



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:40 PM UTC

PDB ID : 9GC7 / pdb\_00009gc7  
Title : Mineralocorticoid receptor in complex with acylurea antagonists.  
Authors : Edman, K.; Aagaard, A.; Barlind, L.  
Deposited on : 2024-08-01  
Resolution : 1.46 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 types of validation reports are described at

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

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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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

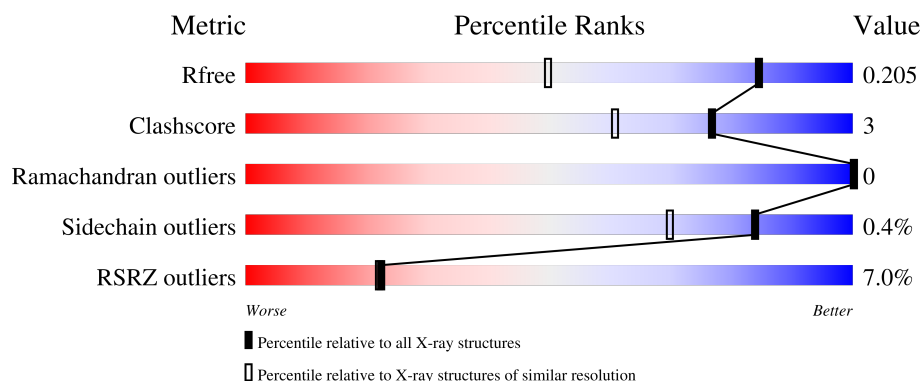
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.46 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	1756 (1.46-1.46)
Clashscore	190562	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)
RSRZ outliers	180081	1756 (1.46-1.46)

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  $\geq 3$ , 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	305	<div> <div>6%</div> <div>74%</div> <div>7%</div> <div>19%</div> </div>
2	B	12	<div> <div>75%</div> <div>8%</div> <div>17%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2445 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 Mineralocorticoid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	12	0
			2127	1368	349	396	14			

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	713	MET	-	initiating methionine	UNP P08235
A	714	HIS	-	expression tag	UNP P08235
A	715	ASN	-	expression tag	UNP P08235
A	716	HIS	-	expression tag	UNP P08235
A	717	ASN	-	expression tag	UNP P08235
A	718	HIS	-	expression tag	UNP P08235
A	719	ASN	-	expression tag	UNP P08235
A	720	HIS	-	expression tag	UNP P08235
A	721	ASN	-	expression tag	UNP P08235
A	722	HIS	-	expression tag	UNP P08235
A	723	ASN	-	expression tag	UNP P08235
A	724	HIS	-	expression tag	UNP P08235
A	725	ASN	-	expression tag	UNP P08235
A	726	GLY	-	expression tag	UNP P08235
A	727	GLY	-	expression tag	UNP P08235
A	728	GLU	-	expression tag	UNP P08235
A	729	ASN	-	expression tag	UNP P08235
A	730	LEU	-	expression tag	UNP P08235
A	731	TYR	-	expression tag	UNP P08235
A	732	PHE	-	expression tag	UNP P08235
A	733	GLN	-	expression tag	UNP P08235
A	734	GLY	-	expression tag	UNP P08235
A	808	SER	CYS	engineered mutation	UNP P08235
A	810	LEU	SER	engineered mutation	UNP P08235
A	910	SER	CYS	engineered mutation	UNP P08235
A	985	GLY	-	expression tag	UNP P08235
A	986	GLY	-	expression tag	UNP P08235

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Chain	Residue	Modelled	Actual	Comment	Reference
A	987	SER	-	expression tag	UNP P08235
A	988	LEU	-	expression tag	UNP P08235
A	989	VAL	-	expression tag	UNP P08235
A	990	PRO	-	expression tag	UNP P08235
A	991	ARG	-	expression tag	UNP P08235
A	992	GLY	-	expression tag	UNP P08235
A	993	SER	-	expression tag	UNP P08235
A	994	GLY	-	expression tag	UNP P08235
A	995	GLY	-	expression tag	UNP P08235
A	996	GLY	-	expression tag	UNP P08235
A	997	SER	-	expression tag	UNP P08235
A	998	GLY	-	expression tag	UNP P08235
A	999	GLY	-	expression tag	UNP P08235
A	1000	SER	-	expression tag	UNP P08235
A	1001	GLY	-	expression tag	UNP P08235
A	1002	GLY	-	expression tag	UNP P08235
A	1003	PRO	-	expression tag	UNP P08235
A	1004	GLN	-	expression tag	UNP P08235
A	1005	ALA	-	expression tag	UNP P08235
A	1006	GLN	-	expression tag	UNP P08235
A	1007	GLN	-	expression tag	UNP P08235
A	1008	LYS	-	expression tag	UNP P08235
A	1009	SER	-	expression tag	UNP P08235
A	1010	LEU	-	expression tag	UNP P08235
A	1011	LEU	-	expression tag	UNP P08235
A	1012	GLN	-	expression tag	UNP P08235
A	1013	GLN	-	expression tag	UNP P08235
A	1014	LEU	-	expression tag	UNP P08235
A	1015	LEU	-	expression tag	UNP P08235
A	1016	THR	-	expression tag	UNP P08235
A	1017	GLU	-	expression tag	UNP P08235

- Molecule 2 is a protein called Nuclear receptor coactivator 1.

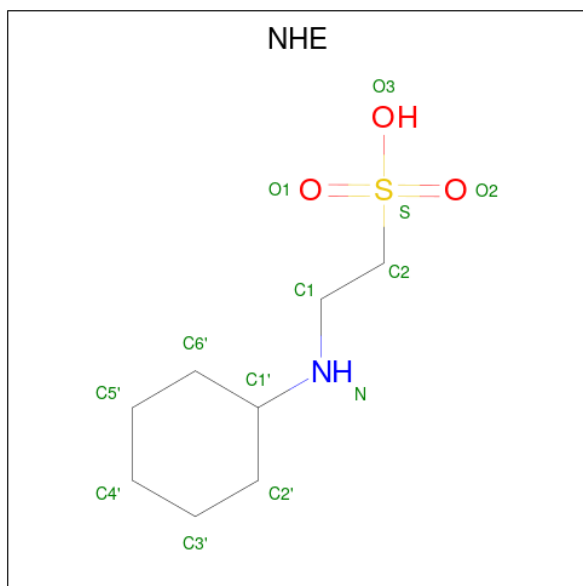
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	10	Total	C	N	O	0	0	0
			82	52	13	17			

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		

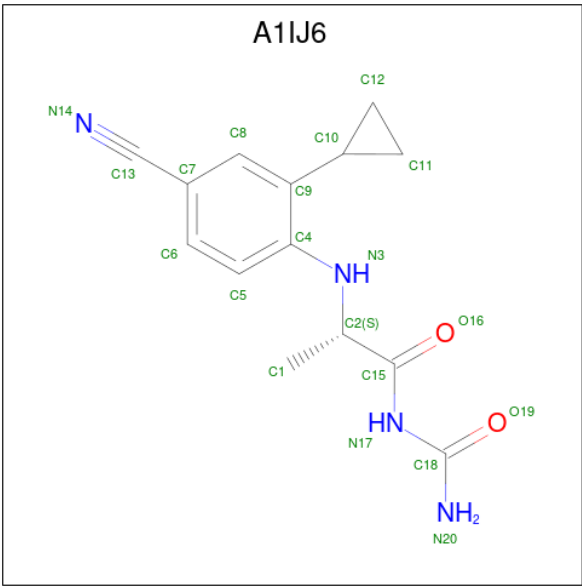
- Molecule 4 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (CCD ID: NHE) (formula:  $C_8H_{17}NO_3S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

- Molecule 5 is (2S)-N-aminocarbonyl-2-[(4-cyano-6-cyclopropyl-cyclohexa-1,2,3,5-tetraen-1-yl)amino]propanamide (CCD ID: A1IJ6) (formula:  $C_{14}H_{14}N_4O_2$ ) (labeled as "Ligand of

Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			20	14	4	2		

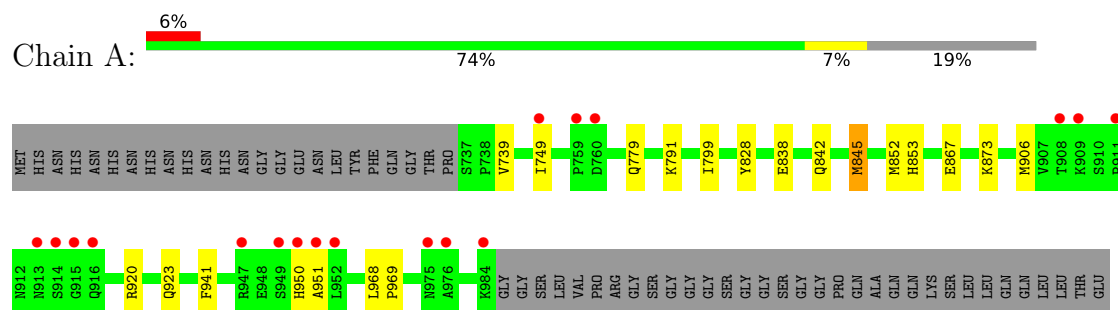
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	189	Total	O	0	0
			189	189		
6	B	6	Total	O	0	0
			6	6		

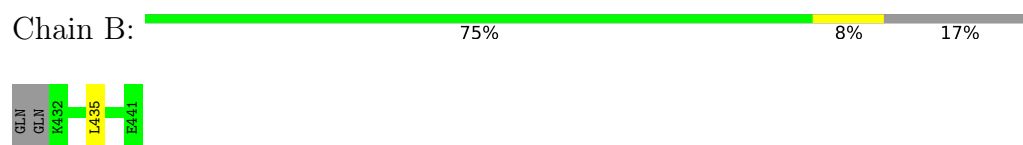
### 3 Residue-property plots [i](#)

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: Mineralocorticoid receptor



- Molecule 2: Nuclear receptor coactivator 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.47Å 77.79Å 78.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.18 – 1.46 41.18 – 1.46	Depositor EDS
% Data completeness (in resolution range)	98.3 (41.18-1.46) 98.3 (41.18-1.46)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.22 (at 1.46Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, $R_{free}$	0.186 , 0.210 0.179 , 0.205	Depositor DCC
$R_{free}$ test set	2595 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.1	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 33.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.022 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2445	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% 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: NHE, A1IJ6, MPD

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	0.80	2/2176 (0.1%)	0.89	2/2939 (0.1%)
2	B	0.67	0/81	0.73	0/106
All	All	0.79	2/2257 (0.1%)	0.88	2/3045 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	845	MET	SD-CE	-6.65	1.62	1.79
1	A	852	MET	SD-CE	5.91	1.94	1.79

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	779	GLN	CB-CG-CD	-5.21	103.74	112.60
1	A	867	GLU	CB-CG-CD	5.19	121.42	112.60

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	2127	0	2116	13	0
2	B	82	0	90	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	8	0	14	1	0
4	A	13	0	17	1	0
5	A	20	0	0	0	0
6	A	189	0	0	2	2
6	B	6	0	0	0	0
All	All	2445	0	2237	13	2

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 3.

All (13) 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:749:ILE:HG23	4:A:1102:NHE:H6'1	1.74	0.70
1:A:853:HIS:HD2	6:A:1225:HOH:O	1.85	0.58
1:A:873:LYS:HD2	3:A:1101:MPD:H53	1.88	0.56
1:A:845:MET:HG2	1:A:941:PHE:CE2	2.42	0.55
1:A:749:ILE:HD13	6:A:1252:HOH:O	2.05	0.55
1:A:739:VAL:HG11	1:A:906:MET:HE3	1.94	0.49
1:A:968:LEU:HD23	1:A:968:LEU:C	2.38	0.49
1:A:950:HIS:CG	1:A:951:ALA:N	2.82	0.47
1:A:920:ARG:HA	1:A:923:GLN:HE21	1.81	0.45
1:A:749:ILE:HD11	1:A:828:TYR:HE1	1.81	0.44
1:A:838:GLU:OE1	1:A:842:GLN:NE2	2.53	0.42
1:A:968:LEU:HB3	1:A:969:PRO:HD3	2.01	0.41
1:A:799:ILE:HG23	2:B:435:LEU:HD23	2.02	0.41

All (2) 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)
6:A:1303:HOH:O	6:A:1361:HOH:O[3_554]	2.08	0.12
6:A:1290:HOH:O	6:A:1303:HOH:O[3_544]	2.11	0.09

## 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	259/305 (85%)	256 (99%)	3 (1%)	0	100	100
2	B	8/12 (67%)	8 (100%)	0	0	100	100
All	All	267/317 (84%)	264 (99%)	3 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	242/272 (89%)	241 (100%)	1 (0%)	84	70
2	B	10/12 (83%)	10 (100%)	0	100	100
All	All	252/284 (89%)	251 (100%)	1 (0%)	84	70

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

Mol	Chain	Res	Type
1	A	791	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	792	ASN
1	A	823	ASN

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Mol	Chain	Res	Type
1	A	853	HIS
1	A	916	GLN
1	A	923	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

3 ligands 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	$\# Z  > 2$
5	A1IJ6	A	1103	-	16,21,21	0.83	0	19,29,29	1.02	1 (5%)
3	MPD	A	1101	-	7,7,7	0.17	0	9,10,10	0.42	0
4	NHE	A	1102	-	13,13,13	0.74	1 (7%)	16,17,17	0.94	2 (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
5	A1IJ6	A	1103	-	-	1/16/20/20	0/2/2/2
3	MPD	A	1101	-	-	0/5/5/5	-
4	NHE	A	1102	-	-	1/7/15/15	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1102	NHE	O3-S	2.44	1.56	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1103	A1IJ6	C7-C13-N14	-2.16	174.74	178.07
4	A	1102	NHE	O3-S-C2	-2.16	101.78	106.00
4	A	1102	NHE	O2-S-O1	2.08	120.59	113.82

There are no chirality outliers.

All (2) torsion outliers are listed below:

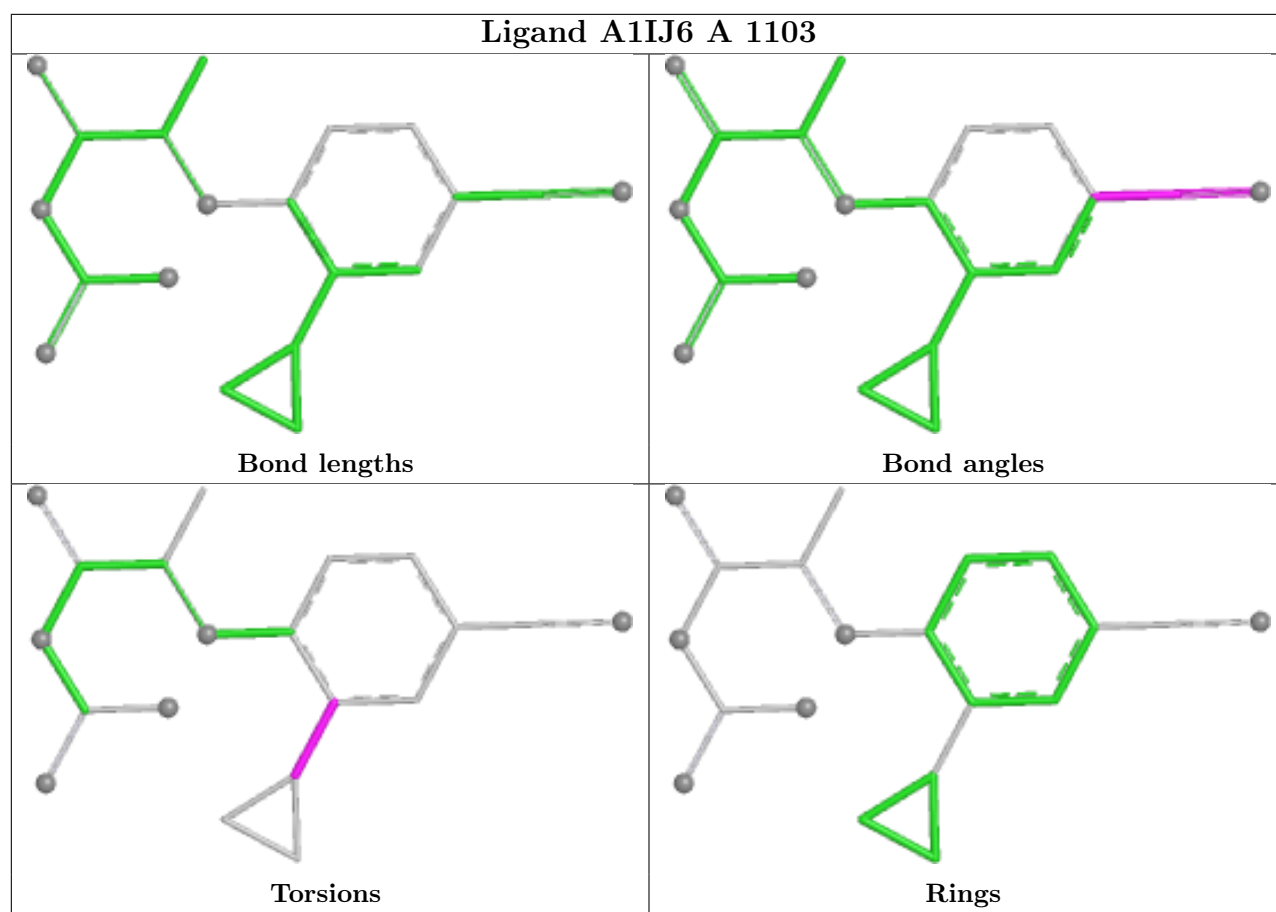
Mol	Chain	Res	Type	Atoms
5	A	1103	A1IJ6	C11-C10-C9-C4
4	A	1102	NHE	C1-C2-S-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1101	MPD	1	0
4	A	1102	NHE	1	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	248/305 (81%)	0.38	18 (7%) 21 20	5, 23, 47, 63	12 (4%)
2	B	10/12 (83%)	0.93	0 100 100	25, 32, 46, 47	0
All	All	258/317 (81%)	0.41	18 (6%) 22 22	5, 24, 47, 63	12 (4%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	951	ALA	6.5
1	A	952	LEU	6.2
1	A	950	HIS	5.5
1	A	908	THR	3.8
1	A	749	ILE	3.3
1	A	911	PRO	3.2
1	A	915	GLY	3.2
1	A	984	LYS	3.2
1	A	949	SER	3.0
1	A	913	ASN	2.9
1	A	760	ASP	2.9
1	A	976	ALA	2.8
1	A	914	SER	2.8
1	A	947	ARG	2.6
1	A	909	LYS	2.2
1	A	916	GLN	2.2
1	A	975	ASN	2.2
1	A	759	PRO	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](#)

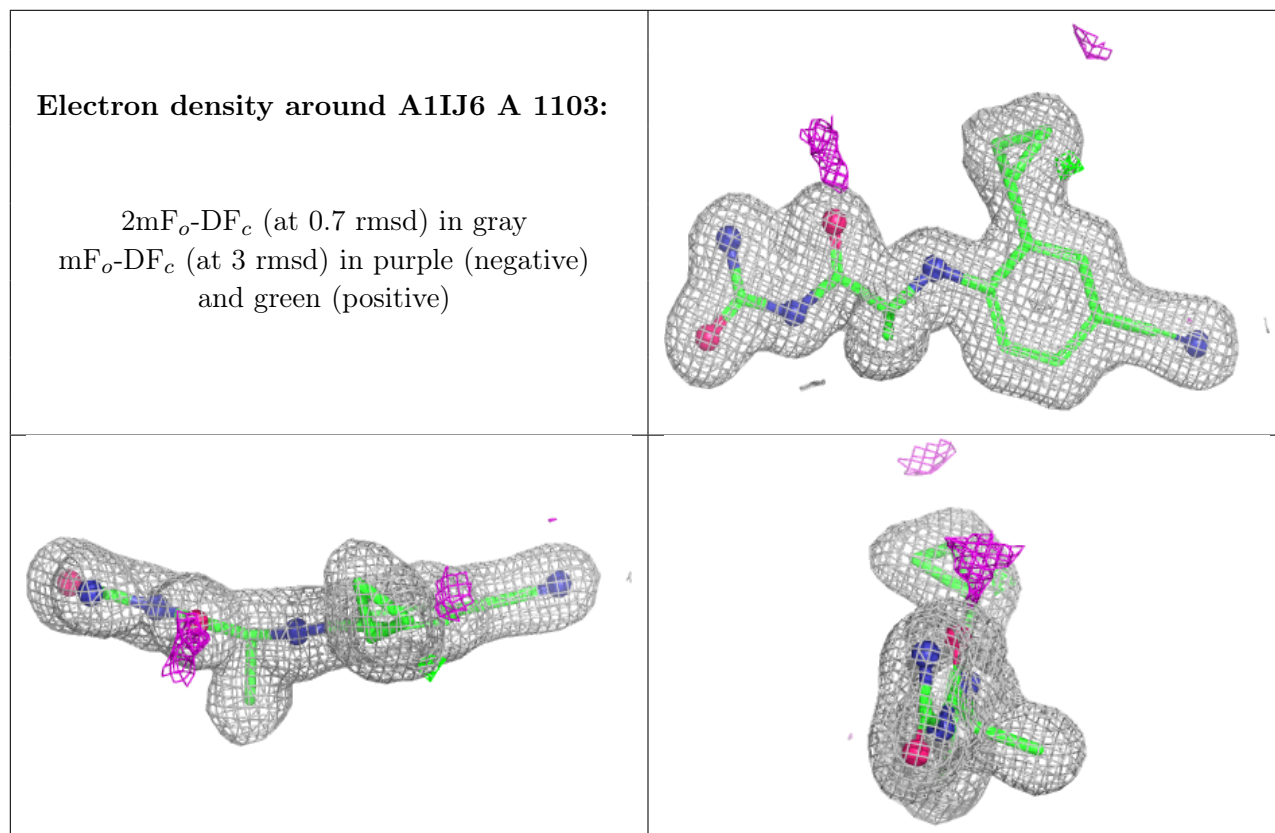
There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

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( $\text{\AA}^2$ )	Q<0.9
4	NHE	A	1102	13/13	0.77	0.18	39,42,43,43	0
3	MPD	A	1101	8/8	0.85	0.16	36,38,39,40	0
5	A1IJ6	A	1103	20/20	0.97	0.06	17,19,24,24	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.