

Phyre²

Email	marius.surleac@gmail.com
Description	rt_____
Date	Fri Oct 13 08:57:50 BST 2017
Unique Job ID	c509c69101c4c3c9
Sequence	PISPIETVPV ... Download FASTA
Job Type	intensive
Job Expiry	

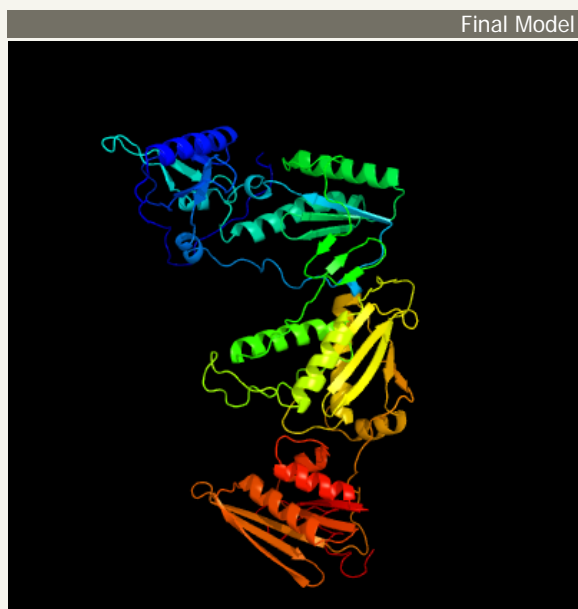


Image coloured by rainbow N → C terminus

Model dimensions (Å): **X**:64.230 **Y**:83.408 **Z**:108.188



Confidence Key
High(9)  Low (0)

97% of residues modelled at >90% confidence ([Details](#))

Publication-ready images

[Hi-Res image \(black background\)](#)
[Hi-Res image \(white background\)](#)

JSmol Viewer

[Interactive 3D view in JSmol](#)

Sequence analysis

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FASTA
version](#)

Secondary structure and disorder prediction [\[Show\]](#)

Domain analysis [\[Show\]](#)

Detailed template information [\[Hide\]](#)



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rthA			100.0	99	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
2	c2opqA			100.0	97	PDB header: transferase Chain: A; PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of I100i mutant hiv-1 reverse transcriptase in2 complex with gw420867x.
3	c1mu2A			100.0	60	PDB header: transferase Chain: A; PDB Molecule: hiv-2 rt; PDBTitle: crystal structure of hiv-2 reverse transcriptase
4	c5dmqA			100.0	20	PDB header: transferase, hydrolase/translation Chain: A; PDB Molecule: reverse transcriptase/ribonuclease h p80; PDBTitle: crystal structure of mouse erf1 in complex with reverse transcriptase2 (rt) of moloney murine leukemia virus
5	d2zd1b1			100.0	100	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
6	c3kk1B			100.0	92	PDB header: transferase/dna Chain: B; PDB Molecule: reverse transcriptase p51 subunit; PDBTitle: hiv-1 reverse transcriptase-dna complex with nucetotide inhibitor gs-2 9148-diphosphate bound in nucleotide site





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Component software

Template detection: [HHpred 1.51](#)
Secondary structure prediction: [Psi-pred 2.5](#)
Disorder prediction: [Disopred 2.4](#)
Transmembrane prediction: [Memsat_SVM](#)
Multi-template modelling and *ab initio*: [Poing 1.0](#)

