



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 09:46 PM GMT

PDB ID : 3V6D  
Title : Crystal structure of HIV-1 reverse transcriptase (RT) cross-linked with AZT-terminated DNA  
Authors : Das, K.; Martinez, S.E.; Arnold, E.  
Deposited on : 2011-12-19  
Resolution : 2.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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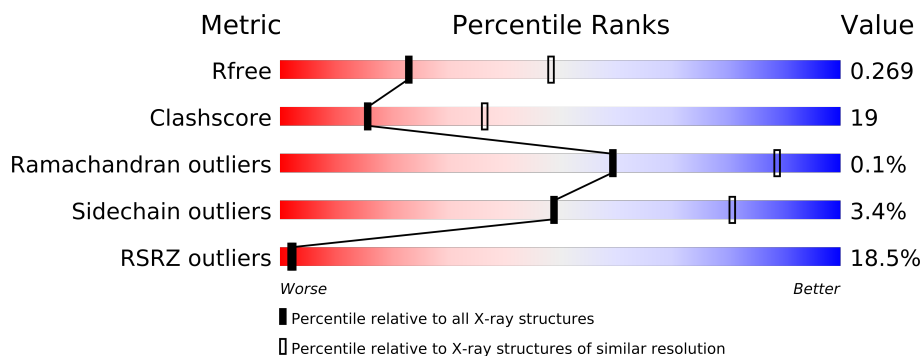
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 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))
$R_{free}$	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	556	
1	C	556	
2	B	428	
2	D	428	
3	E	27	
3	T	27	
4	F	21	
4	P	21	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17627 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HIV-1 REVERSE TRANSCRIPTASE P66 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	0	0
			4511	2920	751	832	8			
1	C	554	Total	C	N	O	S	0	0	0
			4506	2917	750	831	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP P03366
A	0	VAL	-	EXPRESSION TAG	UNP P03366
A	258	CYS	GLN	ENGINEERED MUTATION	UNP P03366
A	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
A	498	ASN	ASP	ENGINEERED MUTATION	UNP P03366
C	-1	MET	-	EXPRESSION TAG	UNP P03366
C	0	VAL	-	EXPRESSION TAG	UNP P03366
C	258	CYS	GLN	ENGINEERED MUTATION	UNP P03366
C	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
C	498	ASN	ASP	ENGINEERED MUTATION	UNP P03366

- Molecule 2 is a protein called HIV-1 REVERSE TRANSCRIPTASE P51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			
2	D	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	ENGINEERED MUTATION	UNP P03366
D	280	SER	CYS	ENGINEERED MUTATION	UNP P03366

- Molecule 3 is a DNA chain called DNA (5'-D(\*AP\*TP\*GP\*GP\*AP\*AP\*GP\*GP\*CP\*GP\*CP\*CP\*GP\*AP\*AP\*CP\*AP\*GP\*GP\*GP\*AP\*CP\*TP\*GP\*TP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	24	Total	C	N	O	P	0	0	0
			497	234	102	138	23			
3	E	24	Total	C	N	O	P	0	0	0
			497	234	102	138	23			

- Molecule 4 is a DNA chain called DNA (5'-D(\*AP\*CP\*AP\*GP\*TP\*CP\*CP\*CP\*TP\*GP\*TP\*TP\*CP\*GP\*GP\*(MRG)P\*CP\*GP\*CP\*CP\*(ATM))-3').

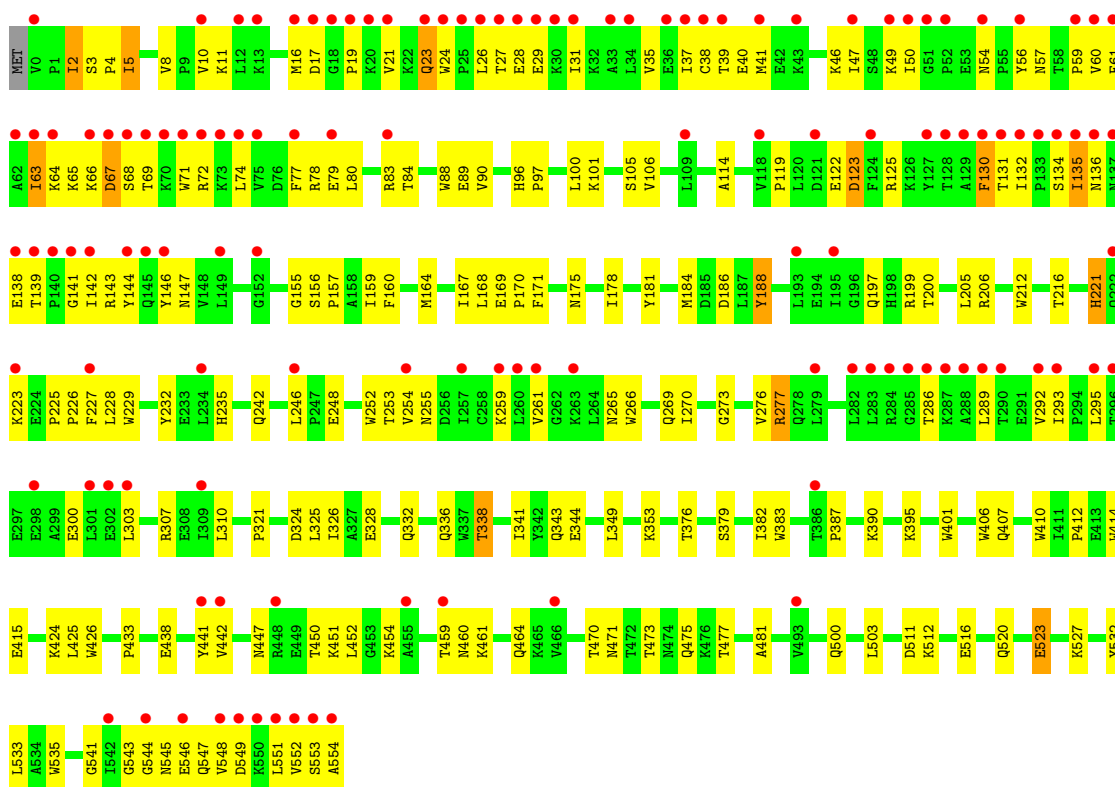
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	P	20	Total	C	N	O	P	S	0	0	0
			408	195	72	121	19	1			
4	F	20	Total	C	N	O	P	S	0	0	0
			408	195	72	121	19	1			

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

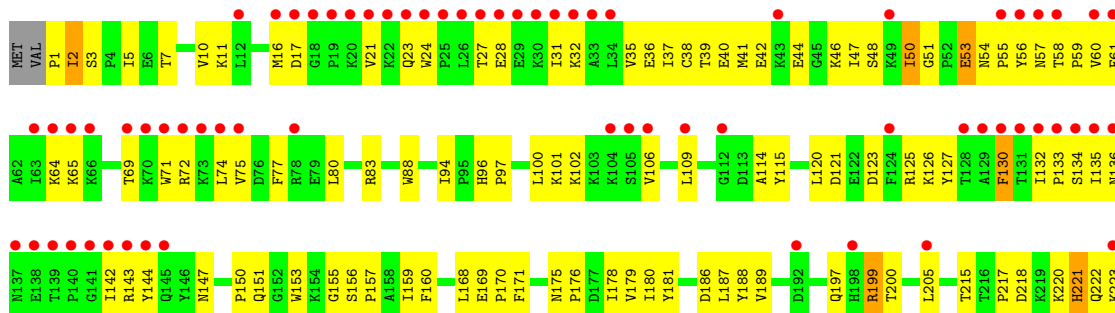
- Molecule 1: HIV-1 REVERSE TRANSCRIPTASE P66 subunit

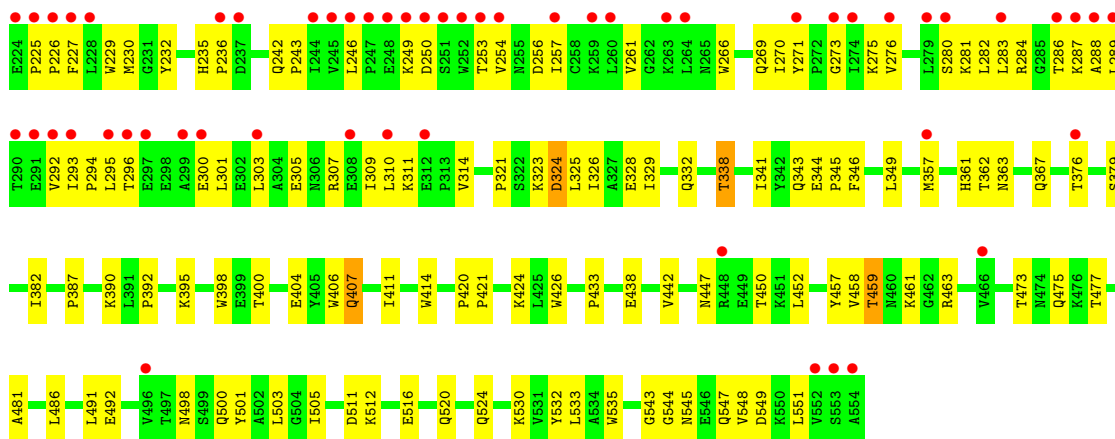
Chain A: 



- Molecule 1: HIV-1 REVERSE TRANSCRIPTASE P66 subunit

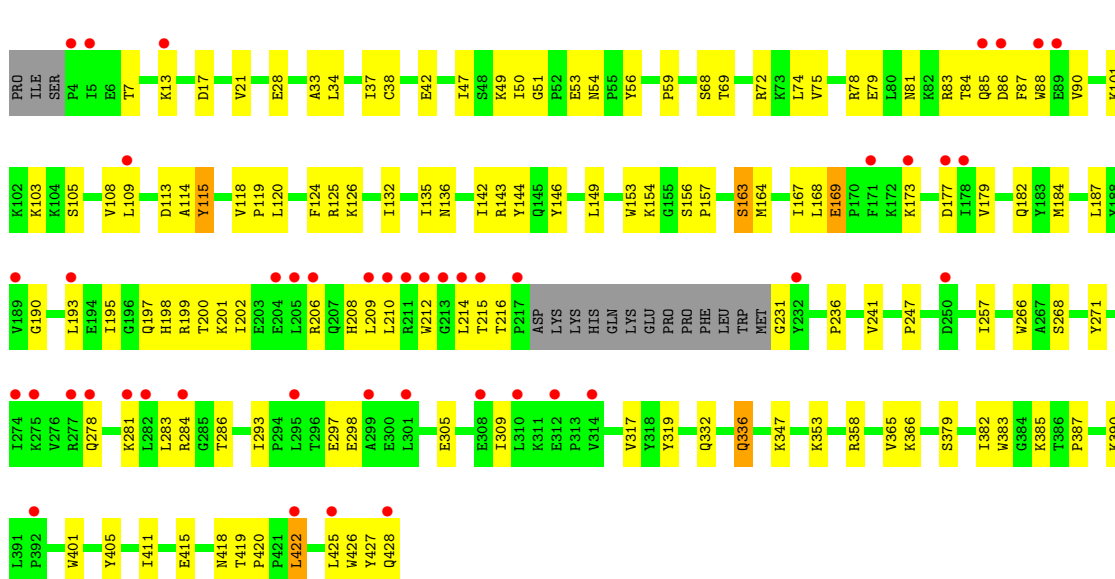
Chain C: 





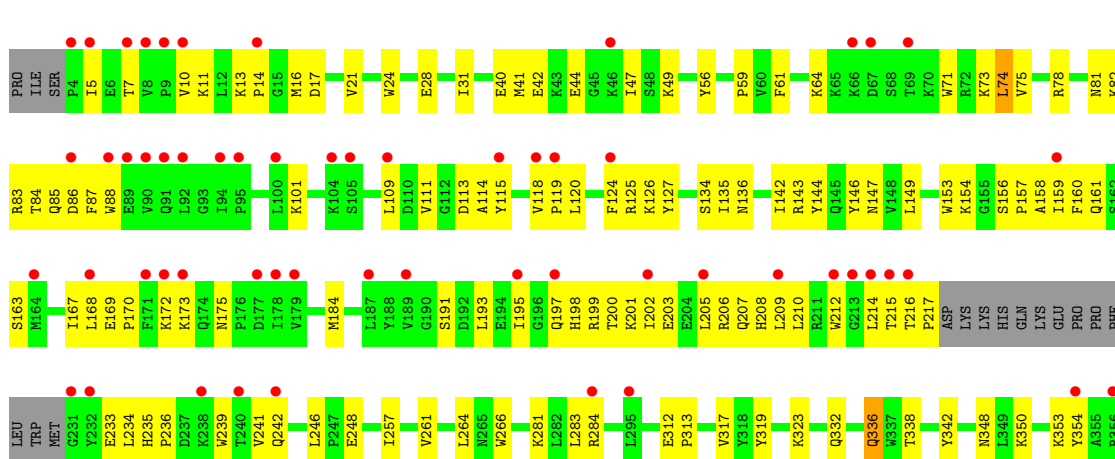
• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE P51 subunit

Chain B:



• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE P51 subunit

Chain D:





- Molecule 3: DNA (5'-D(\*AP\*TP\*GP\*GP\*AP\*AP\*GP\*GP\*CP\*GP\*CP\*CP\*CP\*GP\*AP\*AP\*CP\*AP\*GP\*GP\*GP\*AP\*CP\*TP\*GP\*TP\*G)-3')

Chain T:



- Molecule 3: DNA (5'-D(\*AP\*TP\*GP\*GP\*AP\*AP\*GP\*GP\*CP\*GP\*CP\*CP\*CP\*GP\*AP\*AP\*CP\*AP\*GP\*GP\*GP\*AP\*CP\*TP\*GP\*TP\*G)-3')

Chain E:



- Molecule 4: DNA (5'-D(\*AP\*CP\*AP\*GP\*TP\*CP\*CP\*CP\*TP\*GP\*TP\*TP\*CP\*GP\*GP\*(M RG)P\*CP\*GP\*CP\*CP\*(ATM))-3')

Chain P:



- Molecule 4: DNA (5'-D(\*AP\*CP\*AP\*GP\*TP\*CP\*CP\*CP\*TP\*GP\*TP\*TP\*CP\*GP\*GP\*(M RG)P\*CP\*GP\*CP\*CP\*(ATM))-3')

Chain F:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.48Å 133.17Å 139.90Å 90.00° 98.67° 90.00°	Depositor
Resolution (Å)	44.30 – 2.70 48.21 – 2.71	Depositor EDS
% Data completeness (in resolution range)	97.1 (44.30-2.70) 97.8 (48.21-2.71)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 2.73Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.233 , 0.268 0.234 , 0.269	Depositor DCC
$R_{free}$ test set	2607 reflections (3.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	67.4	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 47.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 86162 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	17627	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.



## 5 Model quality

### 5.1 Standard geometry

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

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	0.46	0/4629	0.61	1/6290 (0.0%)
1	C	0.45	0/4624	0.58	0/6282
2	B	0.48	0/3497	0.60	0/4751
2	D	0.46	0/3497	0.61	0/4751
3	E	0.79	0/560	1.44	10/864 (1.2%)
3	T	0.80	0/560	1.48	11/864 (1.3%)
4	F	0.82	0/400	1.58	9/612 (1.5%)
4	P	0.78	0/400	1.52	6/612 (1.0%)
All	All	0.51	0/18167	0.76	37/25026 (0.1%)

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	810	DT	O4'-C1'-N1	9.89	114.92	108.00
4	F	807	DC	O4'-C1'-N1	8.96	114.27	108.00
4	P	816	DG	O4'-C1'-N9	8.78	114.14	108.00
3	E	721	DG	O4'-C1'-N9	-8.59	101.99	108.00
3	T	703	DG	O4'-C4'-C3'	-7.75	101.35	106.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4511	0	4570	174	0
1	C	4506	0	4568	182	0
2	B	3400	0	3433	117	0
2	D	3400	0	3433	135	0
3	E	497	0	268	14	0
3	T	497	0	268	15	0
4	F	408	0	231	27	0
4	P	408	0	231	20	0
All	All	17627	0	17002	643	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

The worst 5 of 643 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:223:LYS:O	1:C:225:PRO:HD3	1.53	1.09
1:A:541:GLY:HA2	1:A:546:GLU:HB2	1.41	1.01
1:C:500:GLN:HG2	2:D:422:LEU:HD22	1.44	1.00
1:A:459:THR:HG22	1:A:461:LYS:H	1.23	0.99
1:A:2:ILE:HD12	1:A:2:ILE:H	1.26	0.99

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	553/556 (100%)	529 (96%)	23 (4%)	1 (0%)	56	86
1	C	552/556 (99%)	528 (96%)	24 (4%)	0	100	100
2	B	408/428 (95%)	399 (98%)	9 (2%)	0	100	100
2	D	408/428 (95%)	391 (96%)	17 (4%)	0	100	100
All	All	1921/1968 (98%)	1847 (96%)	73 (4%)	1 (0%)	59	89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	ILE

### 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	495/497 (100%)	476 (96%)	19 (4%)	44	76
1	C	495/497 (100%)	475 (96%)	20 (4%)	42	75
2	B	374/390 (96%)	362 (97%)	12 (3%)	51	82
2	D	374/390 (96%)	366 (98%)	8 (2%)	66	91
All	All	1738/1774 (98%)	1679 (97%)	59 (3%)	49	81

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	241	VAL
1	C	5	ILE
2	D	248	GLU
2	B	257	ILE
2	B	336	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	222	GLN
1	C	367	GLN
1	C	547	GLN
2	B	336	GLN
1	C	464	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

4 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	MRG	F	817	1,3,4	26,28,29	2.61	11 (42%)	33,39,42	1.71	7 (21%)
4	ATM	F	822	3,4	21,23,24	1.30	4 (19%)	24,32,35	2.32	7 (29%)
4	MRG	P	817	1,3,4	26,28,29	2.68	11 (42%)	33,39,42	1.73	9 (27%)
4	ATM	P	822	3,4	21,23,24	1.28	3 (14%)	24,32,35	2.10	7 (29%)

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	MRG	F	817	1,3,4	-	0/11/26/27	0/1/3/3
4	ATM	F	822	3,4	-	0/8/24/25	0/2/2/2
4	MRG	P	817	1,3,4	-	0/11/26/27	0/1/3/3
4	ATM	P	822	3,4	-	0/8/24/25	0/2/2/2

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	817	MRG	C2-N2	5.55	1.48	1.32
4	P	817	MRG	C2-N2	5.47	1.48	1.32
4	P	817	MRG	C4-N3	5.43	1.44	1.35
4	F	817	MRG	C4-N3	5.18	1.44	1.35
4	F	817	MRG	P-OP1	4.83	1.52	1.46

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	822	ATM	C6-N1-C2	-6.66	120.51	122.41
4	F	822	ATM	N3-C2-N1	5.76	120.78	115.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	822	ATM	C2'-C1'-N1	-5.36	100.15	114.08
4	P	822	ATM	N3-C2-N1	4.02	119.33	115.97
4	P	817	MRG	C6-C5-N7	-3.99	133.60	134.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	555/556 (99%)	1.60	128 (23%) 1 1	36, 83, 138, 149	0
1	C	554/556 (99%)	1.48	123 (22%) 1 1	34, 81, 136, 148	0
2	B	412/428 (96%)	1.02	45 (10%) 6 6	34, 66, 118, 131	0
2	D	412/428 (96%)	1.11	65 (15%) 3 3	40, 69, 125, 132	0
3	E	24/27 (88%)	0.91	4 (16%) 2 3	67, 104, 156, 164	0
3	T	24/27 (88%)	1.01	4 (16%) 2 3	69, 106, 158, 161	0
4	F	20/21 (95%)	0.60	2 (10%) 8 8	60, 92, 141, 142	0
4	P	20/21 (95%)	0.39	2 (10%) 8 8	68, 90, 142, 144	0
All	All	2021/2064 (97%)	1.31	373 (18%) 2 2	34, 75, 132, 164	0

The worst 5 of 373 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	133	PRO	15.6
1	A	74	LEU	15.5
2	B	214	LEU	14.0
1	C	142	ILE	13.4
1	A	133	PRO	12.5

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	ATM	F	822	22/23	0.20	-0.54	71,78,87,95	0
4	MRG	P	817	26/27	0.18	-0.58	88,102,117,121	0
4	ATM	P	822	22/23	0.18	-0.73	71,82,95,95	0
4	MRG	F	817	26/27	0.18	-0.77	84,99,117,127	0

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

There are no ligands in this entry.

### 6.5 Other polymers

There are no such residues in this entry.