



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:32 AM UTC

PDB ID : 6EVJ / pdb_00006evj
Title : Crystal structure of bat influenza A/H17N10 polymerase with viral RNA promoter and capped RNA primer
Authors : Pflug, A.; Cusack, S.
Deposited on : 2017-11-01
Resolution : 3.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

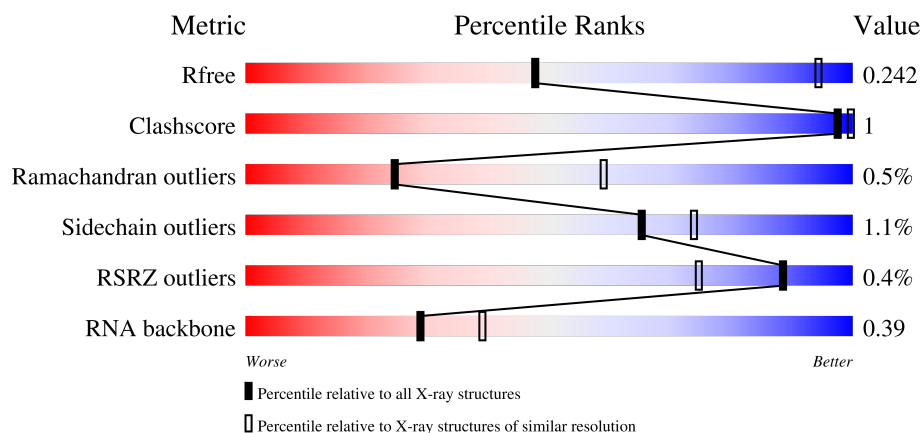
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

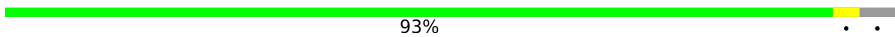
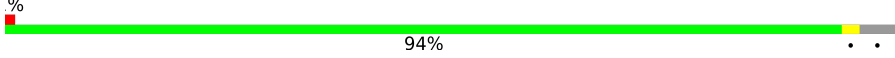
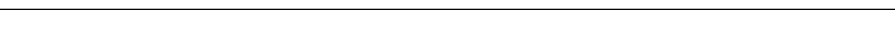
The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1270 (4.10-3.70)
Clashscore	190562	1034 (4.08-3.72)
Ramachandran outliers	187476	1251 (4.10-3.70)
Sidechain outliers	187428	1243 (4.10-3.70)
RSRZ outliers	180081	1269 (4.10-3.70)
RNA backbone	3983	1014 (4.70-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	738	 93%
1	D	738	 94%
2	B	776	 93%
2	E	776	 93%

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Mol	Chain	Length	Quality of chain
3	C	809	 89% 8%
3	F	809	 88% 8%
4	M	13	 8% 15% 8% 69%
4	N	13	 8% 15% 8% 69%
5	R	18	 67% 6% 28%
5	S	18	 67% 6% 28%
6	U	16	 56% 38% 6%
6	V	16	 56% 38% 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 36717 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Polymerase acidic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	709	Total	C	N	O	S	0	0	0
			5775	3671	974	1093	37			
1	D	708	Total	C	N	O	S	0	0	0
			5769	3668	974	1090	37			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	GLY	-	expression tag	UNP H6QM92
A	-12	SER	-	expression tag	UNP H6QM92
A	-11	HIS	-	expression tag	UNP H6QM92
A	-10	HIS	-	expression tag	UNP H6QM92
A	-9	HIS	-	expression tag	UNP H6QM92
A	-8	HIS	-	expression tag	UNP H6QM92
A	-7	HIS	-	expression tag	UNP H6QM92
A	-6	HIS	-	expression tag	UNP H6QM92
A	-5	HIS	-	expression tag	UNP H6QM92
A	-4	HIS	-	expression tag	UNP H6QM92
A	-3	GLY	-	expression tag	UNP H6QM92
A	-2	SER	-	expression tag	UNP H6QM92
A	-1	GLY	-	expression tag	UNP H6QM92
A	0	SER	-	expression tag	UNP H6QM92
A	714	GLY	-	expression tag	UNP H6QM92
A	715	SER	-	expression tag	UNP H6QM92
A	716	GLY	-	expression tag	UNP H6QM92
A	717	SER	-	expression tag	UNP H6QM92
A	718	GLY	-	expression tag	UNP H6QM92
A	719	GLU	-	expression tag	UNP H6QM92
A	720	ASN	-	expression tag	UNP H6QM92
A	721	LEU	-	expression tag	UNP H6QM92
A	722	TYR	-	expression tag	UNP H6QM92
A	723	PHE	-	expression tag	UNP H6QM92
A	724	GLN	-	expression tag	UNP H6QM92

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-13	GLY	-	expression tag	UNP H6QM92
D	-12	SER	-	expression tag	UNP H6QM92
D	-11	HIS	-	expression tag	UNP H6QM92
D	-10	HIS	-	expression tag	UNP H6QM92
D	-9	HIS	-	expression tag	UNP H6QM92
D	-8	HIS	-	expression tag	UNP H6QM92
D	-7	HIS	-	expression tag	UNP H6QM92
D	-6	HIS	-	expression tag	UNP H6QM92
D	-5	HIS	-	expression tag	UNP H6QM92
D	-4	HIS	-	expression tag	UNP H6QM92
D	-3	GLY	-	expression tag	UNP H6QM92
D	-2	SER	-	expression tag	UNP H6QM92
D	-1	GLY	-	expression tag	UNP H6QM92
D	0	SER	-	expression tag	UNP H6QM92
D	714	GLY	-	expression tag	UNP H6QM92
D	715	SER	-	expression tag	UNP H6QM92
D	716	GLY	-	expression tag	UNP H6QM92
D	717	SER	-	expression tag	UNP H6QM92
D	718	GLY	-	expression tag	UNP H6QM92
D	719	GLU	-	expression tag	UNP H6QM92
D	720	ASN	-	expression tag	UNP H6QM92
D	721	LEU	-	expression tag	UNP H6QM92
D	722	TYR	-	expression tag	UNP H6QM92
D	723	PHE	-	expression tag	UNP H6QM92
D	724	GLN	-	expression tag	UNP H6QM92

- Molecule 2 is a protein called RNA-directed RNA polymerase catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	752	Total	C	N	O	S	0	0	0
			5999	3772	1067	1120	40			
2	E	749	Total	C	N	O	S	0	0	0
			5972	3756	1061	1115	40			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	GLY	-	expression tag	UNP H6QM91
B	-7	SER	-	expression tag	UNP H6QM91
B	-6	GLY	-	expression tag	UNP H6QM91
B	-5	SER	-	expression tag	UNP H6QM91
B	-4	GLY	-	expression tag	UNP H6QM91

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	SER	-	expression tag	UNP H6QM91
B	-2	GLY	-	expression tag	UNP H6QM91
B	-1	SER	-	expression tag	UNP H6QM91
B	0	GLY	-	expression tag	UNP H6QM91
B	757	GLY	-	expression tag	UNP H6QM91
B	758	SER	-	expression tag	UNP H6QM91
B	759	GLY	-	expression tag	UNP H6QM91
B	760	SER	-	expression tag	UNP H6QM91
B	761	GLY	-	expression tag	UNP H6QM91
B	762	GLU	-	expression tag	UNP H6QM91
B	763	ASN	-	expression tag	UNP H6QM91
B	764	LEU	-	expression tag	UNP H6QM91
B	765	TYR	-	expression tag	UNP H6QM91
B	766	PHE	-	expression tag	UNP H6QM91
B	767	GLN	-	expression tag	UNP H6QM91
E	-8	GLY	-	expression tag	UNP H6QM91
E	-7	SER	-	expression tag	UNP H6QM91
E	-6	GLY	-	expression tag	UNP H6QM91
E	-5	SER	-	expression tag	UNP H6QM91
E	-4	GLY	-	expression tag	UNP H6QM91
E	-3	SER	-	expression tag	UNP H6QM91
E	-2	GLY	-	expression tag	UNP H6QM91
E	-1	SER	-	expression tag	UNP H6QM91
E	0	GLY	-	expression tag	UNP H6QM91
E	757	GLY	-	expression tag	UNP H6QM91
E	758	SER	-	expression tag	UNP H6QM91
E	759	GLY	-	expression tag	UNP H6QM91
E	760	SER	-	expression tag	UNP H6QM91
E	761	GLY	-	expression tag	UNP H6QM91
E	762	GLU	-	expression tag	UNP H6QM91
E	763	ASN	-	expression tag	UNP H6QM91
E	764	LEU	-	expression tag	UNP H6QM91
E	765	TYR	-	expression tag	UNP H6QM91
E	766	PHE	-	expression tag	UNP H6QM91
E	767	GLN	-	expression tag	UNP H6QM91

- Molecule 3 is a protein called Polymerase basic protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	748	Total	C	N	O	S	0	0	0
			5937	3742	1049	1114	32			
3	F	746	Total	C	N	O	S	0	0	0
			5926	3736	1049	1109	32			

There are 98 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	GLY	-	expression tag	UNP H6QM90
C	-7	SER	-	expression tag	UNP H6QM90
C	-6	GLY	-	expression tag	UNP H6QM90
C	-5	SER	-	expression tag	UNP H6QM90
C	-4	GLY	-	expression tag	UNP H6QM90
C	-3	SER	-	expression tag	UNP H6QM90
C	-2	GLY	-	expression tag	UNP H6QM90
C	-1	SER	-	expression tag	UNP H6QM90
C	0	GLY	-	expression tag	UNP H6QM90
C	761	GLY	-	expression tag	UNP H6QM90
C	762	TRP	-	expression tag	UNP H6QM90
C	763	SER	-	expression tag	UNP H6QM90
C	764	HIS	-	expression tag	UNP H6QM90
C	765	PRO	-	expression tag	UNP H6QM90
C	766	GLN	-	expression tag	UNP H6QM90
C	767	PHE	-	expression tag	UNP H6QM90
C	768	GLU	-	expression tag	UNP H6QM90
C	769	LYS	-	expression tag	UNP H6QM90
C	770	GLY	-	expression tag	UNP H6QM90
C	771	GLY	-	expression tag	UNP H6QM90
C	772	GLY	-	expression tag	UNP H6QM90
C	773	SER	-	expression tag	UNP H6QM90
C	774	GLY	-	expression tag	UNP H6QM90
C	775	GLY	-	expression tag	UNP H6QM90
C	776	GLY	-	expression tag	UNP H6QM90
C	777	SER	-	expression tag	UNP H6QM90
C	778	GLY	-	expression tag	UNP H6QM90
C	779	GLY	-	expression tag	UNP H6QM90
C	780	SER	-	expression tag	UNP H6QM90
C	781	ALA	-	expression tag	UNP H6QM90
C	782	TRP	-	expression tag	UNP H6QM90
C	783	SER	-	expression tag	UNP H6QM90
C	784	HIS	-	expression tag	UNP H6QM90
C	785	PRO	-	expression tag	UNP H6QM90
C	786	GLN	-	expression tag	UNP H6QM90
C	787	PHE	-	expression tag	UNP H6QM90
C	788	GLU	-	expression tag	UNP H6QM90
C	789	LYS	-	expression tag	UNP H6QM90
C	790	GLY	-	expression tag	UNP H6QM90
C	791	ARG	-	expression tag	UNP H6QM90
C	792	SER	-	expression tag	UNP H6QM90
C	793	GLY	-	expression tag	UNP H6QM90

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Chain	Residue	Modelled	Actual	Comment	Reference
C	794	GLY	-	expression tag	UNP H6QM90
C	795	GLU	-	expression tag	UNP H6QM90
C	796	ASN	-	expression tag	UNP H6QM90
C	797	LEU	-	expression tag	UNP H6QM90
C	798	TYR	-	expression tag	UNP H6QM90
C	799	PHE	-	expression tag	UNP H6QM90
C	800	GLN	-	expression tag	UNP H6QM90
F	-8	GLY	-	expression tag	UNP H6QM90
F	-7	SER	-	expression tag	UNP H6QM90
F	-6	GLY	-	expression tag	UNP H6QM90
F	-5	SER	-	expression tag	UNP H6QM90
F	-4	GLY	-	expression tag	UNP H6QM90
F	-3	SER	-	expression tag	UNP H6QM90
F	-2	GLY	-	expression tag	UNP H6QM90
F	-1	SER	-	expression tag	UNP H6QM90
F	0	GLY	-	expression tag	UNP H6QM90
F	761	GLY	-	expression tag	UNP H6QM90
F	762	TRP	-	expression tag	UNP H6QM90
F	763	SER	-	expression tag	UNP H6QM90
F	764	HIS	-	expression tag	UNP H6QM90
F	765	PRO	-	expression tag	UNP H6QM90
F	766	GLN	-	expression tag	UNP H6QM90
F	767	PHE	-	expression tag	UNP H6QM90
F	768	GLU	-	expression tag	UNP H6QM90
F	769	LYS	-	expression tag	UNP H6QM90
F	770	GLY	-	expression tag	UNP H6QM90
F	771	GLY	-	expression tag	UNP H6QM90
F	772	GLY	-	expression tag	UNP H6QM90
F	773	SER	-	expression tag	UNP H6QM90
F	774	GLY	-	expression tag	UNP H6QM90
F	775	GLY	-	expression tag	UNP H6QM90
F	776	GLY	-	expression tag	UNP H6QM90
F	777	SER	-	expression tag	UNP H6QM90
F	778	GLY	-	expression tag	UNP H6QM90
F	779	GLY	-	expression tag	UNP H6QM90
F	780	SER	-	expression tag	UNP H6QM90
F	781	ALA	-	expression tag	UNP H6QM90
F	782	TRP	-	expression tag	UNP H6QM90
F	783	SER	-	expression tag	UNP H6QM90
F	784	HIS	-	expression tag	UNP H6QM90
F	785	PRO	-	expression tag	UNP H6QM90
F	786	GLN	-	expression tag	UNP H6QM90

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Chain	Residue	Modelled	Actual	Comment	Reference
F	787	PHE	-	expression tag	UNP H6QM90
F	788	GLU	-	expression tag	UNP H6QM90
F	789	LYS	-	expression tag	UNP H6QM90
F	790	GLY	-	expression tag	UNP H6QM90
F	791	ARG	-	expression tag	UNP H6QM90
F	792	SER	-	expression tag	UNP H6QM90
F	793	GLY	-	expression tag	UNP H6QM90
F	794	GLY	-	expression tag	UNP H6QM90
F	795	GLU	-	expression tag	UNP H6QM90
F	796	ASN	-	expression tag	UNP H6QM90
F	797	LEU	-	expression tag	UNP H6QM90
F	798	TYR	-	expression tag	UNP H6QM90
F	799	PHE	-	expression tag	UNP H6QM90
F	800	GLN	-	expression tag	UNP H6QM90

- Molecule 4 is a RNA chain called RNA (5'-D(*(GDM))-R(P*AP*AP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	N	4	Total 93	C 40	N 17	O 31	P 5	0	0	0
4	M	4	Total 93	C 40	N 17	O 31	P 5	0	0	0

- Molecule 5 is a RNA chain called RNA (5'-R(*UP*AP*UP*AP*CP*CP*UP*CP*UP*GP*CP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	R	13	Total 246	C 111	N 37	O 86	P 12	0	0	0
5	S	13	Total 247	C 111	N 37	O 87	P 12	0	0	0

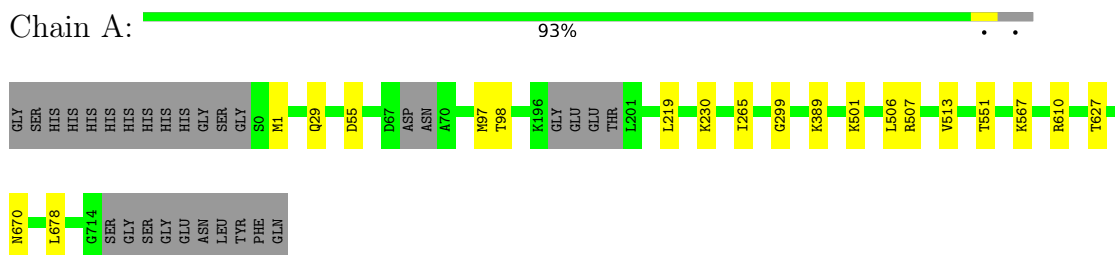
- Molecule 6 is a RNA chain called RNA (5'-R(P*AP*GP*UP*AP*GP*UP*AP*AP*CP*AP*AP*GP*AP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	U	15	Total 330	C 147	N 67	O 101	P 15	0	0	0
6	V	15	Total 330	C 147	N 67	O 101	P 15	0	0	0

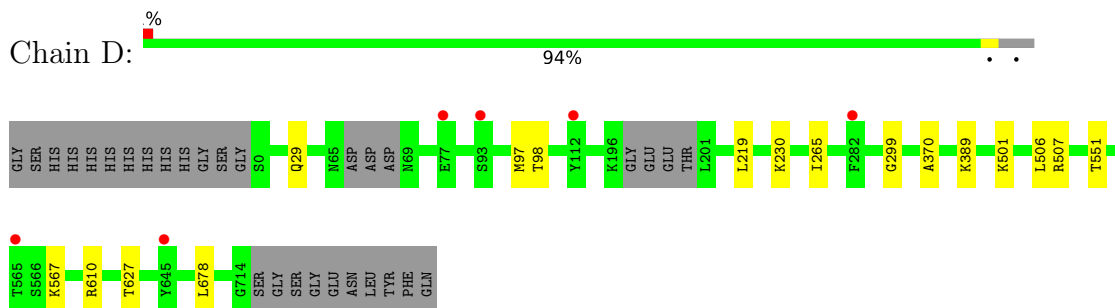
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

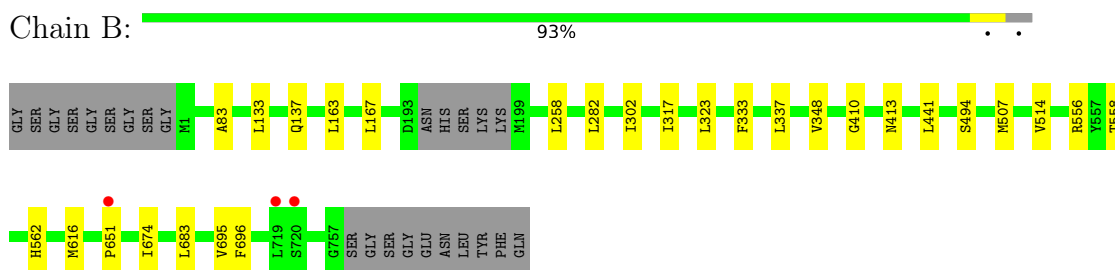
- Molecule 1: Polymerase acidic protein



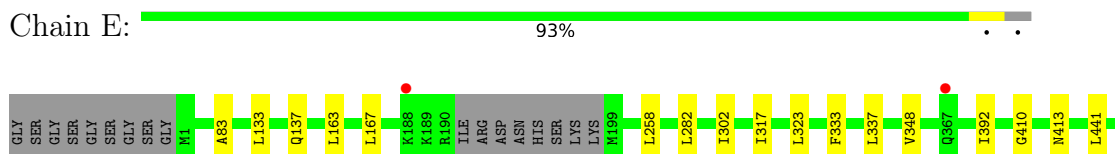
- Molecule 1: Polymerase acidic protein

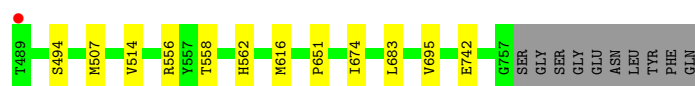


- Molecule 2: RNA-directed RNA polymerase catalytic subunit



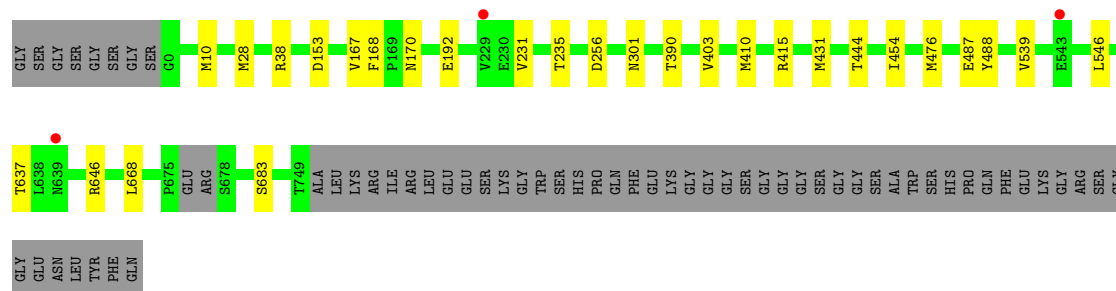
- Molecule 2: RNA-directed RNA polymerase catalytic subunit





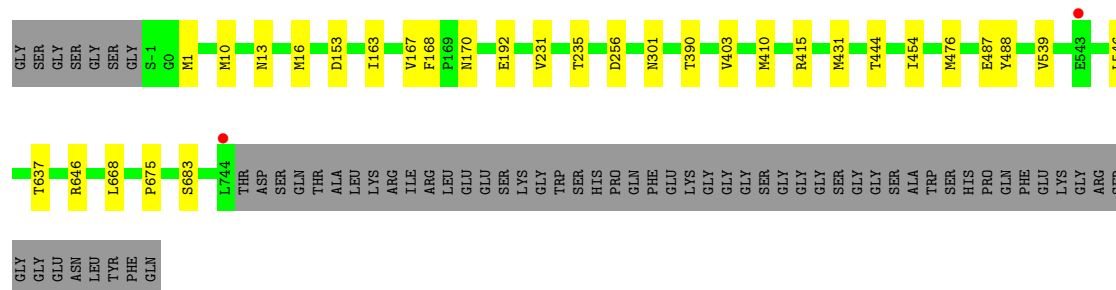
- Molecule 3: Polymerase basic protein 2

Chain C:  89% • 8%

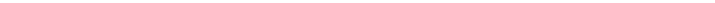


- Molecule 3: Polymerase basic protein 2

Chain F: 88% . 8%

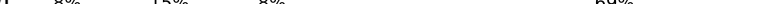


- Molecule 4: RNA (5'-D*(GDM))-R(P*AP*AP*U)-3')

Chain N:  8% 15% 8% 69%



- Molecule 4: RNA (5'-D*(GDM))-R(P*AP*AP*U)-3')

Chain M:  8% 15% 8% 69%



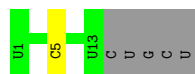
- Molecule 5: RNA (5'-R(*UP*AP*UP*AP*CP*CP*UP*CP*UP*GP*CP*UP*U)-3')

Chain R:  67% 6% 28%



- Molecule 5: RNA (5'-R(*UP*AP*UP*AP*CP*CP*UP*CP*UP*GP*CP*UP*U)-3')

Chain S:  67% 6% 28%



- Molecule 6: RNA (5'-R(P*AP*GP*UP*AP*GP*UP*AP*AP*CP*AP*AP*GP*AP*GP*G)-3')

Chain U:  56% 38% 6%



- Molecule 6: RNA (5'-R(P*AP*GP*UP*AP*GP*UP*AP*AP*CP*AP*AP*GP*AP*GP*G)-3')

Chain V:  56% 38% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	185.46Å 286.17Å 171.93Å 90.00° 93.27° 90.00°	Depositor
Resolution (Å)	50.00 – 3.90 50.00 – 3.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-3.90) 99.7 (50.00-3.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 3.88Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.207 , 0.245 0.206 , 0.242	Depositor DCC
R_{free} test set	4018 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	158.6	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 141.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	36717	wwPDB-VP
Average B, all atoms (Å ²)	186.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: M7G

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.54	0/5897	0.76	0/7939
1	D	0.54	0/5891	0.77	0/7931
2	B	0.56	0/6115	0.80	0/8252
2	E	0.56	0/6088	0.80	0/8216
3	C	0.56	0/6038	0.76	0/8152
3	F	0.55	0/6028	0.76	0/8138
4	M	0.44	0/71	1.14	1/108 (0.9%)
4	N	0.43	0/71	1.11	1/108 (0.9%)
5	R	0.34	0/272	0.64	0/420
5	S	0.34	0/273	0.65	0/421
6	U	0.36	0/371	0.61	0/576
6	V	0.37	0/371	0.61	0/576
All	All	0.54	0/37486	0.77	2/50837 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	1	A	C4'-C3'-O3'	5.68	117.92	109.40
4	N	1	A	C4'-C3'-O3'	5.26	117.29	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5775	0	5690	8	0
1	D	5769	0	5692	8	0
2	B	5999	0	6011	13	0
2	E	5972	0	5983	13	0
3	C	5937	0	6053	9	0
3	F	5926	0	6047	11	0
4	M	93	0	49	0	0
4	N	93	0	49	0	0
5	R	246	0	125	0	0
5	S	247	0	128	0	0
6	U	330	0	164	1	0
6	V	330	0	164	0	0
All	All	36717	0	36155	56	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:695:VAL:HG11	3:C:10:MET:HE2	1.70	0.72
2:E:695:VAL:HG11	3:F:10:MET:HE2	1.75	0.67
3:C:546:LEU:HD12	3:C:668:LEU:HD11	1.79	0.65
3:F:546:LEU:HD12	3:F:668:LEU:HD11	1.79	0.64
3:F:403:VAL:HA	3:F:410:MET:HE3	1.86	0.57
3:C:403:VAL:HA	3:C:410:MET:HE3	1.87	0.57
2:B:258:LEU:HD22	2:B:337:LEU:HD13	1.88	0.55
2:E:258:LEU:HD22	2:E:337:LEU:HD13	1.88	0.55
1:D:265:ILE:HG22	1:D:678:LEU:HD21	1.90	0.54
1:A:265:ILE:HG22	1:A:678:LEU:HD21	1.90	0.53
1:A:506:LEU:HD13	1:A:567:LYS:HG3	1.93	0.50
1:D:506:LEU:HD13	1:D:567:LYS:HG3	1.93	0.50
2:B:494:SER:HB3	2:B:507:MET:HE3	1.95	0.49
2:B:83:ALA:HB3	2:B:317:ILE:HD11	1.96	0.48
3:C:167:VAL:HG23	3:C:168:PHE:CD2	2.49	0.48
3:C:231:VAL:HG23	3:C:235:THR:HG23	1.96	0.48
2:E:83:ALA:HB3	2:E:317:ILE:HD11	1.96	0.48
3:F:231:VAL:HG23	3:F:235:THR:HG23	1.96	0.47
2:E:494:SER:HB3	2:E:507:MET:HE3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:167:VAL:HG23	3:F:168:PHE:CD2	2.49	0.47
1:D:370:ALA:HB2	6:U:10:A:H3'	1.98	0.46
2:E:333:PHE:CZ	2:E:337:LEU:HD11	2.51	0.46
2:B:333:PHE:CZ	2:B:337:LEU:HD11	2.51	0.46
2:E:133:LEU:HD12	2:E:137:GLN:HE21	1.81	0.46
3:C:415:ARG:CG	3:C:444:THR:HG21	2.47	0.45
2:B:133:LEU:HD12	2:B:137:GLN:HE21	1.81	0.45
3:C:637:THR:HG22	3:C:646:ARG:HG2	1.98	0.45
2:B:83:ALA:CB	2:B:317:ILE:HD11	2.47	0.44
2:E:83:ALA:CB	2:E:317:ILE:HD11	2.47	0.44
1:A:230:LYS:HG3	2:B:323:LEU:HD22	1.98	0.44
3:F:415:ARG:CG	3:F:444:THR:HG21	2.47	0.44
1:D:230:LYS:HG3	2:E:323:LEU:HD22	2.00	0.44
3:F:637:THR:HG22	3:F:646:ARG:HG2	1.99	0.43
2:E:674:ILE:HG23	2:E:683:LEU:HD11	2.01	0.43
2:B:674:ILE:HG23	2:B:683:LEU:HD11	2.01	0.42
1:A:506:LEU:HD13	1:A:567:LYS:CG	2.49	0.42
2:B:282:LEU:HG	2:B:441:LEU:HD22	2.01	0.42
1:A:610:ARG:HD2	1:A:627:THR:HG21	2.01	0.42
2:B:696:PHE:CD2	3:C:28:MET:HE3	2.55	0.42
2:B:514:VAL:HG11	2:B:558:THR:HG21	2.02	0.42
2:B:556:ARG:HD3	2:B:562:HIS:HA	2.02	0.42
1:D:610:ARG:HD2	1:D:627:THR:HG21	2.02	0.42
2:E:514:VAL:HG11	2:E:558:THR:HG21	2.02	0.42
1:D:506:LEU:HD13	1:D:567:LYS:CG	2.50	0.41
2:E:282:LEU:HG	2:E:441:LEU:HD22	2.02	0.41
3:C:415:ARG:HG3	3:C:444:THR:HG21	2.03	0.41
1:D:610:ARG:HG3	1:D:627:THR:HG21	2.03	0.41
2:E:742:GLU:HG2	3:F:1:MET:HE3	2.03	0.41
1:D:97:MET:HE2	1:D:98:THR:HG23	2.02	0.41
2:E:556:ARG:HD3	2:E:562:HIS:HA	2.02	0.40
3:F:163:ILE:O	3:F:167:VAL:HG22	2.21	0.40
1:A:610:ARG:HG3	1:A:627:THR:HG21	2.03	0.40
3:F:13:ASN:HD22	3:F:16:MET:HE3	1.86	0.40
3:F:415:ARG:HG3	3:F:444:THR:HG21	2.03	0.40
1:A:97:MET:HE2	1:A:98:THR:HG23	2.02	0.40
1:A:506:LEU:HD11	1:A:513:VAL:CG2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	703/738 (95%)	677 (96%)	23 (3%)	3 (0%)	30	64
1	D	702/738 (95%)	675 (96%)	25 (4%)	2 (0%)	36	69
2	B	748/776 (96%)	710 (95%)	35 (5%)	3 (0%)	30	64
2	E	745/776 (96%)	706 (95%)	36 (5%)	3 (0%)	30	64
3	C	744/809 (92%)	701 (94%)	39 (5%)	4 (0%)	24	59
3	F	744/809 (92%)	703 (94%)	36 (5%)	5 (1%)	18	53
All	All	4386/4646 (94%)	4172 (95%)	194 (4%)	20 (0%)	24	59

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	413	ASN
3	C	683	SER
2	E	413	ASN
3	F	675	PRO
2	B	410	GLY
3	C	153	ASP
3	C	488	TYR
2	E	410	GLY
3	F	153	ASP
3	F	488	TYR
3	F	683	SER
2	B	651	PRO
3	C	476	MET
2	E	651	PRO
3	F	476	MET
1	A	389	LYS
1	D	389	LYS
1	A	670	ASN
1	D	299	GLY
1	A	299	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	633/657 (96%)	626 (99%)	7 (1%)	65	74
1	D	633/657 (96%)	628 (99%)	5 (1%)	73	77
2	B	659/676 (98%)	654 (99%)	5 (1%)	73	77
2	E	656/676 (97%)	650 (99%)	6 (1%)	70	75
3	C	663/706 (94%)	653 (98%)	10 (2%)	57	70
3	F	661/706 (94%)	652 (99%)	9 (1%)	59	71
All	All	3905/4078 (96%)	3863 (99%)	42 (1%)	65	74

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	29	GLN
1	A	55	ASP
1	A	219	LEU
1	A	501	LYS
1	A	507	ARG
1	A	551	THR
2	B	163	LEU
2	B	167	LEU
2	B	302	ILE
2	B	348	VAL
2	B	616	MET
3	C	38	ARG
3	C	170	ASN
3	C	192	GLU
3	C	256	ASP
3	C	301	ASN
3	C	390	THR
3	C	431	MET
3	C	454	ILE
3	C	487	GLU
3	C	539	VAL

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Mol	Chain	Res	Type
1	D	29	GLN
1	D	219	LEU
1	D	501	LYS
1	D	507	ARG
1	D	551	THR
2	E	163	LEU
2	E	167	LEU
2	E	302	ILE
2	E	348	VAL
2	E	392	ILE
2	E	616	MET
3	F	170	ASN
3	F	192	GLU
3	F	256	ASP
3	F	301	ASN
3	F	390	THR
3	F	431	MET
3	F	454	ILE
3	F	487	GLU
3	F	539	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	96	ASN
1	A	180	GLN
1	A	212	GLN
1	A	294	ASN
1	A	387	GLN
1	A	461	ASN
1	A	476	GLN
1	A	612	ASN
1	A	698	ASN
2	B	16	ASN
2	B	58	ASN
2	B	65	GLN
2	B	99	HIS
2	B	127	GLN
2	B	137	GLN
2	B	153	ASN
2	B	158	ASN

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Mol	Chain	Res	Type
2	B	176	ASN
2	B	202	GLN
2	B	312	ASN
2	B	363	HIS
2	B	367	GLN
2	B	413	ASN
2	B	428	GLN
2	B	536	ASN
2	B	537	ASN
2	B	678	ASN
2	B	679	GLN
3	C	13	ASN
3	C	39	GLN
3	C	137	ASN
3	C	170	ASN
3	C	182	GLN
3	C	301	ASN
3	C	306	GLN
3	C	320	ASN
3	C	348	ASN
3	C	350	GLN
3	C	364	ASN
3	C	383	GLN
3	C	482	GLN
3	C	491	ASN
3	C	530	ASN
3	C	532	ASN
3	C	581	GLN
3	C	632	GLN
3	C	728	GLN
1	D	10	ASN
1	D	29	GLN
1	D	96	ASN
1	D	142	ASN
1	D	180	GLN
1	D	212	GLN
1	D	294	ASN
1	D	387	GLN
1	D	416	ASN
1	D	461	ASN
1	D	476	GLN
1	D	612	ASN

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Mol	Chain	Res	Type
2	E	16	ASN
2	E	58	ASN
2	E	65	GLN
2	E	99	HIS
2	E	127	GLN
2	E	137	GLN
2	E	153	ASN
2	E	176	ASN
2	E	312	ASN
2	E	363	HIS
2	E	367	GLN
2	E	413	ASN
2	E	428	GLN
2	E	536	ASN
2	E	537	ASN
2	E	679	GLN
3	F	13	ASN
3	F	39	GLN
3	F	137	ASN
3	F	170	ASN
3	F	182	GLN
3	F	301	ASN
3	F	306	GLN
3	F	320	ASN
3	F	348	ASN
3	F	350	GLN
3	F	383	GLN
3	F	482	GLN
3	F	491	ASN
3	F	530	ASN
3	F	532	ASN
3	F	581	GLN
3	F	632	GLN
3	F	728	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	M	3/13 (23%)	2 (66%)	1 (33%)
4	N	3/13 (23%)	2 (66%)	1 (33%)
5	R	11/18 (61%)	1 (9%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	S	11/18 (61%)	1 (9%)	0
6	U	14/16 (87%)	5 (35%)	1 (7%)
6	V	14/16 (87%)	6 (42%)	1 (7%)
All	All	56/94 (59%)	17 (30%)	4 (7%)

All (17) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	N	2	A
4	N	3	U
5	R	5	C
5	S	5	C
4	M	2	A
4	M	3	U
6	U	5	G
6	U	6	U
6	U	7	A
6	U	11	A
6	U	15	G
6	V	5	G
6	V	6	U
6	V	7	A
6	V	8	A
6	V	11	A
6	V	15	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	N	1	A
4	M	1	A
6	U	5	G
6	V	5	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	709/738 (96%)	-0.53	0 100 100	138, 185, 225, 263	0
1	D	708/738 (95%)	-0.47	6 (0%) 82 64	155, 192, 230, 291	0
2	B	752/776 (96%)	-0.43	3 (0%) 88 74	123, 174, 223, 264	0
2	E	749/776 (96%)	-0.43	3 (0%) 88 74	139, 178, 227, 273	0
3	C	748/809 (92%)	-0.44	3 (0%) 88 74	145, 184, 221, 255	0
3	F	746/809 (92%)	-0.43	2 (0%) 90 78	138, 184, 222, 249	0
4	M	3/13 (23%)	-0.27	0 100 100	232, 232, 259, 281	0
4	N	3/13 (23%)	-0.37	0 100 100	219, 219, 262, 272	0
5	R	13/18 (72%)	-0.95	0 100 100	164, 184, 216, 220	0
5	S	13/18 (72%)	-0.76	0 100 100	179, 195, 220, 232	0
6	U	15/16 (93%)	-0.96	0 100 100	175, 188, 208, 215	0
6	V	15/16 (93%)	-1.14	0 100 100	165, 175, 190, 192	0
All	All	4474/4740 (94%)	-0.46	17 (0%) 88 74	123, 183, 225, 291	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	565	THR	3.4
1	D	77	GLU	2.8
2	E	367	GLN	2.7
2	B	719	LEU	2.6
2	E	489	THR	2.5
3	C	639	ASN	2.5
2	B	720	SER	2.5
2	E	188	LYS	2.4
2	B	651	PRO	2.4
3	C	229	VAL	2.3
1	D	112	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	282	PHE	2.3
3	C	543	GLU	2.3
1	D	645	TYR	2.2
1	D	93	SER	2.1
3	F	744	LEU	2.0
3	F	543	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.