



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 12:57 pm BST

PDB ID : 5B5J  
Title : Hen egg white lysozyme with boron tracedrug UTX-97  
Authors : Morimoto, Y.  
Deposited on : 2016-05-11  
Resolution : 1.26 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](mailto: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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11  
buster-report : 1.1.7 (2018)  
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) : 2.11

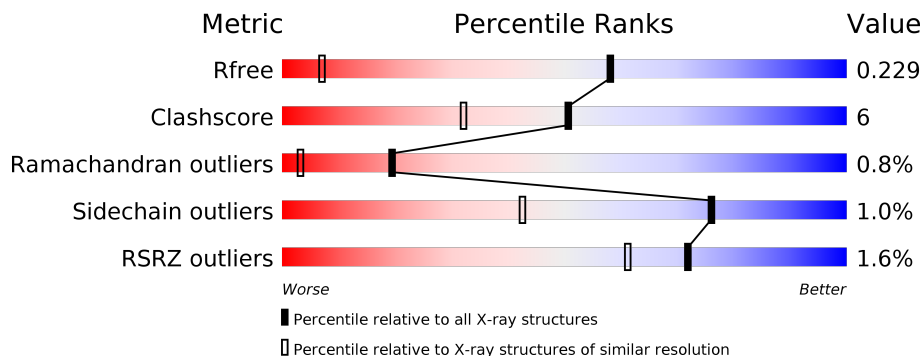
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.26 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	1023 (1.28-1.24)
Clashscore	141614	1060 (1.28-1.24)
Ramachandran outliers	138981	1029 (1.28-1.24)
Sidechain outliers	138945	1028 (1.28-1.24)
RSRZ outliers	127900	1004 (1.28-1.24)

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 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	129	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UTX	A	201	X	-	-	-
2	UTX	A	202	X	-	-	-

## 2 Entry composition [i](#)

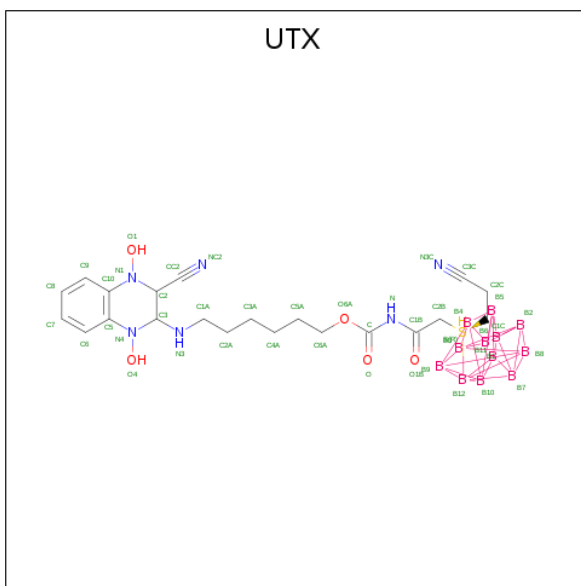
There are 4 unique types of molecules in this entry. The entry contains 1337 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lysozyme C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	129	1020	623	198	189	10	0	3	0

- Molecule 2 is 2-cyano-3-((6-(((2-((2-cyanoethyl)(borocaptate-10B)sulfonio)acetyl)carbamoyl)oxy)hexyl)amino)quinoxaline 1,4-dioxide (three-letter code: UTX) (formula: C<sub>21</sub>H<sub>29</sub>B<sub>12</sub>N<sub>6</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	B	C	N	O			S
2	A	1	45	12	21	6	5	1	0	0
2	A	1	41	12	18	5	5	1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Na 2	0	0


- Molecule 4 is water.

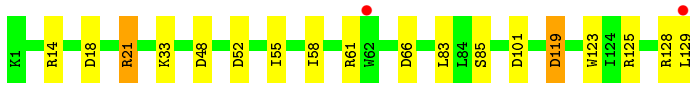
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	222	Total 229	O 229	0	7

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Lysozyme C

Chain A:  2% 86% 12%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.44Å 78.44Å 37.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.76 – 1.26 21.76 – 1.26	Depositor EDS
% Data completeness (in resolution range)	93.7 (21.76-1.26) 93.7 (21.76-1.26)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.84 (at 1.26Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.193 , 0.223 0.201 , 0.229	Depositor DCC
$R_{free}$ test set	1483 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	10.7	Xtrriage
Anisotropy	0.054	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 52.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	1337	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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: NA, UTX

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	1.31	0/1044	1.38	14/1409 (1.0%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	18	ASP	CB-CG-OD2	-10.97	108.42	118.30
1	A	128	ARG	NE-CZ-NH1	10.16	125.38	120.30
1	A	125	ARG	NE-CZ-NH1	7.43	124.02	120.30
1	A	52	ASP	CB-CG-OD2	-7.07	111.94	118.30
1	A	52	ASP	CB-CG-OD1	7.04	124.63	118.30
1	A	61	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	A	66	ASP	CB-CG-OD1	6.71	124.34	118.30
1	A	14[A]	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	14[B]	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	21	ARG	NE-CZ-NH2	5.81	123.20	120.30
1	A	125	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	48	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	18	ASP	CB-CG-OD1	5.14	122.93	118.30
1	A	61	ARG	NE-CZ-NH2	-5.08	117.76	120.30

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	1020	0	978	8	0
2	A	86	0	0	6	0
3	A	2	0	0	0	0
4	A	229	0	0	6	1
All	All	1337	0	978	12	1

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 6.

All (12) 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:A:21:ARG:NH1	4:A:301:HOH:O	1.96	0.96
2:A:202:UTX:O	4:A:302:HOH:O	1.98	0.81
2:A:202:UTX:S	4:A:305:HOH:O	2.51	0.68
2:A:201:UTX:CC2	2:A:201:UTX:C1A	2.74	0.66
1:A:101:ASP:OD1	4:A:303:HOH:O	2.16	0.63
1:A:33:LYS:HG2	1:A:123:TRP:CH2	2.46	0.50
2:A:201:UTX:CC2	2:A:201:UTX:C2A	2.90	0.50
1:A:119:ASP:HB2	2:A:201:UTX:C9	2.43	0.49
1:A:85[A]:SER:OG	4:A:304:HOH:O	2.20	0.47
1:A:55:ILE:HG22	4:A:330:HOH:O	2.17	0.43
1:A:119:ASP:HB2	2:A:201:UTX:C10	2.49	0.43
1:A:58:ILE:HB	1:A:83:LEU:HD13	2.01	0.42

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:475:HOH:O	4:A:475:HOH:O[7_554]	1.68	0.52

## 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	130/129 (101%)	126 (97%)	3 (2%)	1 (1%)	19	3

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	ASP

### 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	108/105 (103%)	107 (99%)	1 (1%)	78	47

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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
2	UTX	A	201	-	58,65,65	6.49	39 (67%)	150,170,170	3.30	49 (32%)
2	UTX	A	202	-	55,61,65	6.14	39 (70%)	153,165,170	2.03	39 (25%)

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
2	UTX	A	201	-	2/2/19/21	4/31/495/495	0/2/21/21
2	UTX	A	202	-	2/2/18/21	7/21/485/495	0/2/21/21

All (78) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	202	UTX	C2-CC2	-13.40	1.29	1.49
2	A	201	UTX	C2-CC2	-13.29	1.29	1.49
2	A	201	UTX	B8-B7	-10.85	1.57	1.78
2	A	201	UTX	B12-B8	-9.87	1.63	1.77
2	A	201	UTX	B12-B9	-9.74	1.63	1.77
2	A	202	UTX	O-C	9.46	1.39	1.21
2	A	202	UTX	B11-B5	-9.43	1.58	1.78
2	A	201	UTX	B11-B10	-9.25	1.60	1.78
2	A	201	UTX	B9-B8	-9.22	1.60	1.78
2	A	202	UTX	B10-B5	-9.19	1.58	1.78
2	A	202	UTX	B10-B9	-9.14	1.60	1.78
2	A	202	UTX	B8-B7	-9.05	1.60	1.78
2	A	201	UTX	O-C	9.01	1.38	1.21
2	A	202	UTX	B1-B2	-9.01	1.52	1.78
2	A	201	UTX	B10-B9	-8.78	1.61	1.78

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	UTX	B12-S	-8.77	1.84	1.90
2	A	202	UTX	B11-B10	-8.73	1.61	1.78
2	A	201	UTX	B12-B7	-8.73	1.64	1.77
2	A	201	UTX	B12-B11	-8.65	1.64	1.77
2	A	201	UTX	B8-B3	-8.62	1.60	1.78
2	A	201	UTX	B11-B7	-8.59	1.61	1.78
2	A	201	UTX	B1-B4	-8.53	1.53	1.78
2	A	202	UTX	B7-B2	-8.42	1.60	1.78
2	A	201	UTX	B7-B2	-8.41	1.60	1.78
2	A	202	UTX	O1B-C1B	8.40	1.40	1.23
2	A	201	UTX	B1-B6	-8.38	1.54	1.78
2	A	202	UTX	B11-B7	-8.37	1.62	1.78
2	A	202	UTX	B9-B4	-8.36	1.60	1.78
2	A	202	UTX	B8-B3	-8.32	1.60	1.78
2	A	201	UTX	B7-B6	-8.24	1.60	1.78
2	A	201	UTX	B1-B2	-8.23	1.54	1.78
2	A	201	UTX	B3-B2	-8.22	1.54	1.78
2	A	201	UTX	B1-B3	-8.15	1.55	1.78
2	A	202	UTX	B9-B8	-7.99	1.62	1.78
2	A	201	UTX	B9-B4	-7.90	1.61	1.78
2	A	202	UTX	B11-B6	-7.83	1.61	1.78
2	A	201	UTX	B11-B6	-7.82	1.61	1.78
2	A	202	UTX	B1-B3	-7.70	1.56	1.78
2	A	201	UTX	B12-B10	-7.70	1.66	1.77
2	A	201	UTX	B10-B5	-7.61	1.62	1.78
2	A	202	UTX	B8-B2	-7.46	1.62	1.78
2	A	201	UTX	B1-B5	-7.32	1.57	1.78
2	A	202	UTX	B1-B4	-7.32	1.57	1.78
2	A	202	UTX	B1-B5	-7.30	1.57	1.78
2	A	202	UTX	B4-B3	-7.22	1.57	1.78
2	A	201	UTX	C2-C3	-7.21	1.40	1.53
2	A	202	UTX	B9-B3	-7.13	1.63	1.78
2	A	202	UTX	B3-B2	-7.07	1.58	1.78
2	A	202	UTX	B7-B6	-7.01	1.63	1.78
2	A	201	UTX	B9-B3	-6.90	1.63	1.78
2	A	202	UTX	B10-B4	-6.90	1.63	1.78
2	A	201	UTX	B8-B2	-6.87	1.63	1.78
2	A	201	UTX	B4-B3	-6.81	1.58	1.78
2	A	201	UTX	B5-B4	-6.76	1.59	1.78
2	A	201	UTX	B6-B2	-6.76	1.59	1.78
2	A	201	UTX	B11-B5	-6.59	1.64	1.78
2	A	201	UTX	B10-B4	-6.56	1.64	1.78

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	UTX	B6-B5	-6.17	1.60	1.78
2	A	202	UTX	B12-B10	-6.10	1.63	1.78
2	A	202	UTX	B1-B6	-6.04	1.61	1.78
2	A	202	UTX	B12-B9	-5.86	1.63	1.78
2	A	202	UTX	B5-B4	-5.81	1.61	1.78
2	A	202	UTX	B6-B2	-5.56	1.62	1.78
2	A	202	UTX	B12-B7	-5.40	1.64	1.78
2	A	202	UTX	B12-B8	-5.19	1.65	1.78
2	A	202	UTX	B6-B5	-5.10	1.63	1.78
2	A	202	UTX	B12-B11	-5.04	1.65	1.78
2	A	202	UTX	C2-C3	-4.81	1.44	1.53
2	A	202	UTX	C10-C5	4.18	1.48	1.40
2	A	201	UTX	C10-C5	4.01	1.47	1.40
2	A	201	UTX	C-N	3.85	1.44	1.37
2	A	202	UTX	C-N	3.18	1.42	1.37
2	A	202	UTX	C2B-S	-3.09	1.73	1.80
2	A	201	UTX	C9-C10	2.66	1.44	1.39
2	A	201	UTX	O4-N4	-2.52	1.26	1.42
2	A	201	UTX	O1-N1	-2.51	1.26	1.42
2	A	202	UTX	O4-N4	-2.43	1.26	1.42
2	A	202	UTX	O1-N1	-2.38	1.27	1.42

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	UTX	B9-B12-B7	-11.34	103.36	110.86
2	A	201	UTX	B10-B12-B7	-10.42	103.97	110.86
2	A	202	UTX	O-C-N	-10.27	111.38	125.44
2	A	201	UTX	B11-B12-B9	-10.24	104.09	110.86
2	A	201	UTX	B11-B12-B8	-9.67	104.47	110.86
2	A	201	UTX	B12-B7-B2	8.95	111.26	106.38
2	A	201	UTX	B10-B12-B8	-8.69	105.12	110.86
2	A	202	UTX	C1A-N3-C3	8.05	126.61	114.39
2	A	201	UTX	B8-B12-B7	-7.69	57.38	61.09
2	A	201	UTX	B12-B9-B4	7.49	110.46	106.38
2	A	201	UTX	B12-B8-B2	7.45	110.44	106.38
2	A	201	UTX	B12-B8-B3	7.44	110.44	106.38
2	A	201	UTX	O-C-N	-7.26	115.51	125.44
2	A	201	UTX	B12-B10-B5	7.02	110.21	106.38
2	A	201	UTX	C1A-N3-C3	6.58	124.38	114.39
2	A	201	UTX	B11-B12-B10	-6.36	58.03	61.09
2	A	201	UTX	B12-B11-B5	6.30	109.81	106.38

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	UTX	B12-B7-B6	6.19	109.75	106.38
2	A	201	UTX	CC2-C2-N1	5.93	121.02	111.37
2	A	201	UTX	B12-B8-B7	5.74	61.83	59.45
2	A	202	UTX	B7-B6-B1	-5.61	102.59	108.16
2	A	201	UTX	B12-B11-B6	5.29	109.26	106.38
2	A	201	UTX	B12-B9-B10	5.10	61.56	59.45
2	A	201	UTX	B10-B12-B9	-4.99	58.69	61.09
2	A	201	UTX	O6A-C-O	-4.90	114.85	124.25
2	A	201	UTX	B12-B11-B10	4.74	61.41	59.45
2	A	201	UTX	B11-B12-B7	-4.68	58.84	61.09
2	A	202	UTX	B11-B6-B1	-4.55	103.64	108.16
2	A	202	UTX	B6-B1-B4	4.52	113.41	108.06
2	A	201	UTX	B9-B12-B8	-4.42	58.96	61.09
2	A	201	UTX	O1-N1-C2	4.21	123.25	107.37
2	A	202	UTX	B6-B1-B3	4.20	113.03	108.06
2	A	201	UTX	B5-B1-B2	4.16	112.99	108.06
2	A	202	UTX	B5-B6-B2	-4.09	103.22	108.06
2	A	201	UTX	B12-B9-B3	3.97	108.54	106.38
2	A	202	UTX	O1-N1-C2	3.77	121.61	107.37
2	A	202	UTX	B7-B6-B5	-3.71	104.48	108.16
2	A	202	UTX	B1-B6-B2	-3.62	56.30	60.00
2	A	201	UTX	B3-B8-B2	-3.60	57.09	59.91
2	A	201	UTX	C9-C10-N1	3.53	124.05	118.24
2	A	202	UTX	C9-C10-N1	3.27	123.61	118.24
2	A	201	UTX	B8-B3-B2	3.25	62.65	60.05
2	A	201	UTX	B12-B7-B8	3.23	60.79	59.45
2	A	201	UTX	B5-B1-B3	3.17	111.82	108.06
2	A	202	UTX	B11-B12-B8	-3.12	104.91	108.61
2	A	201	UTX	B11-B5-B1	-3.00	105.19	108.16
2	A	202	UTX	C2B-C1B-N	2.96	118.46	114.38
2	A	202	UTX	B10-B12-B7	-2.93	105.13	108.61
2	A	202	UTX	B8-B7-B6	2.90	110.42	107.98
2	A	202	UTX	CC2-C2-N1	2.86	116.03	111.37
2	A	201	UTX	B12-B7-B11	2.81	60.62	59.45
2	A	202	UTX	B10-B4-B1	-2.81	105.38	108.16
2	A	202	UTX	B12-B11-B6	2.80	110.95	107.46
2	A	202	UTX	B9-B12-B7	-2.80	105.28	108.61
2	A	202	UTX	B6-B2-B3	2.77	111.34	108.06
2	A	201	UTX	B4-B1-B2	2.75	111.32	108.06
2	A	202	UTX	B11-B12-B9	-2.74	105.35	108.61
2	A	201	UTX	B12-B8-B9	2.71	60.58	59.45
2	A	202	UTX	C8-C7-C6	2.70	124.31	120.19

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	UTX	B8-B7-B2	2.69	62.03	59.94
2	A	201	UTX	B8-B2-B7	-2.69	58.02	60.12
2	A	201	UTX	B12-B10-B11	2.68	60.56	59.45
2	A	202	UTX	B10-B12-B8	-2.65	105.46	108.61
2	A	201	UTX	B12-B11-B7	2.65	60.55	59.45
2	A	201	UTX	B6-B1-B4	2.64	111.19	108.06
2	A	202	UTX	B4-B1-B2	2.56	111.09	108.06
2	A	202	UTX	B10-B11-B6	2.56	110.13	107.98
2	A	202	UTX	B5-B1-B2	2.52	111.05	108.06
2	A	202	UTX	B12-B7-B6	2.46	110.53	107.46
2	A	201	UTX	B12-B9-B8	2.45	60.46	59.45
2	A	201	UTX	B7-B8-B3	-2.42	105.95	107.98
2	A	202	UTX	B8-B12-S	2.40	128.77	122.72
2	A	202	UTX	B11-B6-B2	-2.39	105.79	108.16
2	A	202	UTX	B11-B12-S	-2.35	116.77	122.72
2	A	202	UTX	B10-B5-B6	2.33	110.47	108.16
2	A	201	UTX	B12-B10-B4	2.30	107.63	106.38
2	A	202	UTX	C6-C5-N4	2.28	121.99	118.24
2	A	202	UTX	B11-B6-B5	-2.27	58.23	60.05
2	A	202	UTX	B6-B1-B2	2.26	62.30	60.00
2	A	201	UTX	B6-B5-B4	-2.20	105.45	108.06
2	A	202	UTX	B9-B12-S	2.17	128.20	122.72
2	A	201	UTX	B5-B10-B4	-2.14	58.24	59.91
2	A	202	UTX	B4-B9-B3	-2.11	58.26	59.91
2	A	202	UTX	B9-B4-B3	2.07	61.70	60.05
2	A	201	UTX	B11-B10-B4	-2.06	106.25	107.98
2	A	202	UTX	B6-B11-B5	2.04	61.50	59.91
2	A	201	UTX	B6-B1-B5	2.00	62.04	60.00
2	A	202	UTX	B10-B4-B5	-2.00	58.44	60.05

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	201	UTX	C3
2	A	201	UTX	C2
2	A	202	UTX	C3
2	A	202	UTX	C2

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	UTX	O-C-N-C1B

*Continued on next page...*

*Continued from previous page...*

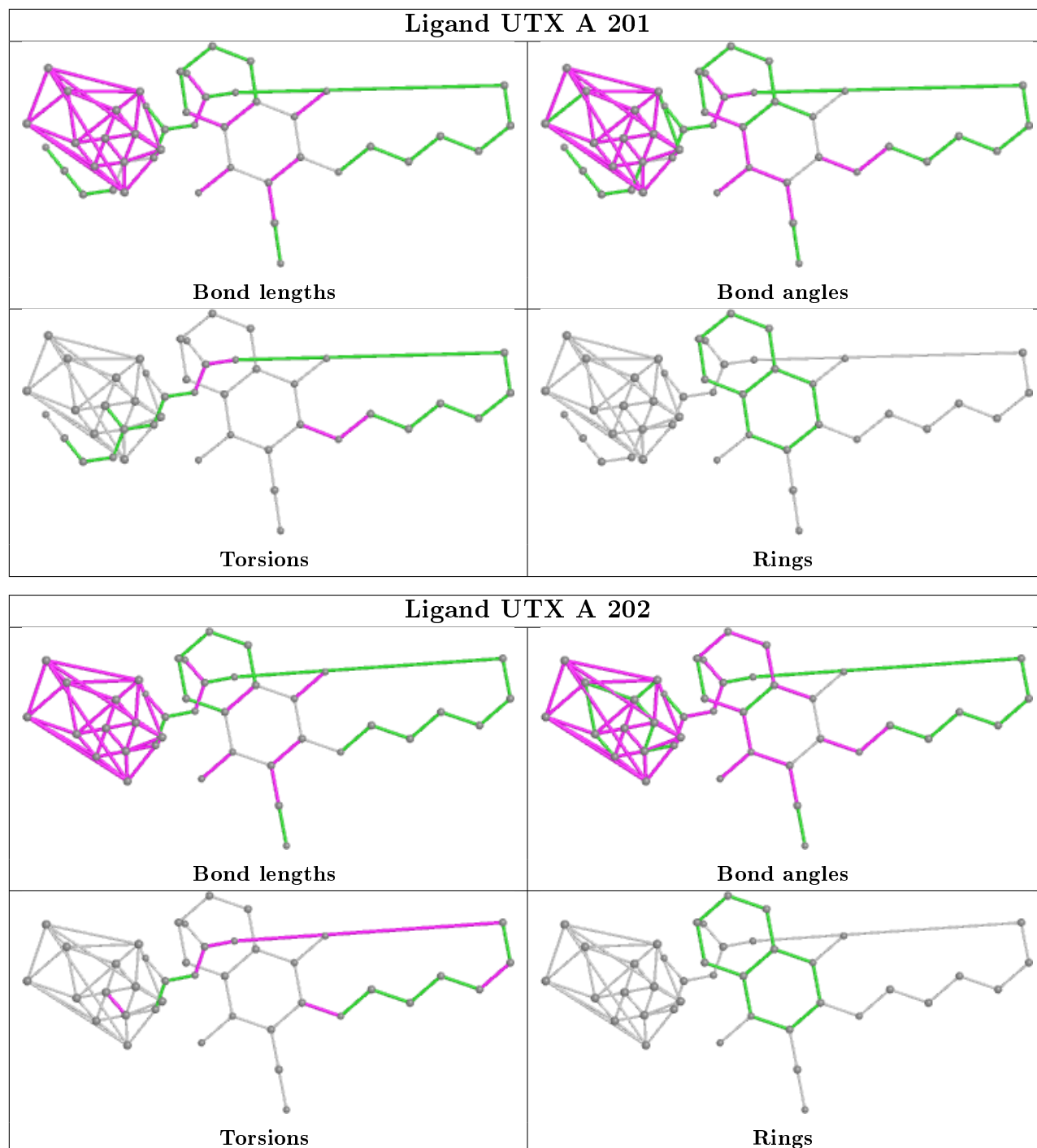
Mol	Chain	Res	Type	Atoms
2	A	201	UTX	C2-C3-N3-C1A
2	A	202	UTX	O-C-N-C1B
2	A	202	UTX	C2-C3-N3-C1A
2	A	201	UTX	O-C-O6A-C6A
2	A	202	UTX	O-C-O6A-C6A
2	A	202	UTX	C3A-C4A-C5A-C6A
2	A	201	UTX	C2A-C1A-N3-C3
2	A	202	UTX	C5A-C6A-O6A-C
2	A	202	UTX	B10-B12-S-C2B
2	A	202	UTX	B11-B12-S-C2B

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	UTX	4	0
2	A	202	UTX	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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, 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	129/129 (100%)	0.22	2 (1%) 72 61	6, 10, 16, 26	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	129	LEU	3.8
1	A	62	TRP	2.6

### 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 carbohydrates in this entry.

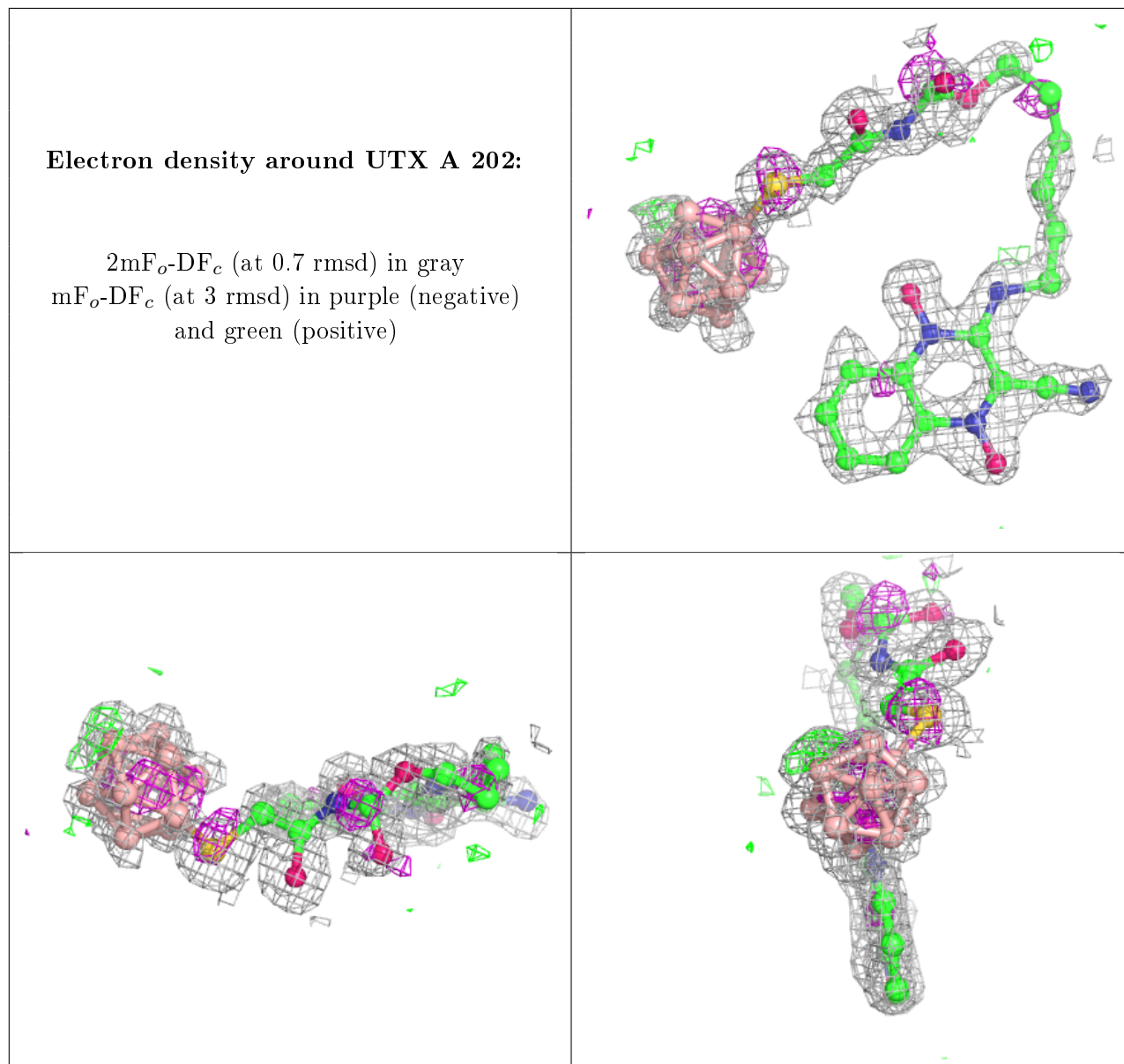
### 6.4 Ligands [i](#)

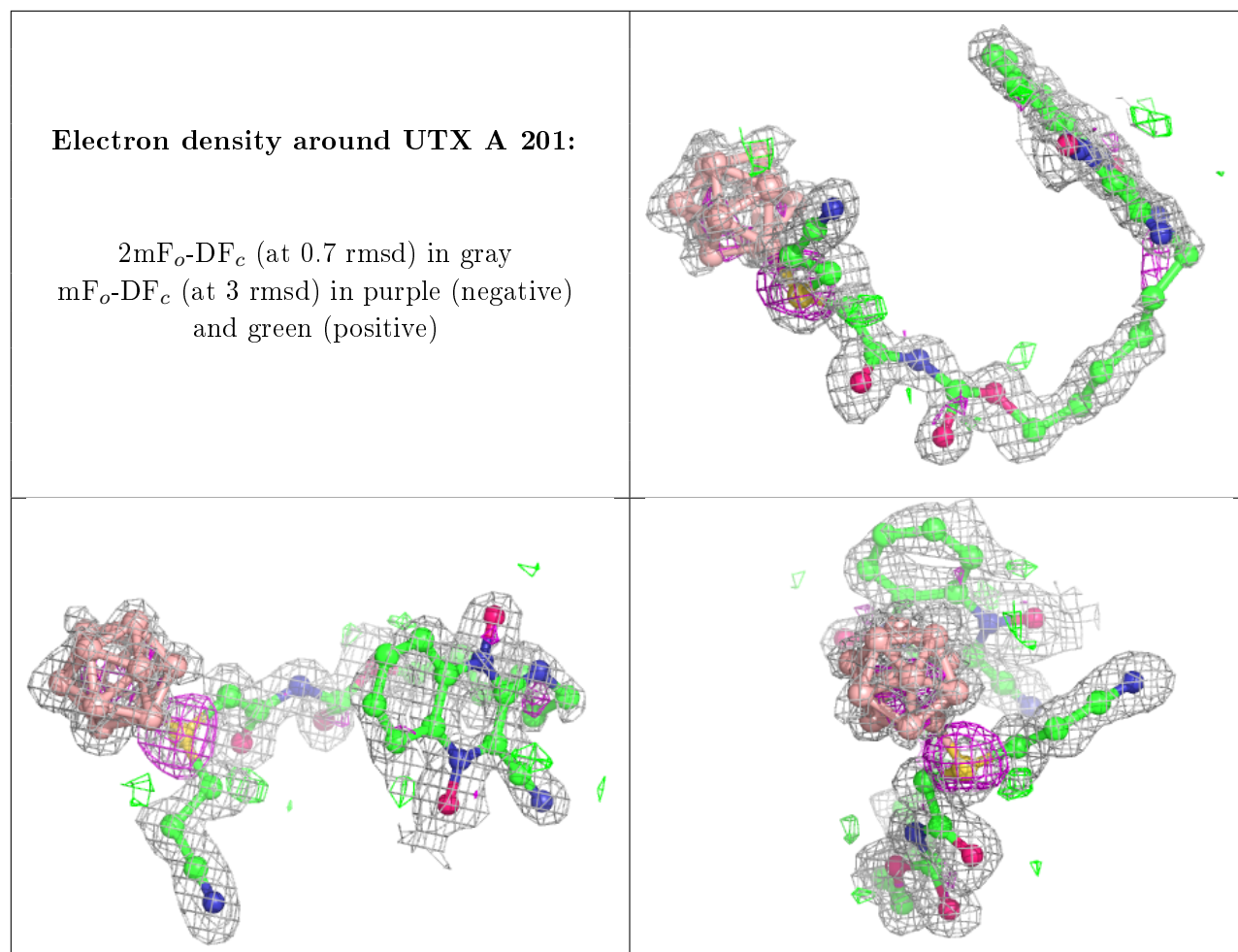
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	UTX	A	202	41/45	0.82	0.24	14,20,26,35	0
2	UTX	A	201	45/45	0.84	0.24	13,17,27,28	0
3	NA	A	204	1/1	0.98	0.21	24,24,24,24	0
3	NA	A	203	1/1	1.00	0.05	10,10,10,10	0

The following is a graphical depiction of the model fit to experimental electron density of all

instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.