDBTitle:</b> two chain form of the 66.3 kda protein at 1.8 angstrom
38	<a href="#">d1r8ea2</a>	Alignment	not modelled	9.1	12	<b>Fold:</b> Probable bacterial effector-binding domain <b>Superfamily:</b> Probable bacterial effector-binding domain <b>Family:</b> Multidrug-binding domain of transcription activator BmrR
39	<a href="#">c2wzoA_</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> transforming growth factor beta regulator 1; <b>PDBTitle:</b> the structure of the fyr domain
40	<a href="#">d1xoub_</a>	Alignment	not modelled	8.3	28	<b>Fold:</b> EspA/CesA-like <b>Superfamily:</b> EspA/CesA-like <b>Family:</b> EspA chaperone CesA
41	<a href="#">c6fmgC_</a>	Alignment	not modelled	8.0	33	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system mannose-specific transporter subunit iiaB; <b>PDBTitle:</b> structure of the mannose transporter iia domain from streptococcus2 pneumoniae
42	<a href="#">c4fp9F_</a>	Alignment	not modelled	7.9	14	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> methyltransferase nsun4; <b>PDBTitle:</b> human mterf4-nsun4 protein complex
43	<a href="#">d1ueza_</a>	Alignment	not modelled	7.7	29	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
44	<a href="#">c3lfhF_</a>	Alignment	not modelled	7.7	17	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> phosphotransferase system, mannose/fructose-specific <b>PDBTitle:</b> crystal structure of manxa from thermoanaerobacter tengcongensis
45	<a href="#">d1pdoa_</a>	Alignment	not modelled	7.3	27	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> EIIA-man component-like
46	<a href="#">c6cjdA_</a>	Alignment	not modelled	7.1	40	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> nmr structure of salmonella type iii secretion system protein orgc
47	<a href="#">c1sqqA_</a>	Alignment	not modelled	7.1	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sun protein; <b>PDBTitle:</b> the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
48	<a href="#">c2lifA_</a>	Alignment	not modelled	7.1	20	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> core protein p21; <b>PDBTitle:</b> solution structure of kkgf
49	<a href="#">c3mtqA_</a>	Alignment	not modelled	7.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphoenolpyruvate-dependent sugar <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
50	<a href="#">d2ezla_</a>	Alignment	not modelled	6.6	3	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
51	<a href="#">c1piwA_</a>	Alignment	not modelled	6.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical zinc-type alcohol dehydrogenase- <b>PDBTitle:</b> apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae
52	<a href="#">d1wgna_</a>	Alignment	not modelled	5.9	9	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
53	<a href="#">c5t3uA_</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae

54	<a href="#">d1pi1a_</a>	Alignment	not modelled	5.6	23	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Mob1/phocein <b>Family:</b> Mob1/phocein
55	<a href="#">c2lndA_</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein, pfk fold; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
56	<a href="#">c3j47O_</a>	Alignment	not modelled	5.5	6	<b>PDB header:</b> protein binding <b>Chain:</b> O: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn9; <b>PDBTitle:</b> formation of an intricate helical bundle dictates the assembly of the2 26s proteasome lid
57	<a href="#">c3iprC_</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pts system, iia component; <b>PDBTitle:</b> crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
58	<a href="#">d1j3wa_</a>	Alignment	not modelled	5.3	10	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
59	<a href="#">c6iczX_</a>	Alignment	not modelled	5.3	16	<b>PDB header:</b> splicing <b>Chain:</b> X: <b>PDB Molecule:</b> prkr-interacting protein 1; <b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
60	<a href="#">c3dhiA_</a>	Alignment	not modelled	5.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 4-monooxygenase hydroxylase alpha subunit; <b>PDBTitle:</b> crystal structure of reduced toluene 4-monooxygenase hydroxylase2 complexed with effector protein
61	<a href="#">c5yf4A_</a>	Alignment	not modelled	5.1	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mob-like protein phocein; <b>PDBTitle:</b> a kinase complex mst4-mob4
62	<a href="#">c4q9aA_</a>	Alignment	not modelled	5.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tat pathway signal sequence domain protein; <b>PDBTitle:</b> crystal structure of a putative gdsl-like lipase (parmer_00689) from2 parabacteroides merdae atcc 43184 at 2.86 a resolution
63	<a href="#">d1eyra_</a>	Alignment	not modelled	5.0	8	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase