



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:35 AM GMT

PDB ID : 2XMC  
Title : G117H mutant of human butyrylcholinesterase in complex with fluoride anion  
Authors : Nachon, F.; Carletti, E.; Wandhammer, M.; Nicolet, Y.; Schopfer, L.M.; Masson, P.; Lockridge, O.  
Deposited on : 2010-07-27  
Resolution : 2.40 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

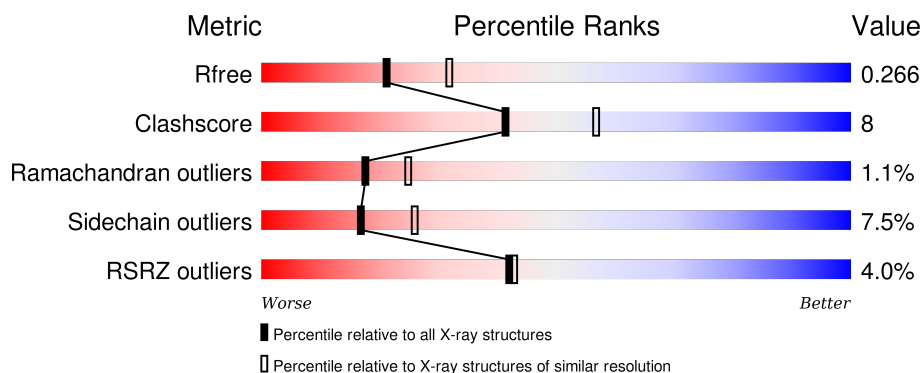
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	529	<div> <div>4%</div> <div>81%</div> <div>15%</div> <div>..</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
2	UNX	A	1531	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	A	1532	-	-	-	X
2	UNX	A	1535	-	-	-	X
2	UNX	A	1546	-	-	-	X
2	UNX	A	1547	-	-	-	X
7	FUC	A	1556	X	-	-	-
7	NAG	A	1562	-	-	-	X
7	FUC	A	1564	X	-	-	X
8	FUC	A	1558	X	-	-	X
9	NAG	A	1560	-	-	-	X
9	NAG	A	1561	X	-	-	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 4616 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 CHOLINESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	527	Total	C	N	O	S	0	1	0
			4216	2721	710	770	15			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLN	ASN	ENGINEERED MUTATION	UNP P06276
A	117	HIS	GLY	ENGINEERED MUTATION	UNP P06276
A	455	GLN	ASN	ENGINEERED MUTATION	UNP P06276
A	481	GLN	ASN	ENGINEERED MUTATION	UNP P06276
A	486	GLN	ASN	ENGINEERED MUTATION	UNP P06276

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	17	Total	X	0	0
			17	17		

- Molecule 3 is FLUORIDE ION (three-letter code: F) (formula: F).

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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	5	Total	Cl	0	0
			5	5		

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	K	0	0
			1	1		

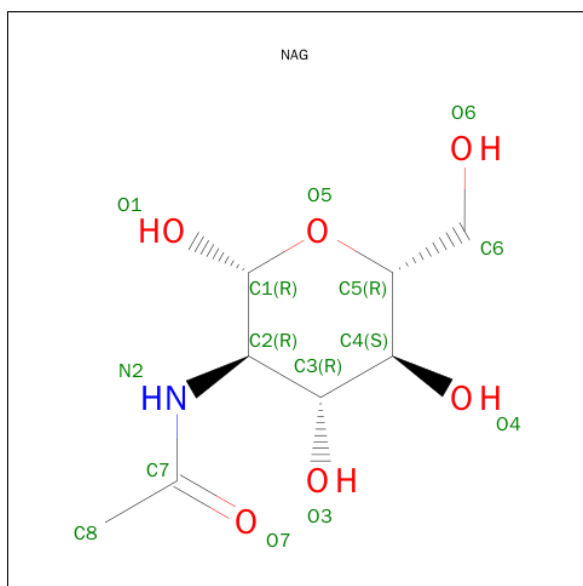
- Molecule 7 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	3	Total	C	N	O	0	0
			38	22	2	14		
7	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 8 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 9 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

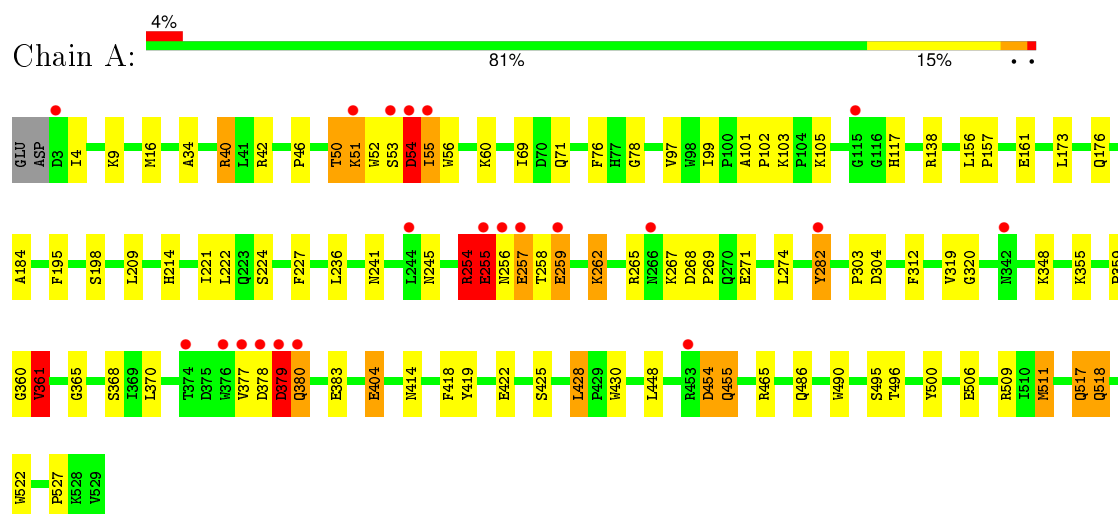
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	229	Total	O	0	0
			229	229		

### 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 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: CHOLINESTERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.59Å 155.59Å 127.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	109.76 – 2.40 41.14 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.7 (109.76-2.40) 96.7 (41.14-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.57 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.192 , 0.253 0.207 , 0.266	Depositor DCC
$R_{free}$ test set	980 reflections (3.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.8	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 41.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 29897 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4616	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NAG, F, UNX, K, CL, FUC, SO4

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	1.03	2/4340 (0.0%)	0.90	7/5892 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
7	A	2	0
8	A	1	0
All	All	3	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	490	TRP	CG-CD1	5.39	1.44	1.36
1	A	404	GLU	CG-CD	5.33	1.59	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	ARG	NE-CZ-NH2	-7.56	116.52	120.30
1	A	465	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	A	511	MET	CG-SD-CE	-5.84	90.85	100.20
1	A	448	LEU	CA-CB-CG	5.71	128.43	115.30
1	A	448	LEU	CB-CG-CD2	5.33	120.05	111.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	1556	FUC	C1
8	A	1558	FUC	C1
7	A	1564	FUC	C1

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	254	ARG	Peptide
1	A	255	GLU	Peptide
1	A	360	GLY	Peptide
1	A	380	GLN	Peptide
1	A	53	SER	Peptide

## 5.2 Too-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 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	4216	0	4111	71	0
2	A	17	0	0	2	0
3	A	1	0	0	0	0
4	A	5	0	0	0	0
5	A	5	0	0	0	0
6	A	1	0	0	0	0
7	A	76	0	68	4	0
8	A	24	0	22	0	0
9	A	42	0	39	0	0
10	A	229	0	0	15	0
All	All	4616	0	4240	73	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 8.

The worst 5 of 73 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:40:ARG:HG2	1:A:40:ARG:HH11	1.08	1.09
1:A:518:GLN:H	1:A:518:GLN:HE21	1.20	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:GLN:HG2	10:A:2034:HOH:O	1.73	0.88
1:A:117:HIS:HD2	10:A:2120:HOH:O	1.59	0.84
1:A:40:ARG:HG2	1:A:40:ARG:NH1	1.83	0.81

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	526/529 (99%)	492 (94%)	28 (5%)	6 (1%)	17 25

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	ASP
1	A	255	GLU
1	A	361	VAL
1	A	379	ASP
1	A	496	THR

### 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	454/455 (100%)	420 (92%)	34 (8%)	17 26

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	254	ARG
1	A	274	LEU
1	A	506	GLU
1	A	259	GLU
1	A	54	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	380	GLN
1	A	518	GLN
1	A	414	ASN
1	A	275	ASN
1	A	517	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 ⓘ

8 carbohydrates 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	$\# Z  > 2$
7	NAG	A	1554	1,7	14,14,15	0.86	0	15,19,21	2.41	7 (46%)
7	NAG	A	1555	7	14,14,15	0.83	0	15,19,21	2.28	6 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	FUC	A	1556	7	10,10,11	1.25	1 (10%)	14,14,16	3.29	8 (57%)
8	NAG	A	1557	1,8	14,14,15	1.16	1 (7%)	15,19,21	1.66	6 (40%)
8	FUC	A	1558	8	10,10,11	1.18	1 (10%)	14,14,16	2.28	6 (42%)
7	NAG	A	1562	1,7	14,14,15	0.97	1 (7%)	15,19,21	3.05	7 (46%)
7	NAG	A	1563	7	14,14,15	1.26	1 (7%)	15,19,21	2.38	7 (46%)
7	FUC	A	1564	7	10,10,11	0.82	0	14,14,16	2.53	6 (42%)

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
7	NAG	A	1554	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	1555	7	-	0/6/23/26	0/1/1/1
7	FUC	A	1556	7	1/1/4/5	0/0/17/20	0/1/1/1
8	NAG	A	1557	1,8	-	0/6/23/26	0/1/1/1
8	FUC	A	1558	8	1/1/4/5	0/0/17/20	0/1/1/1
7	NAG	A	1562	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	1563	7	-	0/6/23/26	0/1/1/1
7	FUC	A	1564	7	1/1/4/5	0/0/17/20	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1562	NAG	C2-N2	2.06	1.50	1.46
7	A	1556	FUC	C4-C5	2.28	1.57	1.52
8	A	1558	FUC	C2-C3	2.55	1.56	1.52
8	A	1557	NAG	C1-C2	2.90	1.56	1.52
7	A	1563	NAG	C1-C2	4.21	1.58	1.52

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1556	FUC	C1-C2-C3	-8.07	99.99	109.54
7	A	1556	FUC	C1-O5-C5	-5.27	104.23	112.38
7	A	1563	NAG	C3-C4-C5	-4.76	101.90	110.20
7	A	1564	FUC	C1-C2-C3	-4.57	104.13	109.54
7	A	1562	NAG	O7-C7-C8	-4.23	114.30	122.06

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	1564	FUC	C1
8	A	1558	FUC	C1
7	A	1556	FUC	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1562	NAG	4	0

## 5.6 Ligand geometry

Of 28 ligands modelled in this entry, 17 are unknown and 7 are monoatomic - leaving 4 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	SO4	A	1548	-	4,4,4	0.38	0	6,6,6	0.49	0
9	NAG	A	1559	1	14,14,15	0.72	0	15,19,21	2.84	5 (33%)
9	NAG	A	1560	1	14,14,15	0.71	0	15,19,21	2.65	4 (26%)
9	NAG	A	1561	1	14,14,15	0.89	0	15,19,21	2.94	5 (33%)

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	SO4	A	1548	-	-	0/0/0/0	0/0/0/0
9	NAG	A	1559	1	-	0/6/23/26	0/1/1/1
9	NAG	A	1560	1	-	0/6/23/26	0/1/1/1
9	NAG	A	1561	1	1/1/5/7	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
9	A	1559	NAG	C4-C3-C2	-4.61	104.07	111.23
9	A	1560	NAG	C4-C3-C2	-3.91	105.14	111.23
9	A	1561	NAG	O7-C7-C8	-2.05	118.29	122.06
9	A	1561	NAG	O4-C4-C5	2.31	115.36	109.24
9	A	1559	NAG	O4-C4-C3	2.59	116.16	110.34

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	A	1561	NAG	C1

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	527/529 (99%)	0.10	21 (3%) 42 43	26, 42, 74, 108	9 (1%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	379	ASP	4.8
1	A	377	VAL	4.3
1	A	255	GLU	4.3
1	A	282	TYR	4.2
1	A	378	ASP	4.2

### 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](#)

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
8	FUC	A	1558	10/11	0.87	0.33	5.32	66,70,73,73	0
7	NAG	A	1562	14/15	0.77	0.30	3.62	75,87,92,93	0
7	FUC	A	1564	10/11	0.87	0.34	2.62	89,91,92,93	0
7	NAG	A	1554	14/15	0.96	0.18	0.12	46,56,70,78	0
8	NAG	A	1557	14/15	0.87	0.23	-	56,64,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
7	FUC	A	1556	10/11	0.81	0.41	-	84,86,88,88	0
7	NAG	A	1555	14/15	0.79	0.23	-	76,83,87,88	0
7	NAG	A	1563	14/15	0.75	0.49	-	88,96,98,99	0

## 6.4 Ligands ⓘ

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( $\text{\AA}^2$ )	Q<0.9
2	UNX	A	1546	1/1	0.86	0.28	17.33	43,43,43,43	0
2	UNX	A	1535	1/1	0.94	0.34	8.26	35,35,35,35	0
2	UNX	A	1531	1/1	0.92	0.35	3.74	33,33,33,33	0
2	UNX	A	1532	1/1	0.96	0.35	3.47	38,38,38,38	0
2	UNX	A	1547	1/1	0.95	0.16	2.38	28,28,28,28	0
9	NAG	A	1560	14/15	0.77	0.22	2.02	69,77,83,85	0
2	UNX	A	1539	1/1	0.95	0.27	1.77	22,22,22,22	0
2	UNX	A	1537	1/1	0.89	0.20	1.30	28,28,28,28	0
3	F	A	1530	1/1	0.93	0.23	0.35	34,34,34,34	0
2	UNX	A	1540	1/1	0.96	0.08	-5.30	16,16,16,16	0
2	UNX	A	1541	1/1	0.94	0.07	-7.42	34,34,34,34	0
5	CL	A	1552	1/1	0.95	0.24	-	63,63,63,63	0
2	UNX	A	1534	1/1	0.97	0.43	-	24,24,24,24	0
2	UNX	A	1542	1/1	0.93	0.14	-	13,13,13,13	0
2	UNX	A	1543	1/1	0.95	0.16	-	23,23,23,23	0
5	CL	A	1550	1/1	0.81	0.19	-	72,72,72,72	0
2	UNX	A	1544	1/1	0.96	0.15	-	12,12,12,12	0
5	CL	A	1565	1/1	0.94	0.12	-	71,71,71,71	0
5	CL	A	1549	1/1	0.60	0.22	-	91,91,91,91	0
5	CL	A	1551	1/1	0.90	0.05	-	77,77,77,77	0
2	UNX	A	1533	1/1	0.96	0.41	-	23,23,23,23	0
9	NAG	A	1559	14/15	0.73	0.40	-	72,81,83,85	0
9	NAG	A	1561	14/15	0.58	0.53	-	80,90,95,95	0
2	UNX	A	1545	1/1	0.51	0.56	-	59,59,59,59	0
2	UNX	A	1536	1/1	0.94	0.23	-	51,51,51,51	0
6	K	A	1553	1/1	0.94	0.17	-	79,79,79,79	0
4	SO4	A	1548	5/5	0.94	0.33	-	68,68,69,71	0
2	UNX	A	1538	1/1	0.89	0.30	-	33,33,33,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.