







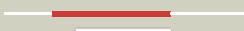
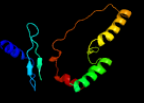



















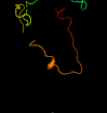



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0071 (-)_79483_80190
Date	Tue Jul 23 14:50:10 BST 2019
Unique Job ID	f9203d38ca5b12bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ar3A_</a>	 Alignment		100.0	35	<b>PDB header:</b> rna binding protein/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> gsi-iiic rt; <b>PDBTitle:</b> structure of a thermostable group ii intron reverse transcriptase with2 template-primer and its functional and evolutionary implications3 (rt/duplex (se-met))
2	<a href="#">c5g2xC_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> group ii intron-encoded protein ltra; <b>PDBTitle:</b> structure a of group ii intron complexed with its reverse2 transcriptase
3	<a href="#">c5hh1A_</a>	 Alignment		100.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> retron-type reverse transcriptase; <b>PDBTitle:</b> reverse transcriptase domain of group ii intron maturase from2 eubacterium rectale in p21 space group
4	<a href="#">c3du6A_</a>	 Alignment		98.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> telomerase reverse transcriptase; <b>PDBTitle:</b> structure of the catalytic subunit of telomerase, tert
5	<a href="#">c6d6vA_</a>	 Alignment		98.4	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> telomerase reverse transcriptase; <b>PDBTitle:</b> cryoem structure of tetrahymena telomerase with telomeric dna at 4.82 angstrom resolution
6	<a href="#">d1xr7a_</a>	 Alignment		95.6	14	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
7	<a href="#">d1u09a_</a>	 Alignment		94.7	11	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
8	<a href="#">c4nz0F_</a>	 Alignment		93.6	14	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> the emcv 3dpol structure at 2.8a resolution
9	<a href="#">d1xr6a_</a>	 Alignment		93.1	15	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
10	<a href="#">c1rthA_</a>	 Alignment		89.2	22	<b>PDB header:</b> nucleotidyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> hiv-1 reverse transcriptase; <b>PDBTitle:</b> high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes
11	<a href="#">d1sh0a_</a>	 Alignment		85.7	16	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase

12	<a href="#">d2zd1b1</a>	Alignment		84.7	20	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> Reverse transcriptase
13	<a href="#">c3n6mA</a>	Alignment		81.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of ev71 rdrp in complex with gtp
14	<a href="#">c2uutA</a>	Alignment		80.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna-directed rna polymerase; <b>PDBTitle:</b> the 2.4 angstrom resolution structure of the d346g mutant2 of the sapporo virus rdrp polymerase
15	<a href="#">c3nahC</a>	Alignment		78.1	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> rna dependent rna polymerase; <b>PDBTitle:</b> crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
16	<a href="#">c3kk1B</a>	Alignment		77.6	19	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> reverse transcriptase p51 subunit; <b>PDBTitle:</b> hiv-1 reverse transcriptase-dna complex with nucleotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
17	<a href="#">d1khva</a>	Alignment		75.1	14	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
18	<a href="#">d1ra6a</a>	Alignment		70.2	15	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
19	<a href="#">c5ovnA</a>	Alignment		65.4	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> pol protein; <b>PDBTitle:</b> crystal strucre of fiv reverse transcriptase
20	<a href="#">c2b43D</a>	Alignment		65.3	16	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> non-structural polyprotein; <b>PDBTitle:</b> crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
21	<a href="#">d1nb4a</a>	Alignment	not modelled	54.1	13	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
22	<a href="#">c2novD</a>	Alignment	not modelled	51.5	21	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> breakage-reunion domain of s.pneumoniae topo iv: crystal structure of f2 a gram-positive quinolone target
23	<a href="#">c2ijd1</a>	Alignment	not modelled	47.4	15	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> 1: <b>PDB Molecule:</b> picornain 3c, rna-directed rna polymerase; <b>PDBTitle:</b> crystal structure of the poliovirus precursor protein 3cd
24	<a href="#">d1gx5a</a>	Alignment	not modelled	43.5	13	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
25	<a href="#">c5i62A</a>	Alignment	not modelled	42.3	14	<b>PDB header:</b> viral protein, replication <b>Chain:</b> A: <b>PDB Molecule:</b> potential rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the insertion loop deletion mutant of the rna-2 dependent rna polymerase of a human picorbinavirus
26	<a href="#">c3rafA</a>	Alignment	not modelled	38.3	15	<b>PDB header:</b> isomerase/dna/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> quinazolinedione-dna cleavage complex of type iv topoisomerase from s.2 pneumoniae
27	<a href="#">c4z2cA</a>	Alignment	not modelled	34.1	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
28	<a href="#">d1ab4a</a>	Alignment	not modelled	27.9	12	<b>Fold:</b> Type II DNA topoisomerase <b>Superfamily:</b> Type II DNA topoisomerase <b>Family:</b> Type II DNA topoisomerase
						<b>Fold:</b> DNA/RNA polymerases

29	<a href="#">d1xr5a_</a>	Alignment	not modelled	26.8	15	<b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
30	<a href="#">c2wl2B_</a>	Alignment	not modelled	25.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a; <b>PDBTitle:</b> crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
31	<a href="#">c3mmpG_</a>	Alignment	not modelled	19.7	16	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> rna-directed rna polymerase beta chain; <b>PDBTitle:</b> structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
32	<a href="#">c2ze3A_</a>	Alignment	not modelled	18.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
33	<a href="#">d1s2wa_</a>	Alignment	not modelled	18.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
34	<a href="#">c2inrA_</a>	Alignment	not modelled	16.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (gria) from staphylococcus aureus
35	<a href="#">c5ovnB_</a>	Alignment	not modelled	15.6	32	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> pol protein; <b>PDBTitle:</b> crystal strcure of fiv reverse transcriptase
36	<a href="#">c5fszA_</a>	Alignment	not modelled	15.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> macrodomain; <b>PDBTitle:</b> crystal structure of trypanosoma cruzi macrodomain
37	<a href="#">c4i3hA_</a>	Alignment	not modelled	15.2	18	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit b, dna topoisomerase 4 subunit a <b>PDBTitle:</b> a three-gate structure of topoisomerase iv from streptococcus2 pneumoniae
38	<a href="#">c3ih1A_</a>	Alignment	not modelled	12.7	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
39	<a href="#">c3m1fv_</a>	Alignment	not modelled	11.5	38	<b>PDB header:</b> contractile protein <b>Chain:</b> V: <b>PDB Molecule:</b> putative uncharacterized protein vpa1370; <b>PDBTitle:</b> crosslinked complex of actin with first w domain of vibrio2 parahaemolyticus vopl
40	<a href="#">c4pa5A_</a>	Alignment	not modelled	10.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> tgl - a bacterial spore coat transglutaminase - cystamine complex
41	<a href="#">c2hjpA_</a>	Alignment	not modelled	10.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
42	<a href="#">d1muma_</a>	Alignment	not modelled	9.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
43	<a href="#">c3b8iF_</a>	Alignment	not modelled	9.2	16	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
44	<a href="#">c2xcsD_</a>	Alignment	not modelled	9.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna gyrase subunit b, dna gyrase subunit a; <b>PDBTitle:</b> the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
45	<a href="#">c4k2wA_</a>	Alignment	not modelled	8.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> x-ray crystal structure of superoxide dismutase from babesia bovis2 solved by sulfur/zinc sad
46	<a href="#">c2xcqA_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit b, dna gyrase subunit a; <b>PDBTitle:</b> the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
47	<a href="#">d1ujqa_</a>	Alignment	not modelled	8.4	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
48	<a href="#">c4uecB_</a>	Alignment	not modelled	8.2	33	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 4g, isoform a; <b>PDBTitle:</b> complex of d. melanogaster eif4e with eif4g and cap analog
49	<a href="#">c1zlpA_</a>	Alignment	not modelled	8.1	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
50	<a href="#">d1p9ya_</a>	Alignment	not modelled	7.9	21	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
51	<a href="#">c4mg4G_</a>	Alignment	not modelled	7.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
52	<a href="#">d2z15a1</a>	Alignment	not modelled	7.7	24	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
53	<a href="#">d1l8qa1</a>	Alignment	not modelled	7.7	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Chromosomal replication initiation factor DnaA C-terminal domain IV

54	<a href="#">d2cupa3</a>	Alignment	not modelled	7.0	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
55	<a href="#">c2xkjE</a>	Alignment	not modelled	7.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> E; <b>PDB Molecule:</b> topoisomerase iv; <b>PDBTitle:</b> crystal structure of catalytic core of a. baumannii topo iv (pare-2 parc fusion truncate)
56	<a href="#">c2d3o1</a>	Alignment	not modelled	6.9	67	<b>PDB header:</b> ribosome <b>Chain:</b> 1; <b>PDB Molecule:</b> trigger factor; <b>PDBTitle:</b> structure of ribosome binding domain of the trigger factor on the 50s2 ribosomal subunit from d. radiodurans
57	<a href="#">d1t11a2</a>	Alignment	not modelled	6.8	29	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
58	<a href="#">d1w26a2</a>	Alignment	not modelled	6.8	29	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Trigger factor ribosome-binding domain <b>Family:</b> Trigger factor ribosome-binding domain
59	<a href="#">c5fsuA</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> macrodomein; <b>PDBTitle:</b> crystal structure of trypanosoma brucei macrodomain2 (crystal form 1)
60	<a href="#">c3eool</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> lyase <b>Chain:</b> L; <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
61	<a href="#">d1wgla</a>	Alignment	not modelled	6.2	14	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
62	<a href="#">d1d6za2</a>	Alignment	not modelled	6.0	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
63	<a href="#">c1b06A</a>	Alignment	not modelled	6.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (superoxide dismutase); <b>PDBTitle:</b> superoxide dismutase from sulfolobus acidocaldarius
64	<a href="#">c2dhyA</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedcl1)
65	<a href="#">d1wb8a2</a>	Alignment	not modelled	6.0	5	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
66	<a href="#">c4lsbA</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
67	<a href="#">c3k9aA</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> hiv glycoprotein gp41; <b>PDBTitle:</b> crystal structure of hiv gp41 with mper
68	<a href="#">c2qiwa</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> pep phosphonmutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
69	<a href="#">c5td6A</a>	Alignment	not modelled	5.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> fog-3 protein; <b>PDBTitle:</b> c. elegans fog-3 btg/tob domain - h47n, c117a
70	<a href="#">d1dt0a2</a>	Alignment	not modelled	5.5	9	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
71	<a href="#">d1j1va</a>	Alignment	not modelled	5.4	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Chromosomal replication initiation factor DnaA C-terminal domain IV
72	<a href="#">c3pvpA</a>	Alignment	not modelled	5.3	32	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
73	<a href="#">c3gpqA</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> viral protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> non-structural protein 3; <b>PDBTitle:</b> crystal structure of macro domain of chikungunya virus in complex with2 rna
74	<a href="#">d1b06a2</a>	Alignment	not modelled	5.3	14	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
75	<a href="#">c3lyeA</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase