



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 05:38 AM GMT

PDB ID : 3KLG
Title : Crystal structure of AZT-resistant HIV-1 Reverse Transcriptase crosslinked to pre-translocation AZTMP-Terminated DNA (COMPLEX N)
Authors : Tu, X.; Sarafianos, S.G.; Arnold, E.
Deposited on : 2009-11-07
Resolution : 3.65 Å(reported)

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

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

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

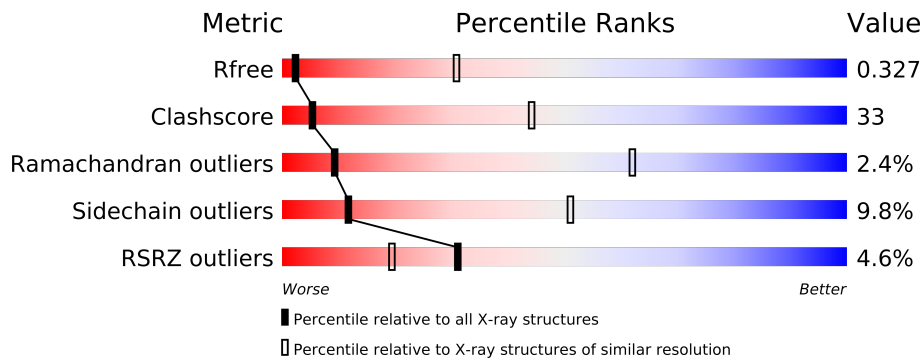
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.65 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	1021 (3.94-3.38)
Clashscore	79885	1025 (3.90-3.42)
Ramachandran outliers	78287	1195 (3.92-3.40)
Sidechain outliers	78261	1193 (3.92-3.40)
RSRZ outliers	66119	1021 (3.94-3.38)

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 ≥ 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	562	
1	E	562	
2	B	437	
2	F	437	
3	C	27	
3	G	27	
4	D	22	
4	H	22	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17640 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 Reverse transcriptase/ribonucleaseH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	554	Total	C	N	O	S	0	0	0
			4513	2922	752	832	7			
1	E	554	Total	C	N	O	S	0	0	0
			4513	2922	752	832	7			

There are 20 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	41	LEU	MET	ENGINEERED	UNP P03366
A	67	ASN	ASP	ENGINEERED	UNP P03366
A	70	ARG	LYS	ENGINEERED	UNP P03366
A	215	TYR	THR	ENGINEERED	UNP P03366
A	219	GLN	LYS	ENGINEERED	UNP P03366
A	258	CYS	GLN	ENGINEERED	UNP P03366
A	280	SER	CYS	ENGINEERED	UNP P03366
A	559	VAL	ILE	SEE REMARK 999	UNP P03366
E	-1	MET	-	EXPRESSION TAG	UNP P03366
E	0	VAL	-	EXPRESSION TAG	UNP P03366
E	41	LEU	MET	ENGINEERED	UNP P03366
E	67	ASN	ASP	ENGINEERED	UNP P03366
E	70	ARG	LYS	ENGINEERED	UNP P03366
E	215	TYR	THR	ENGINEERED	UNP P03366
E	219	GLN	LYS	ENGINEERED	UNP P03366
E	258	CYS	GLN	ENGINEERED	UNP P03366
E	280	SER	CYS	ENGINEERED	UNP P03366
E	559	VAL	ILE	SEE REMARK 999	UNP P03366

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	413	Total 3405	C 2215	N 564	O 620	S 6	0	0	0
2	F	413	Total 3405	C 2215	N 564	O 620	S 6	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	ENGINEERED	UNP P03366
B	429	GLY	-	EXPRESSION TAG	UNP P03366
B	430	GLY	-	EXPRESSION TAG	UNP P03366
B	431	HIS	-	EXPRESSION TAG	UNP P03366
B	432	HIS	-	EXPRESSION TAG	UNP P03366
B	433	HIS	-	EXPRESSION TAG	UNP P03366
B	434	HIS	-	EXPRESSION TAG	UNP P03366
B	435	HIS	-	EXPRESSION TAG	UNP P03366
B	436	HIS	-	EXPRESSION TAG	UNP P03366
B	437	HIS	-	EXPRESSION TAG	UNP P03366
F	280	SER	CYS	ENGINEERED	UNP P03366
F	429	GLY	-	EXPRESSION TAG	UNP P03366
F	430	GLY	-	EXPRESSION TAG	UNP P03366
F	431	HIS	-	EXPRESSION TAG	UNP P03366
F	432	HIS	-	EXPRESSION TAG	UNP P03366
F	433	HIS	-	EXPRESSION TAG	UNP P03366
F	434	HIS	-	EXPRESSION TAG	UNP P03366
F	435	HIS	-	EXPRESSION TAG	UNP P03366
F	436	HIS	-	EXPRESSION TAG	UNP P03366
F	437	HIS	-	EXPRESSION TAG	UNP P03366

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*T*GP*CP*AP*TP*GP*GP*CP*GP*C
P*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	C	23	Total 473	C 223	N 95	O 133	P 22	0	0	0
3	G	23	Total 473	C 223	N 95	O 133	P 22	0	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(*A*CP*AP*GP*TP*CP*CP*CP*TP*GP*T
P*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*AP*(ATM))-3').

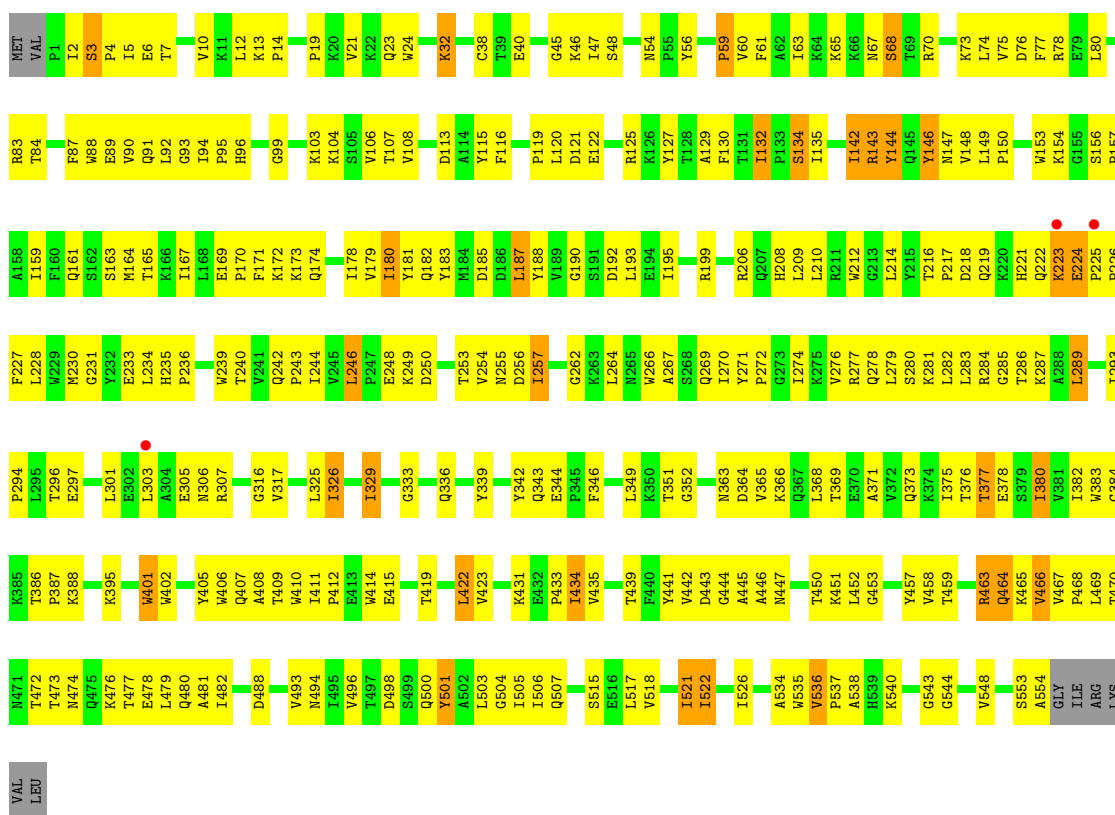
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	21	Total 429	C 205	N 77	O 126	P 20	S 1	0	0	0
4	H	21	Total 429	C 205	N 77	O 126	P 20	S 1	0	0	0

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.

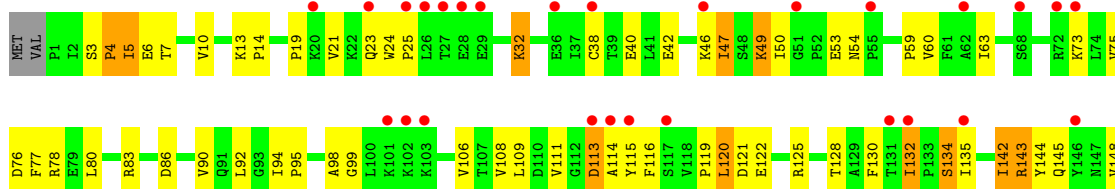
• Molecule 1: Reverse transcriptase/ribonucleaseH

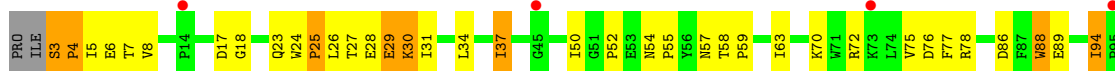
Chain A: 



• Molecule 1: Reverse transcriptase/ribonucleaseH

Chain E: 







4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.12Å 154.40Å 277.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.97 – 3.65 39.97 – 3.65	Depositor EDS
% Data completeness (in resolution range)	85.0 (39.97-3.65) 83.4 (39.97-3.65)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.66Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.312 , 0.350 0.305 , 0.327	Depositor DCC
R_{free} test set	652 reflections (2.02%)	DCC
Wilson B-factor (Å ²)	120.0	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 50.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	2 of 32217 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	17640	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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	0.54	0/4632	0.68	0/6295
1	E	0.43	1/4632 (0.0%)	0.64	2/6295 (0.0%)
2	B	0.62	1/3502 (0.0%)	0.76	4/4760 (0.1%)
2	F	0.41	0/3502	0.63	1/4760 (0.0%)
3	C	0.83	0/532	0.92	0/820
3	G	0.61	0/532	0.86	0/820
4	D	0.75	0/424	0.88	0/649
4	H	0.64	0/424	0.89	0/649
All	All	0.53	2/18180 (0.0%)	0.70	7/25048 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	478	GLU	CD-OE2	5.98	1.32	1.25
2	B	79	GLU	CG-CD	5.07	1.59	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	34	LEU	CB-CA-C	-5.98	98.84	110.20
2	F	353	LYS	N-CA-CB	-5.98	99.84	110.60
2	B	213	GLY	N-CA-C	5.57	127.03	113.10
1	E	539	HIS	N-CA-C	-5.54	96.05	111.00
2	B	315	HIS	CB-CA-C	5.48	121.37	110.40

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	4513	0	4568	350	0
1	E	4513	0	4568	293	0
2	B	3405	0	3437	244	0
2	F	3405	0	3437	207	0
3	C	473	0	257	37	0
3	G	473	0	257	32	0
4	D	429	0	243	36	0
4	H	429	0	243	35	0
All	All	17640	0	17010	1127	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 33.

The worst 5 of 1127 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:142:ILE:H	1:E:142:ILE:HD13	1.01	1.16
1:A:24:TRP:HA	3:C:703:DG:H21	1.09	1.10
2:B:5:ILE:HG22	2:B:6:GLU:N	1.53	1.10
2:B:5:ILE:HG22	2:B:6:GLU:H	0.94	1.08
1:E:540:LYS:O	1:E:542:ILE:HD12	1.53	1.08

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	552/562 (98%)	469 (85%)	71 (13%)	12 (2%)	10	64
1	E	552/562 (98%)	460 (83%)	78 (14%)	14 (2%)	9	61
2	B	409/437 (94%)	352 (86%)	45 (11%)	12 (3%)	7	57
2	F	409/437 (94%)	348 (85%)	53 (13%)	8 (2%)	11	66
All	All	1922/1998 (96%)	1629 (85%)	247 (13%)	46 (2%)	9	62

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	SER
1	A	134	SER
2	B	358	ARG
1	E	134	SER
1	E	345	PRO

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	495/502 (99%)	445 (90%)	50 (10%)	11	49
1	E	495/502 (99%)	446 (90%)	49 (10%)	11	50
2	B	375/397 (94%)	339 (90%)	36 (10%)	12	52
2	F	375/397 (94%)	340 (91%)	35 (9%)	13	54
All	All	1740/1798 (97%)	1570 (90%)	170 (10%)	12	51

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	357	MET
1	E	120	LEU
2	F	318	TYR
2	B	382	ILE
1	E	5	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	363	ASN
1	E	182	GLN
2	F	330	GLN
2	B	373	GLN
2	B	428	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	D	817	3,4	26,28,29	1.26	1 (3%)	33,39,42	5.63	8 (24%)
4	ATM	D	823	3,4	21,23,24	1.26	2 (9%)	24,32,35	1.53	5 (20%)
4	MRG	H	817	3,4	26,28,29	1.24	2 (7%)	33,39,42	5.35	6 (18%)
4	ATM	H	823	3,4	21,23,24	1.27	3 (14%)	24,32,35	1.45	5 (20%)

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	D	817	3,4	-	0/11/26/27	0/1/3/3
4	ATM	D	823	3,4	-	0/8/24/25	0/2/2/2
4	MRG	H	817	3,4	-	1/11/26/27	0/1/3/3
4	ATM	H	823	3,4	-	0/8/24/25	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	817	MRG	C21-N2	-5.00	1.34	1.46
4	H	817	MRG	C21-N2	-4.85	1.34	1.46
4	D	823	ATM	N5'-N4'	4.46	1.32	1.15
4	H	823	ATM	N5'-N4'	3.93	1.30	1.15
4	H	823	ATM	P-OP1	2.23	1.49	1.46

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	817	MRG	C6-C5-N7	-29.88	130.12	134.14
4	H	817	MRG	C6-C5-N7	-28.32	130.33	134.14
4	D	817	MRG	C21-N2-C2	-9.84	100.14	122.84
4	H	817	MRG	C21-N2-C2	-9.47	100.99	122.84
4	D	823	ATM	C6-N1-C2	-5.08	120.96	122.41

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	817	MRG	N1-C2-N2-C21

There are no ring outliers.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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	554/562 (98%)	0.03	3 (0%) 88 72	26, 89, 115, 135	0
1	E	554/562 (98%)	0.75	58 (10%) 7 7	33, 154, 164, 172	0
2	B	413/437 (94%)	0.10	9 (2%) 59 36	54, 84, 119, 143	0
2	F	413/437 (94%)	0.61	21 (5%) 27 16	127, 153, 165, 171	0
3	C	23/27 (85%)	0.06	1 (4%) 34 20	65, 90, 125, 141	0
3	G	23/27 (85%)	0.49	1 (4%) 34 20	151, 159, 167, 178	0
4	D	21/22 (95%)	-0.28	0 100 100	75, 96, 121, 136	0
4	H	21/22 (95%)	0.43	1 (4%) 29 18	149, 159, 169, 171	0
All	All	2022/2096 (96%)	0.37	94 (4%) 31 19	26, 122, 162, 178	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	231	GLY	5.9
3	C	703	DG	4.7
1	E	26	LEU	4.4
1	E	271	TYR	4.4
2	F	232	TYR	4.2

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, 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	ATM	D	823	22/23	0.27	0.91	87,90,92,94	0
4	MRG	H	817	26/27	0.25	0.23	154,157,167,167	0
4	ATM	H	823	22/23	0.33	-0.58	155,157,158,158	0
4	MRG	D	817	26/27	0.17	-0.75	89,93,101,108	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.