wwPDB X-ray Structure Validation Summary Report (i)

Jun 24, 2024 – 11:12 PM EDT

PDB ID	:	6F5P
Title	:	A mechanism for the activation of the influenza virus transcriptase
Authors	:	Serna Martin, I.; Grimes, J.M.
Deposited on	:	2017-12-02
Resolution	:	4.14 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

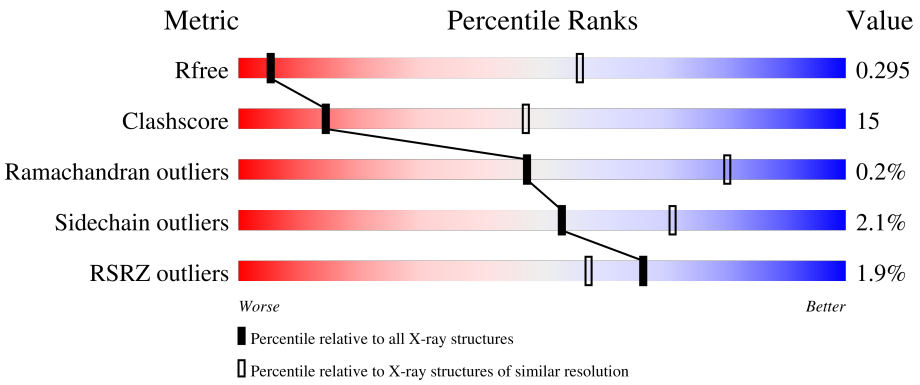
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.14 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}	130704	1018 (4.52-3.76)
Clashscore	141614	1041 (4.50-3.78)
Ramachandran outliers	138981	1036 (4.52-3.76)
Sidechain outliers	138945	1022 (4.52-3.76)
RSRZ outliers	127900	1042 (4.58-3.70)

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 <=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	709	2% 64% 34%
1	D	709	% 65% 32%
2	B	754	% 66% 27% 6%
2	C	754	2% 66% 28%
3	E	774	2% 66% 33%

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Mol	Chain	Length	Quality of chain
3	F	774	3%, 65%, 34%
4	G	28	18%, 18%, 7%, 57%
5	H	10	70%, 30%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 35282 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
			Total	C	N	O	S			
1	A	708	5736	3654	972	1065	45	0	0	0
1	D	708	5736	3654	972	1065	45	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	710	5643	3584	948	1057	54	0	0	0
2	C	721	5736	3638	971	1073	54	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	771	6140	3883	1079	1141	37	0	0	0
3	F	771	6140	3883	1079	1141	37	0	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	G	12	97	56	12	27	2	0	0	0

- Molecule 5 is a protein called ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	H	10	50	30	10	10	50	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

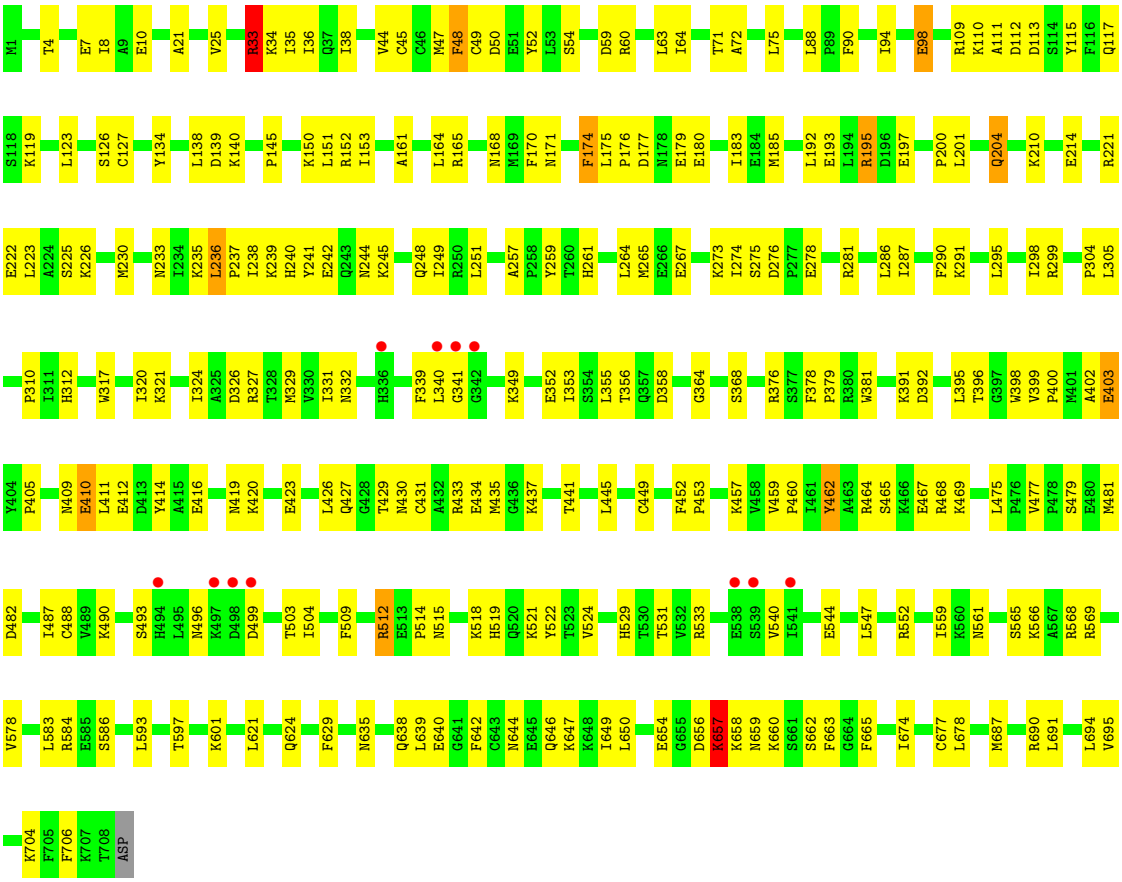
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	2	2	2	0	0
6	D	2	2	2	0	0

3 Residue-property plots (i)

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.

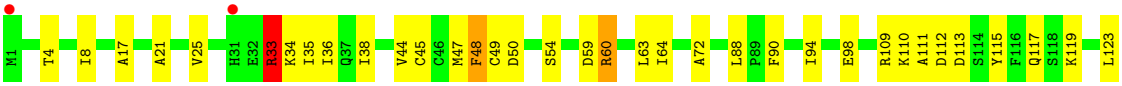
• Molecule 1: Polymerase acidic protein

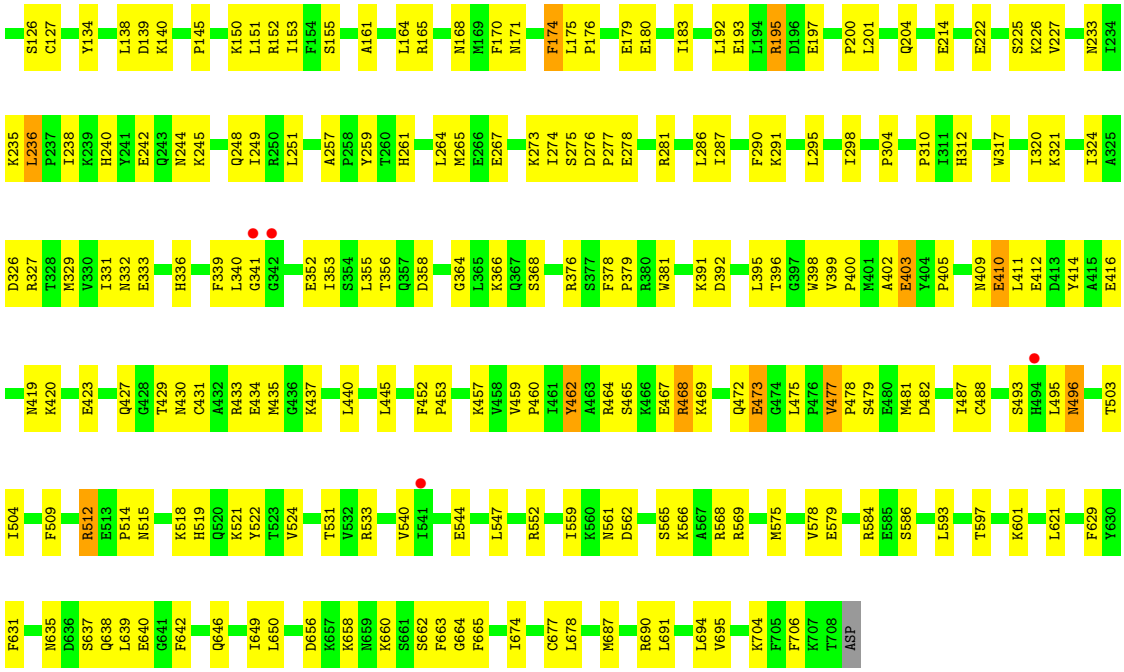
Chain A:



• Molecule 1: Polymerase acidic protein

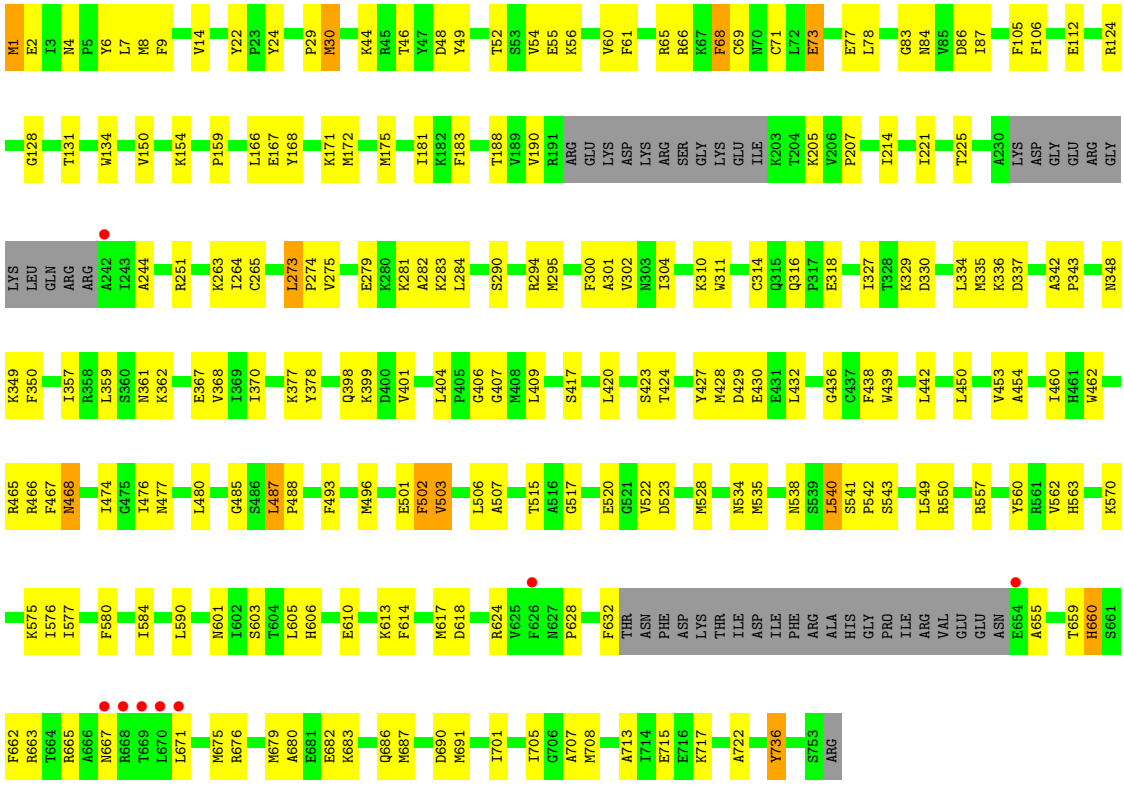
Chain D:





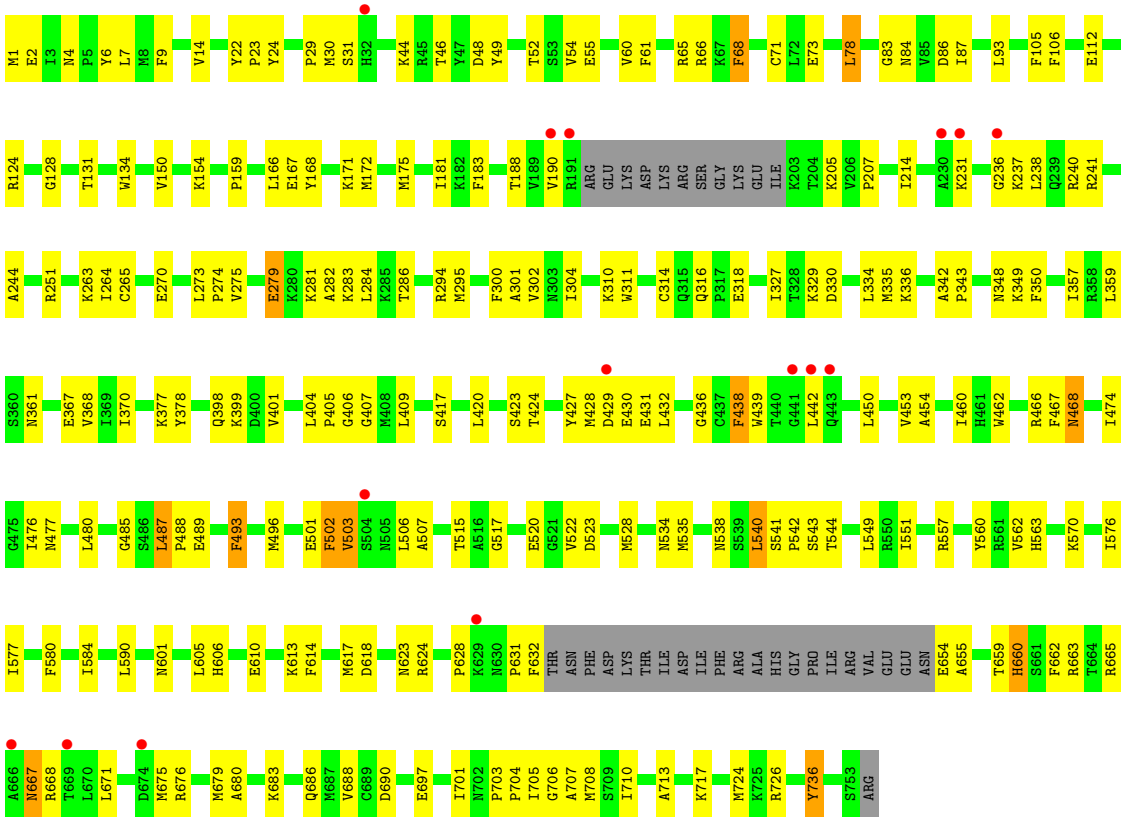
• Molecule 2: RNA-directed RNA polymerase catalytic subunit

Chain B:



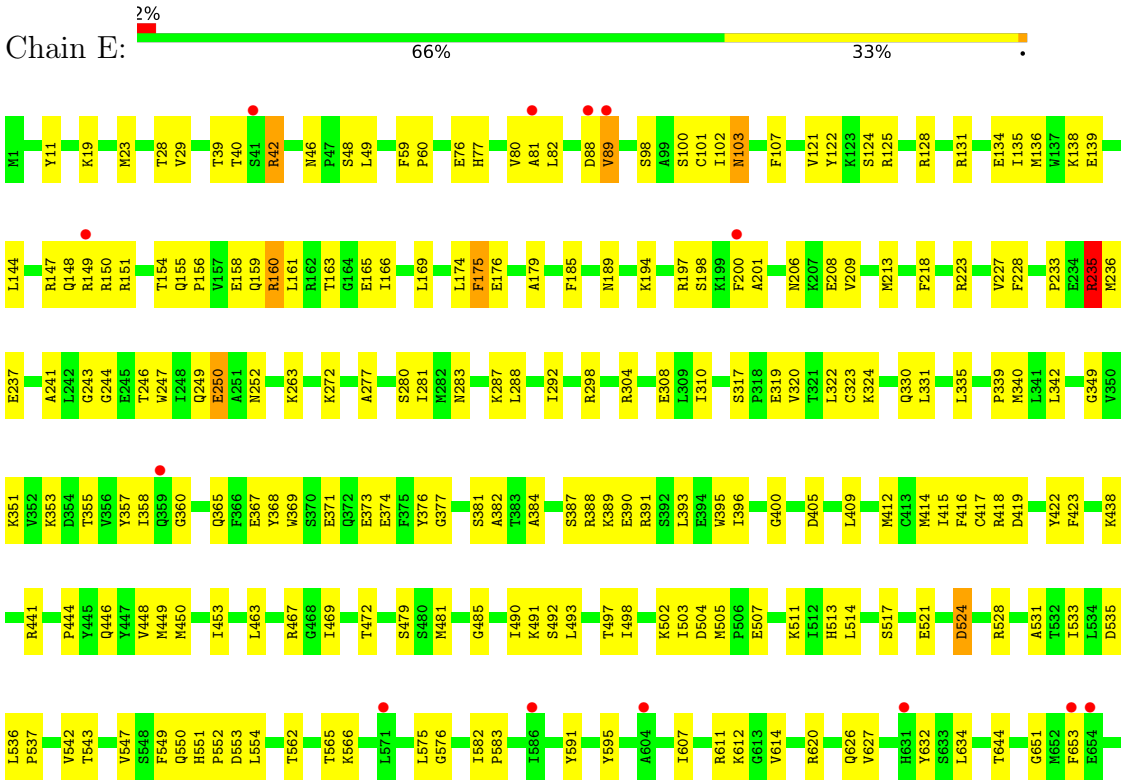
• Molecule 2: RNA-directed RNA polymerase catalytic subunit

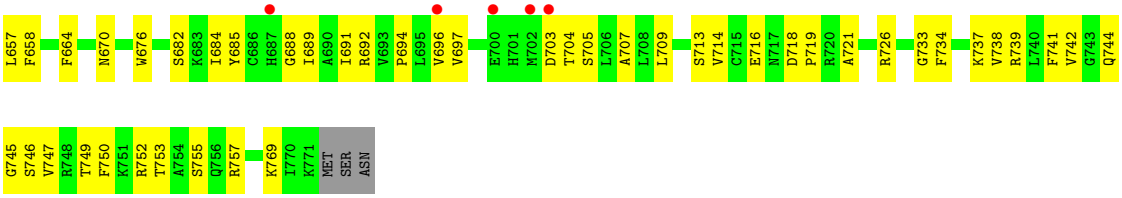
Chain C:



• Molecule 3: Polymerase basic protein 2

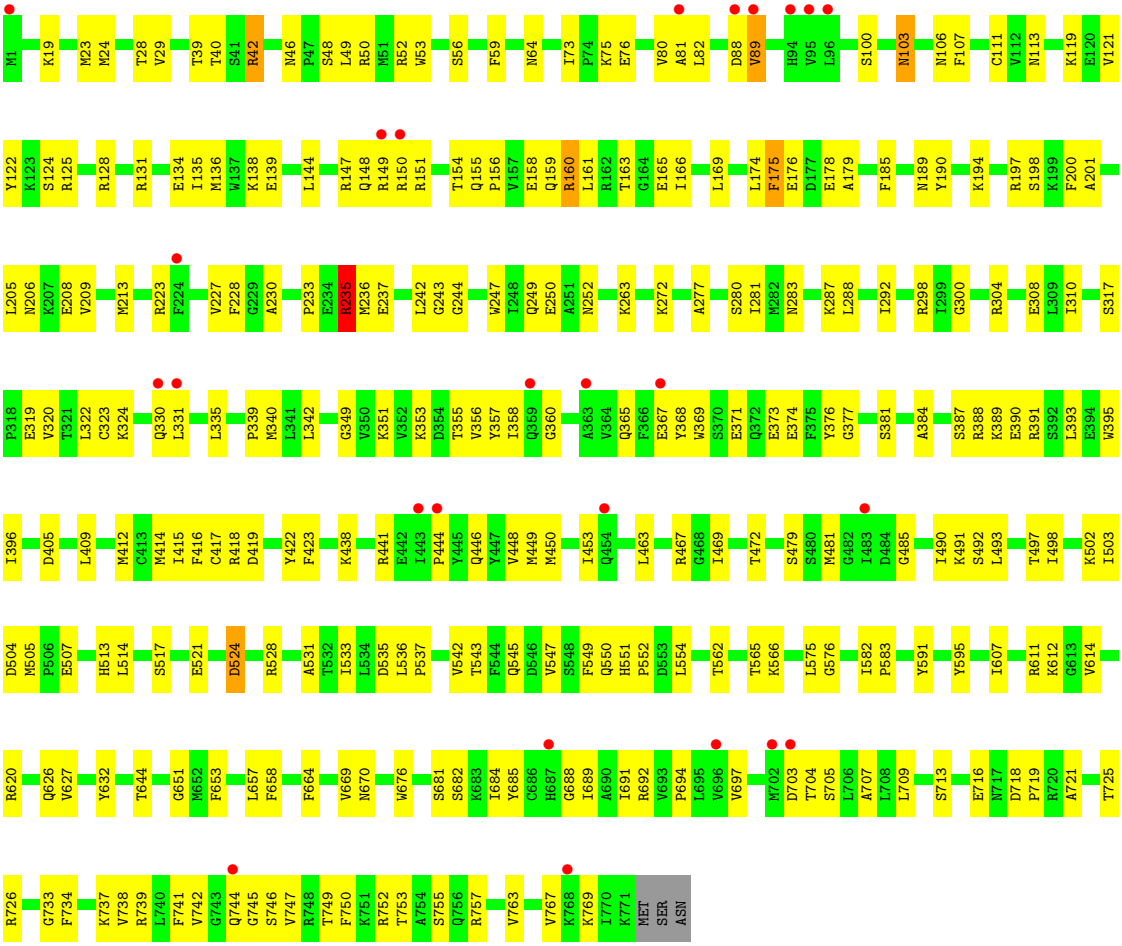
Chain E:





• Molecule 3: Polymerase basic protein 2

Chain F:

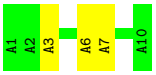


• Molecule 4: DNA-directed RNA polymerase subunit

Chain G:

• Molecule 5: ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA

Chain H:


A1
A2
A3
A6
A7
A10

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	185.70Å 185.70Å 597.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	131.31 – 4.14 131.31 – 4.14	Depositor EDS
% Data completeness (in resolution range)	68.9 (131.31-4.14) 68.9 (131.31-4.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.35 (at 4.15Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.260 , 0.296 0.260 , 0.295	Depositor DCC
R_{free} test set	2816 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	105.8	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 79.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.80	EDS
Total number of atoms	35282	wwPDB-VP
Average B, all atoms (Å^2)	145.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: SEP, MG

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	0.34	2/5855 (0.0%)	0.62	13/7866 (0.2%)
1	D	0.34	2/5855 (0.0%)	0.62	12/7866 (0.2%)
2	B	0.33	2/5741 (0.0%)	0.50	5/7716 (0.1%)
2	C	0.35	2/5835 (0.0%)	0.52	6/7839 (0.1%)
3	E	0.28	2/6251 (0.0%)	0.51	2/8415 (0.0%)
3	F	0.28	2/6251 (0.0%)	0.51	2/8415 (0.0%)
4	G	0.39	0/79	0.57	0/105
5	H	0.30	0/49	2.45	4/67 (6.0%)
All	All	0.32	12/35916 (0.0%)	0.56	44/48289 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	D	0	4
2	B	0	1
2	C	0	1
All	All	0	7

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	462	TYR	CE1-CZ	-9.52	1.26	1.38
2	B	736	TYR	CE1-CZ	-9.29	1.26	1.38
1	A	462	TYR	CE1-CZ	-9.20	1.26	1.38
2	C	736	TYR	CE1-CZ	-9.17	1.26	1.38
2	C	736	TYR	CG-CD1	-7.77	1.29	1.39

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	33	ARG	NE-CZ-NH2	-14.79	112.91	120.30
1	D	33	ARG	NE-CZ-NH2	14.15	127.37	120.30
1	D	33	ARG	NE-CZ-NH1	-14.14	113.23	120.30
1	A	33	ARG	NE-CZ-NH1	12.64	126.62	120.30
1	D	512	ARG	NE-CZ-NH2	-12.58	114.01	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	204	GLN	Sidechain
1	D	204	GLN	Sidechain
1	D	472	GLN	Peptide
1	D	473	GLU	Peptide
1	D	664	GLY	Peptide

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	5736	0	5749	227	0
1	D	5736	0	5749	220	0
2	B	5643	0	5736	185	0
2	C	5736	0	5837	205	0
3	E	6140	0	6250	207	0
3	F	6140	0	6250	226	0
4	G	97	0	73	11	0
5	H	50	0	52	0	0
6	A	2	0	0	0	0
6	D	2	0	0	0	0
All	All	35282	0	35696	1098	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 15.

The worst 5 of 1098 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)
1:D:410:GLU:OE1	1:D:411:LEU:N	1.59	1.34
1:A:410:GLU:OE1	1:A:411:LEU:N	1.59	1.34
3:E:367:GLU:O	3:E:418:ARG:NH1	1.87	1.08
3:F:367:GLU:O	3:F:418:ARG:NH1	1.87	1.07
1:A:410:GLU:OE1	1:A:411:LEU:HB2	1.57	1.05

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	706/709 (100%)	674 (96%)	31 (4%)	1 (0%)	51	85
1	D	706/709 (100%)	678 (96%)	27 (4%)	1 (0%)	51	85
2	B	702/754 (93%)	678 (97%)	23 (3%)	1 (0%)	51	85
2	C	715/754 (95%)	691 (97%)	23 (3%)	1 (0%)	51	85
3	E	769/774 (99%)	732 (95%)	35 (5%)	2 (0%)	41	76
3	F	769/774 (99%)	731 (95%)	36 (5%)	2 (0%)	41	76
4	G	8/28 (29%)	6 (75%)	1 (12%)	1 (12%)	0	5
5	H	8/10 (80%)	6 (75%)	2 (25%)	0	100	100
All	All	4383/4512 (97%)	4196 (96%)	178 (4%)	9 (0%)	47	80

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	G	13	PRO
3	E	89	VAL
3	E	533	ILE
3	F	89	VAL
3	F	533	ILE

5.3.2 Protein sidechains (i)

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	630/631 (100%)	614 (98%)	16 (2%)	47	68
1	D	630/631 (100%)	616 (98%)	14 (2%)	52	70
2	B	630/669 (94%)	614 (98%)	16 (2%)	47	68
2	C	639/669 (96%)	622 (97%)	17 (3%)	44	66
3	E	676/679 (100%)	667 (99%)	9 (1%)	69	82
3	F	676/679 (100%)	667 (99%)	9 (1%)	69	82
4	G	10/24 (42%)	10 (100%)	0	100	100
All	All	3891/3982 (98%)	3810 (98%)	81 (2%)	53	71

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	502	PHE
3	E	611	ARG
2	C	618	ASP
3	E	136	MET
3	F	136	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	545	GLN
3	F	766	ASN
2	B	348	ASN
2	C	348	ASN
2	C	660	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SEP	G	12	4	8,9,10	1.43	1 (12%)	8,12,14	2.15	2 (25%)
4	SEP	G	5	4	8,9,10	1.55	1 (12%)	8,12,14	1.47	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SEP	G	12	4	-	5/5/8/10	-
4	SEP	G	5	4	-	5/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	5	SEP	P-O1P	3.41	1.61	1.50
4	G	12	SEP	P-O1P	2.97	1.60	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	G	12	SEP	OG-CB-CA	5.12	113.13	108.14
4	G	5	SEP	P-OG-CB	-2.94	110.20	118.30
4	G	12	SEP	O3P-P-OG	2.65	113.79	106.73

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	5	SEP	N-CA-CB-OG
4	G	5	SEP	CB-OG-P-O2P
4	G	5	SEP	CB-OG-P-O3P
4	G	12	SEP	N-CA-CB-OG
4	G	12	SEP	CB-OG-P-O2P

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	12	SEP	2	0
4	G	5	SEP	3	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	708/709 (99%)	0.05	11 (1%)	72	62	65, 123, 199, 259	0
1	D	708/709 (99%)	0.05	6 (0%)	86	79	67, 140, 219, 293	0
2	B	710/754 (94%)	0.06	8 (1%)	80	72	63, 115, 202, 293	0
2	C	721/754 (95%)	0.20	15 (2%)	63	53	75, 135, 203, 265	0
3	E	771/774 (99%)	0.19	18 (2%)	60	51	71, 161, 254, 321	0
3	F	771/774 (99%)	0.22	25 (3%)	47	37	82, 161, 229, 299	0
4	G	10/28 (35%)	-0.53	0	100	100	167, 181, 197, 197	0
5	H	0/10	-	-			-	-
All	All	4399/4512 (97%)	0.13	83 (1%)	66	57	63, 139, 226, 321	0

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	341	GLY	5.7
1	A	498	ASP	4.7
1	A	342	GLY	4.3
3	F	149	ARG	4.3
2	B	242	ALA	4.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	SEP	G	12	10/11	0.76	0.22	191,224,246,253	0
4	SEP	G	5	10/11	0.83	0.21	184,191,200,207	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	MG	A	801	1/1	0.31	0.30	103,103,103,103	0
6	MG	D	801	1/1	0.73	0.28	145,145,145,145	0
6	MG	A	800	1/1	0.84	0.41	116,116,116,116	0
6	MG	D	800	1/1	0.91	0.58	193,193,193,193	0

6.5 Other polymers (i)

There are no such residues in this entry.