



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 27, 2017 – 02:46 AM EDT

PDB ID : 5INH  
Title : Crystal structure of Autotaxin/ENPP2 with a covalent fragment  
Authors : Klein, M.G.; Tjhen, R.  
Deposited on : 2016-03-07  
Resolution : 1.84 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029077  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029077

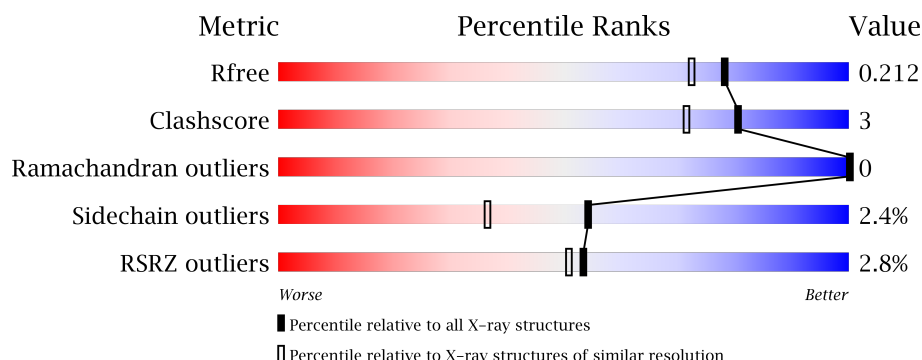
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.84 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))
$R_{free}$	100719	2964 (1.86-1.82)
Clashscore	112137	3197 (1.86-1.82)
Ramachandran outliers	110173	3164 (1.86-1.82)
Sidechain outliers	110143	3165 (1.86-1.82)
RSRZ outliers	101464	2973 (1.86-1.82)

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. 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	879	<div> <div>3%</div> <div>82%</div> <div>7%</div> <div>11%</div> </div>

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
4	NAG	A	912	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6709 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	780	Total	C	N	O	S	0	6	0
			6311	4006	1086	1170	49			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	initiating methionine	UNP Q9R1E6
A	-7	LEU	-	expression tag	UNP Q9R1E6
A	-6	LEU	-	expression tag	UNP Q9R1E6
A	-5	VAL	-	expression tag	UNP Q9R1E6
A	-4	ASN	-	expression tag	UNP Q9R1E6
A	-3	GLN	-	expression tag	UNP Q9R1E6
A	-2	SER	-	expression tag	UNP Q9R1E6
A	-1	HIS	-	expression tag	UNP Q9R1E6
A	0	GLN	-	expression tag	UNP Q9R1E6
A	1	GLY	-	expression tag	UNP Q9R1E6
A	2	PHE	-	expression tag	UNP Q9R1E6
A	3	ASN	-	expression tag	UNP Q9R1E6
A	4	LYS	-	expression tag	UNP Q9R1E6
A	5	GLU	-	expression tag	UNP Q9R1E6
A	6	HIS	-	expression tag	UNP Q9R1E6
A	7	THR	-	expression tag	UNP Q9R1E6
A	8	SER	-	expression tag	UNP Q9R1E6
A	9	LYS	-	expression tag	UNP Q9R1E6
A	10	MET	-	expression tag	UNP Q9R1E6
A	11	VAL	-	expression tag	UNP Q9R1E6
A	12	SER	-	expression tag	UNP Q9R1E6
A	13	ALA	-	expression tag	UNP Q9R1E6
A	14	ILE	-	expression tag	UNP Q9R1E6
A	15	VAL	-	expression tag	UNP Q9R1E6
A	16	LEU	-	expression tag	UNP Q9R1E6
A	17	TYR	-	expression tag	UNP Q9R1E6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	18	VAL	-	expression tag	UNP Q9R1E6
A	19	LEU	-	expression tag	UNP Q9R1E6
A	20	LEU	-	expression tag	UNP Q9R1E6
A	21	ALA	-	expression tag	UNP Q9R1E6
A	22	ALA	-	expression tag	UNP Q9R1E6
A	23	ALA	-	expression tag	UNP Q9R1E6
A	24	ALA	-	expression tag	UNP Q9R1E6
A	25	HIS	-	expression tag	UNP Q9R1E6
A	26	SER	-	expression tag	UNP Q9R1E6
A	27	ALA	-	expression tag	UNP Q9R1E6
A	28	PHE	-	expression tag	UNP Q9R1E6
A	29	ALA	-	expression tag	UNP Q9R1E6
A	30	ALA	-	expression tag	UNP Q9R1E6
A	31	ASP	-	expression tag	UNP Q9R1E6
A	32	PRO	-	expression tag	UNP Q9R1E6
A	33	GLY	-	expression tag	UNP Q9R1E6
A	34	GLY	-	expression tag	UNP Q9R1E6
A	35	SER	-	expression tag	UNP Q9R1E6
A	859	SER	-	expression tag	UNP Q9R1E6
A	860	ALA	-	expression tag	UNP Q9R1E6
A	861	GLU	-	expression tag	UNP Q9R1E6
A	862	ASN	-	expression tag	UNP Q9R1E6
A	863	LEU	-	expression tag	UNP Q9R1E6
A	864	TYR	-	expression tag	UNP Q9R1E6
A	865	PHE	-	expression tag	UNP Q9R1E6
A	866	GLN	-	expression tag	UNP Q9R1E6

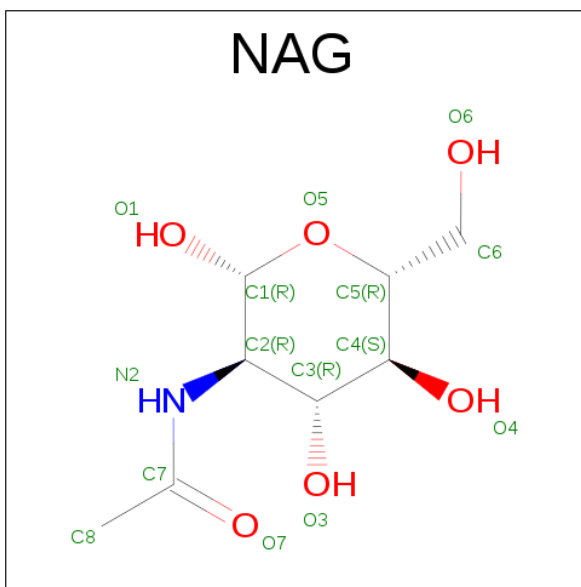
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Zn 2 2	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

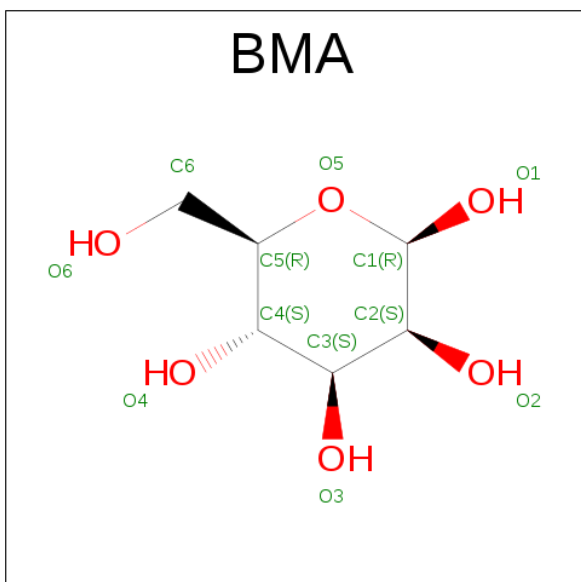
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0

- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



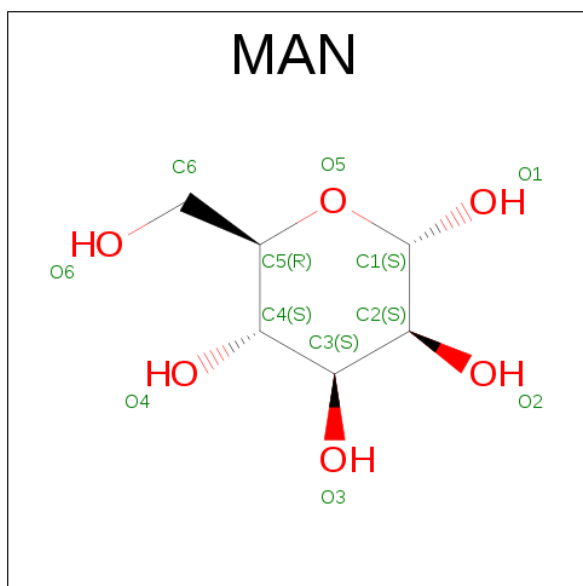
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is BETA-D-MANNOSE (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



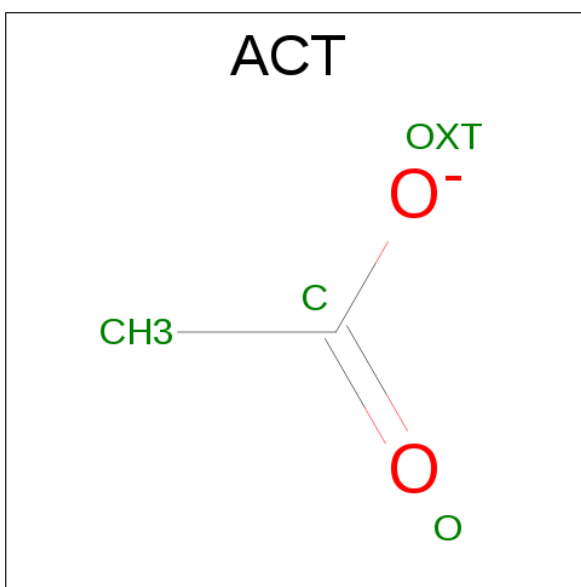
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



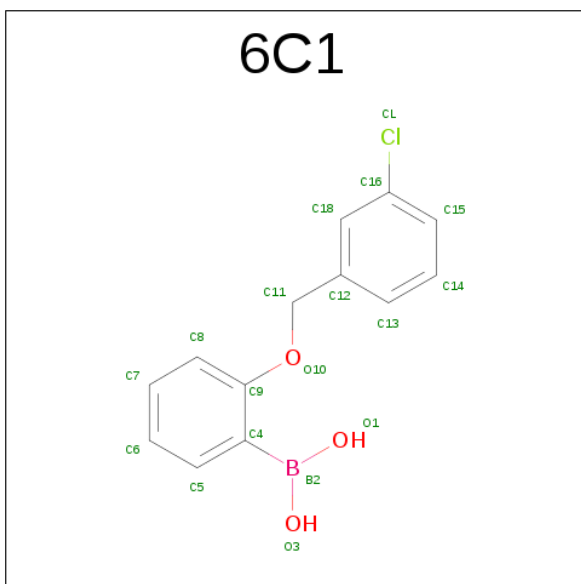
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O		0	0
			4	2	2			

- Molecule 8 is {2-[(3-chlorophenyl)methoxy]phenyl}boronic acid (three-letter code: 6C1) (formula:  $C_{13}H_{12}BClO_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	B	C	Cl	O	0	0
			18	1	13	1	3		

- Molecule 9 is water.

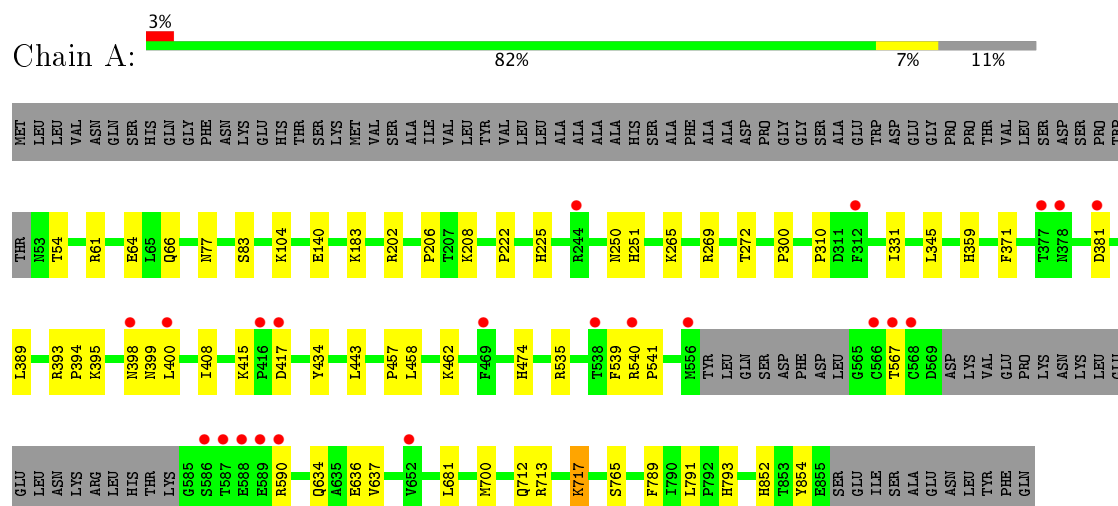
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	259	Total 259	O 259	0	0



### 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 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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.36Å 80.75Å 76.48Å 90.00° 102.86° 90.00°	Depositor
Resolution (Å)	44.51 – 1.84 44.47 – 1.83	Depositor EDS
% Data completeness (in resolution range)	95.5 (44.51-1.84) 95.5 (44.47-1.83)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.31 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.7.0025	Depositor
R, $R_{free}$	0.172 , 0.207 0.179 , 0.212	Depositor DCC
$R_{free}$ test set	3120 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.3	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6709	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: ZN, BMA, NAG, CA, 6C1, ACT, MAN

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	0.52	0/6509	0.70	2/8832 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	202	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	A	202	ARG	NE-CZ-NH1	5.46	123.03	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	6311	0	6077	39	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	70	0	62	0	0
5	A	11	0	9	0	0
6	A	33	0	28	0	0
7	A	4	0	3	0	0
8	A	18	0	0	0	0
9	A	259	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6709	0	6179	39	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 3.

The worst 5 of 39 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:712:GLN:O	1:A:717:LYS:NZ	1.96	0.96
1:A:381:ASP:HB2	9:A:1104:HOH:O	1.77	0.84
1:A:77:ASN:ND2	1:A:272:THR:HG21	2.03	0.72
1:A:717:LYS:HE3	1:A:717:LYS:H	1.58	0.69
1:A:717:LYS:H	1:A:717:LYS:CE	2.05	0.69

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	780/879 (89%)	763 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	711/792 (90%)	694 (98%)	17 (2%)	54 37

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	395	LYS
1	A	400	LEU
1	A	567	THR
1	A	345	LEU
1	A	590	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	77	ASN
1	A	634	GLN
1	A	646	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

5 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	NAG	A	905	5,4	14,14,15	0.49	0	15,19,21	0.93	0
6	MAN	A	908	6	11,11,12	1.11	1 (9%)	13,15,17	2.50	4 (30%)
6	MAN	A	909	6	11,11,12	0.94	1 (9%)	13,15,17	2.40	4 (30%)
4	NAG	A	911	1,4	14,14,15	0.51	0	15,19,21	1.20	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	A	912	4	14,14,15	0.81	1 (7%)	15,19,21	1.12	2 (13%)

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	NAG	A	905	5,4	-	0/6/23/26	0/1/1/1
6	MAN	A	908	6	-	0/2/19/22	0/1/1/1
6	MAN	A	909	6	-	0/2/19/22	0/1/1/1
4	NAG	A	911	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	912	4	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	908	MAN	O5-C1	-2.98	1.38	1.43
6	A	909	MAN	O5-C1	-2.68	1.39	1.43
4	A	912	NAG	O5-C1	-2.46	1.39	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	908	MAN	C1-O5-C5	-6.69	102.95	112.17
6	A	909	MAN	C1-O5-C5	-5.24	104.94	112.17
6	A	909	MAN	C1-C2-C3	-4.73	103.66	109.65
6	A	908	MAN	C1-C2-C3	-2.53	106.45	109.65
4	A	911	NAG	O5-C1-C2	-2.47	108.03	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 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$
4	NAG	A	904	1,4	14,14,15	0.68	0	15,19,21	1.51	4 (26%)
4	NAG	A	905	5,4	14,14,15	0.49	0	15,19,21	0.93	0
5	BMA	A	906	4,6	11,11,12	0.45	0	13,15,17	1.07	1 (7%)
6	MAN	A	907	5,6	11,11,12	1.33	2 (18%)	13,15,17	4.57	5 (38%)
6	MAN	A	908	6	11,11,12	1.11	1 (9%)	13,15,17	2.50	4 (30%)
6	MAN	A	909	6	11,11,12	0.94	1 (9%)	13,15,17	2.40	4 (30%)
4	NAG	A	910	1	14,14,15	0.43	0	15,19,21	1.74	4 (26%)
4	NAG	A	911	1,4	14,14,15	0.51	0	15,19,21	1.20	2 (13%)
4	NAG	A	912	4	14,14,15	0.81	1 (7%)	15,19,21	1.12	2 (13%)
7	ACT	A	913	2	1,3,3	1.48	0	0,3,3	0.00	-
8	6C1	A	914	1,2	19,19,19	3.12	4 (21%)	24,25,25	2.15	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	NAG	A	904	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	905	5,4	-	0/6/23/26	0/1/1/1
5	BMA	A	906	4,6	-	0/2/19/22	0/1/1/1
6	MAN	A	907	5,6	-	0/2/19/22	0/1/1/1
6	MAN	A	908	6	-	0/2/19/22	0/1/1/1
6	MAN	A	909	6	-	0/2/19/22	0/1/1/1
4	NAG	A	910	1	-	0/6/23/26	0/1/1/1
4	NAG	A	911	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	912	4	-	0/6/23/26	0/1/1/1
7	ACT	A	913	2	-	0/0/0/0	0/0/0/0
8	6C1	A	914	1,2	-	0/9/9/9	0/2/2/2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	907	MAN	O5-C1	-3.36	1.38	1.43
6	A	908	MAN	O5-C1	-2.98	1.38	1.43
6	A	909	MAN	O5-C1	-2.68	1.39	1.43
4	A	912	NAG	O5-C1	-2.46	1.39	1.43
6	A	907	MAN	C2-C3	2.05	1.55	1.52

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	907	MAN	C1-C2-C3	-10.48	96.37	109.65
6	A	907	MAN	C1-O5-C5	-7.94	101.22	112.17
6	A	908	MAN	C1-O5-C5	-6.69	102.95	112.17
8	A	914	6C1	O1-B2-C4	-5.54	103.89	120.61
6	A	909	MAN	C1-O5-C5	-5.24	104.94	112.17

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, 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	780/879 (88%)	-0.14	22 (2%) 53 51	18, 33, 60, 86	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	400	LEU	6.1
1	A	556	MET	5.9
1	A	469	PHE	5.2
1	A	587	THR	5.0
1	A	586	SER	4.0

### 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	A	912	14/15	0.80	0.19	2.28	45,49,53,53	0
4	NAG	A	911	14/15	0.84	0.16	1.43	43,47,49,50	0
6	MAN	A	909	11/12	0.93	0.09	0.12	35,37,39,42	0
6	MAN	A	908	11/12	0.94	0.09	-0.27	32,34,35,36	0
4	NAG	A	905	14/15	0.93	0.08	-	27,31,38,38	0

### 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	A	912	14/15	0.80	0.19	2.28	45,49,53,53	0
7	ACT	A	913	4/4	0.98	0.10	1.43	33,35,36,38	0
4	NAG	A	911	14/15	0.84	0.16	1.43	43,47,49,50	0
4	NAG	A	910	14/15	0.88	0.17	0.13	48,52,57,58	0
6	MAN	A	909	11/12	0.93	0.09	0.12	35,37,39,42	0
8	6C1	A	914	18/18	0.92	0.10	-0.21	18,28,40,52	0
6	MAN	A	908	11/12	0.94	0.09	-0.27	32,34,35,36	0
4	NAG	A	904	14/15	0.98	0.11	-0.31	20,21,23,24	0
2	ZN	A	901	1/1	1.00	0.08	-0.32	24,24,24,24	0
6	MAN	A	907	11/12	0.92	0.08	-0.34	27,30,33,33	0
3	CA	A	903	1/1	0.99	0.09	-0.68	24,24,24,24	0
2	ZN	A	902	1/1	0.99	0.06	-2.04	25,25,25,25	0
4	NAG	A	905	14/15	0.93	0.08	-	27,31,38,38	0
5	BMA	A	906	11/12	0.91	0.09	-	28,30,34,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.