Phyre^2

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Description	Q47688
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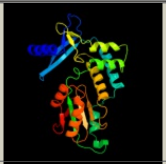
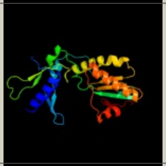
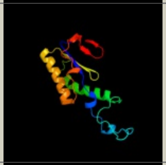
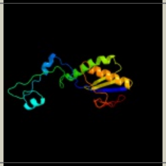
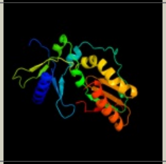
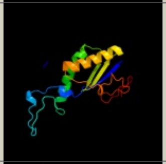
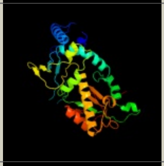
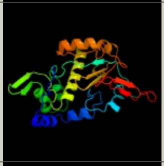
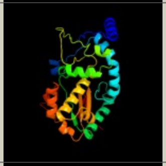
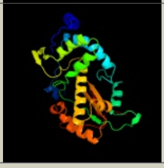
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3du6A_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**telomerase reverse transcriptase; **PDBTitle:** structure of the catalytic subunit of telomerase, tert
2	c1rthA_	Alignment		99.5	20	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**hiv-1 reverse transcriptase; **PDBTitle:** high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes
3	c1mu2A_	Alignment		99.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hiv-2 rt; **PDBTitle:** crystal structure of hiv-2 reverse transcriptase
4	c2opqA_	Alignment		98.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**reverse transcriptase/ribonuclease h; **PDBTitle:** crystal structure of l100i mutant hiv-1 reverse2 transcriptase in complex with gw420867x.
5	d1xr7a_	Alignment		98.7	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
6	d2zd1b1	Alignment		98.7	21	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
7	d1u09a_	Alignment		98.7	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
8	c3n6mA_	Alignment		98.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-dependent rna polymerase; **PDBTitle:** crystal structure of ev71 rdrp in complex with gtp
9	d1mu2a2	Alignment		98.7	18	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
10	d1xr6a_	Alignment		98.6	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
11	d1ra6a_	Alignment		98.5	13	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase

12	d1ztwa1	Alignment		98.5	24	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
13	d1khva_	Alignment		98.5	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
14	c2ijd1_	Alignment		98.3	13	**PDB header:**hydrolase, transferase **Chain: 1: PDB Molecule:**picornain 3c, rna-directed rna polymerase; **PDBTitle:** crystal structure of the poliovirus precursor protein 3cd
15	c3kk1B_	Alignment		98.3	18	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**reverse transcriptase p51 subunit; **PDBTitle:** hiv-1 reverse transcriptase-dna complex with nuceotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
16	d1xr5a_	Alignment		98.3	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
17	c2uutA_	Alignment		98.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** the 2.4 angstrom resolution structure of the d346g mutant2 of the sapporo virus rdrp polymerase
18	c3nahC_	Alignment		98.1	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**rna dependent rna polymerase; **PDBTitle:** crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
19	d1sh0a_	Alignment		97.9	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
20	c2b43D_	Alignment		97.9	15	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**non-structural polyprotein; **PDBTitle:** crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
21	d1rw3a_	Alignment	not modelled	97.3	19	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
22	d1hara_	Alignment	not modelled	96.5	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
23	d1raja_	Alignment	not modelled	93.9	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
24	c3mmpG_	Alignment	not modelled	88.7	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**rna-directed rna polymerase beta chain; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
25	c3agqA_	Alignment	not modelled	72.6	17	**PDB header:**translation,transferase **Chain:** A: **PDB Molecule:**elongation factor ts, elongation factor tu 1, linker, q **PDBTitle:** structure of viral polymerase form ii
26	d1nb4a_	Alignment	not modelled	71.3	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
27	d1gx5a_	Alignment	not modelled	41.9	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
28	c1nh2D_	Alignment	not modelled	35.3	23	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia small chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
29	c1nvpD_	Alignment	not modelled	33.2	19	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia gamma

29	c1nvpD_	Alignment	not modelled	53.2	19	chain; **PDBTitle:** human tfiia/tbp/dna complex
30	d1c0aa2	Alignment	not modelled	15.8	19	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
31	d1l0wa2	Alignment	not modelled	14.3	22	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
32	d1nh2d1	Alignment	not modelled	11.2	26	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
33	d1nvpd1	Alignment	not modelled	9.5	25	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
34	d1p9ya_	Alignment	not modelled	7.3	14	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
35	d1w26a2	Alignment	not modelled	6.3	21	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain