



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:37 AM GMT

PDB ID : 2XQK  
Title : X-ray Structure of human butyrylcholinesterase inhibited by pure enantiomer VX-(S)  
Authors : Wandhammer, M.; Carletti, E.; Gillon, E.; Masson, P.; Goeldner, M.; Noort, D.; Nachon, F.  
Deposited on : 2010-09-02  
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.

---

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

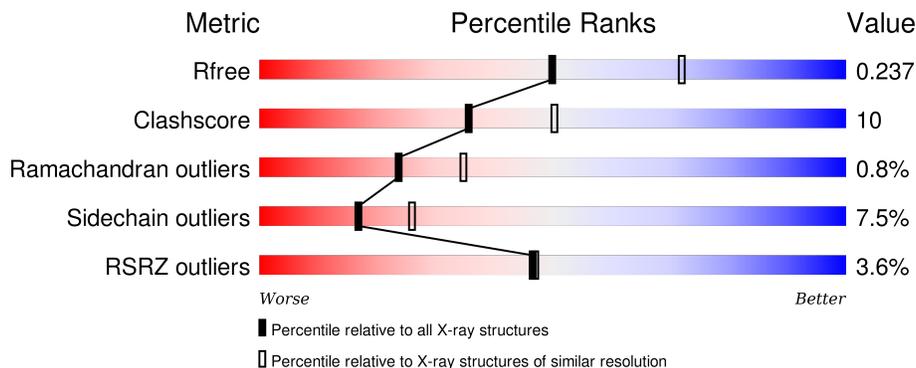
# 1 Overall quality at a glance

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	527	

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
10	FUC	A	1548	-	-	-	X

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
12	UNX	A	1553	-	-	-	X
12	UNX	A	1555	-	-	-	X
12	UNX	A	1570	-	-	-	X
5	CA	A	1534	-	-	-	X

## 2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 4771 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.

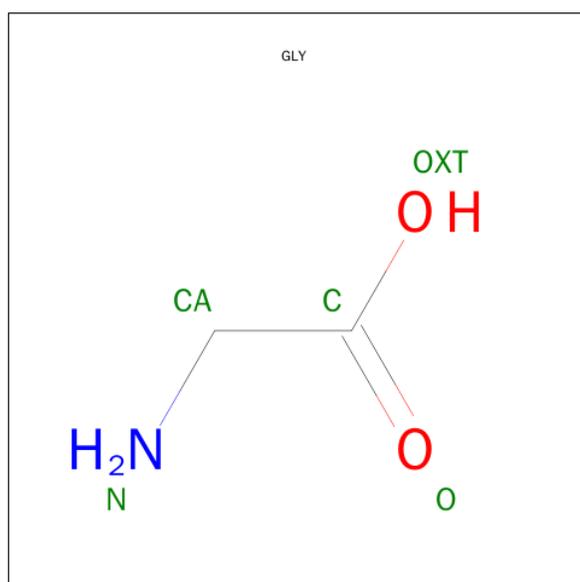
- Molecule 1 is a protein called CHOLINESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	527	4265	2755	713	781	16	0	10	0

There are 4 discrepancies between the modelled and reference sequences:

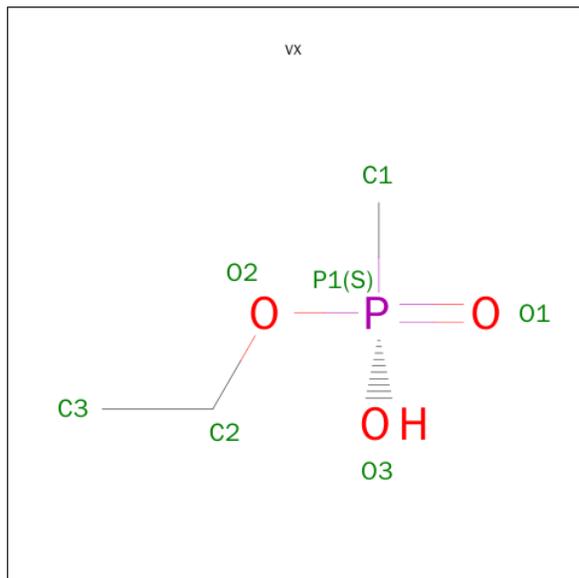
Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLN	ASN	ENGINEERED MUTATION	UNP P06276
A	455	GLN	ASN	ENGINEERED MUTATION	UNP P06276
A	481	GLN	ASN	ENGINEERED MUTATION	UNP P06276
A	486	GLN	ASN	ENGINEERED MUTATION	UNP P06276

- Molecule 2 is GLYCINE (three-letter code: GLY) (formula: C<sub>2</sub>H<sub>5</sub>NO<sub>2</sub>).



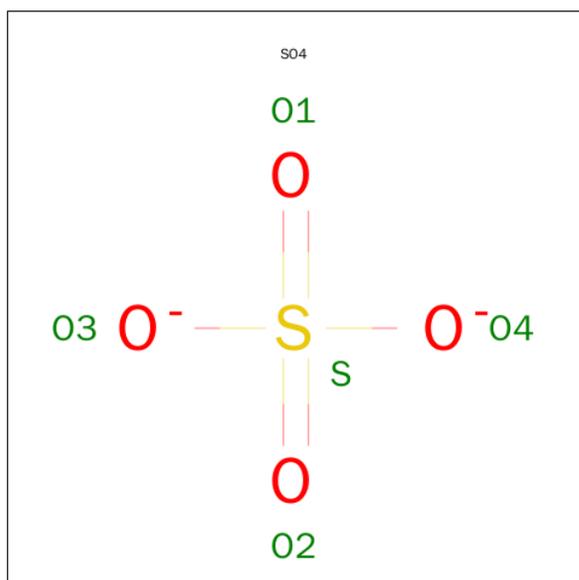
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	5	2	1	2	0	0

- Molecule 3 is O-ETHYLMETHYLPHOSPHONIC ACID ESTER GROUP (three-letter code: VX) (formula:  $C_3H_9O_3P$ ).



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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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

*Continued on next page...*

*Continued from previous page...*

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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total Cl 2 2	0	0

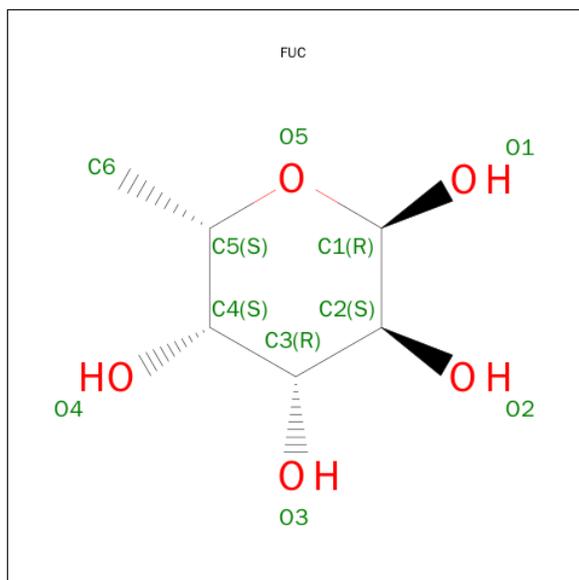
- Molecule 8 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 9 is a polymer of unknown type called SUGAR (2-MER).

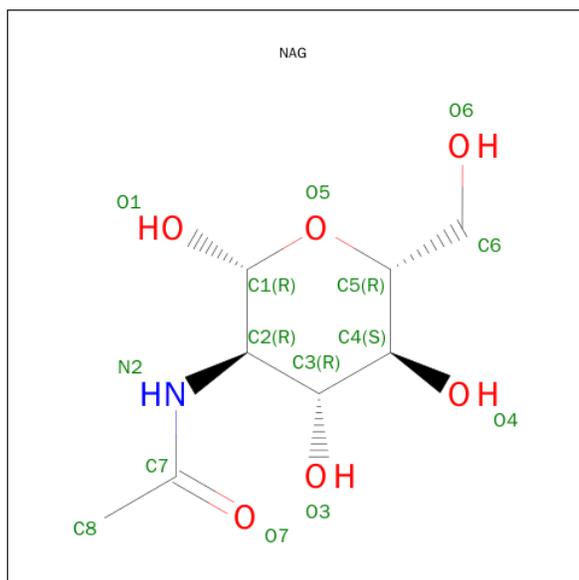
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	2	Total C N O 28 16 2 10	0	0

- Molecule 10 is SUGAR (ALPHA-L-FUCOSE) (three-letter code: FUC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			10	6	4		
10	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 11 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

*Continued on next page...*

*Continued from previous page...*

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

- Molecule 12 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	25	Total	X	0	0
			25	25		

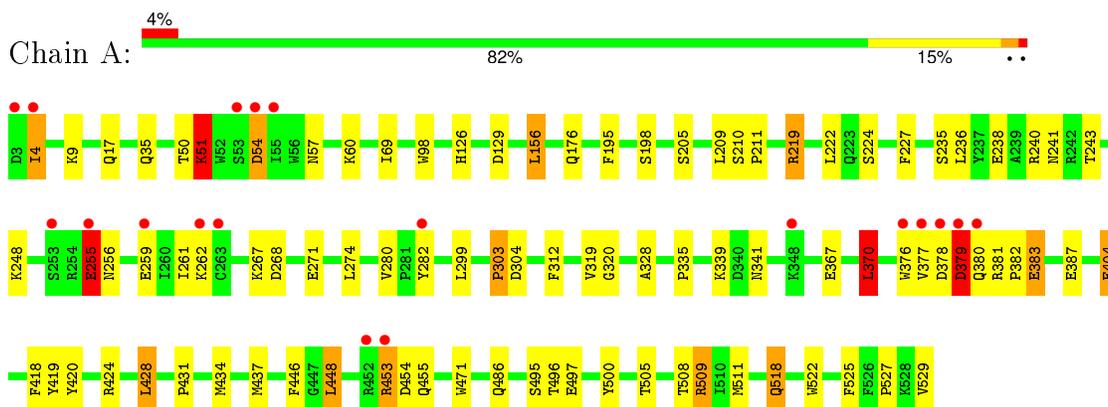
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	323	Total	O	0	0
			323	323		

### 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, $\alpha$ , $\beta$ , $\gamma$	154.92Å 154.92Å 127.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.53 – 2.40 41.53 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.5 (41.53-2.40) 99.5 (41.53-2.40)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.81 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.157 , 0.217 0.186 , 0.237	Depositor DCC
$R_{free}$ test set	1216 reflections (4.17%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.5	Xtrriage
Anisotropy	0.760	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.9	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Outliers	0 of 30392 reflections	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4771	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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, CL, UNX, NA, K, FUC, VX, CA, 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	1.13	5/4413 (0.1%)	0.94	5/5989 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	255	GLU	CB-CG	8.15	1.67	1.52
1	A	404	GLU	CG-CD	6.05	1.61	1.51
1	A	255	GLU	CG-CD	5.48	1.60	1.51
1	A	446	PHE	CE2-CZ	5.40	1.47	1.37
1	A	420	TYR	CE2-CZ	5.26	1.45	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	LEU	CA-CB-CG	7.65	132.90	115.30
1	A	219	ARG	NE-CZ-NH1	-7.15	116.72	120.30
1	A	448	LEU	CB-CG-CD2	5.69	120.68	111.00
1	A	219	ARG	CG-CD-NE	-5.41	100.44	111.80
1	A	448	LEU	CA-CB-CG	5.37	127.66	115.30

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	4265	0	4173	80	0
2	A	5	0	2	2	0
3	A	6	0	8	1	0
4	A	10	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	2	0	0	0	0
8	A	1	0	0	0	0
9	A	28	0	24	4	0
10	A	20	0	20	4	0
11	A	84	0	78	9	0
12	A	25	0	0	0	0
13	A	323	0	0	12	0
All	All	4771	0	4305	85	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 10.

The worst 5 of 85 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:241:ASN:HD21	11:A:1546:NAG:C1	1.38	1.36
1:A:4:ILE:H	1:A:4:ILE:HD12	1.10	1.16
1:A:241:ASN:ND2	11:A:1546:NAG:C1	2.08	1.15
1:A:453:ARG:HG3	1:A:453:ARG:NH1	1.52	1.12
1:A:4:ILE:N	1:A:4:ILE:HD12	1.69	1.07

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	535/527 (102%)	509 (95%)	22 (4%)	4 (1%)	26 38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	51	LYS
1	A	496	THR
1	A	379	ASP
1	A	54	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	462/452 (102%)	428 (93%)	34 (7%)	17 26

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

Mol	Chain	Res	Type
1	A	268	ASP
1	A	303	PRO
1	A	508	THR
1	A	280	VAL
1	A	69	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	214	HIS
1	A	518	GLN
1	A	275	ASN
1	A	71	GLN
1	A	241	ASN

### 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](#)

2 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
9	NAG	A	1539	1,9	14,14,15	0.97	0	15,19,21	1.87	2 (13%)
9	NAG	A	1540	9	14,14,15	0.75	0	15,19,21	2.69	6 (40%)

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
9	NAG	A	1539	1,9	-	0/6/23/26	0/1/1/1
9	NAG	A	1540	9	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
9	A	1540	NAG	C3-C4-C5	-6.61	98.67	110.20
9	A	1539	NAG	C3-C4-C5	-5.33	100.90	110.20
9	A	1540	NAG	C3-C2-N2	-4.61	99.53	110.56
9	A	1540	NAG	O6-C6-C5	-2.64	102.61	111.33
9	A	1540	NAG	O4-C4-C5	2.34	115.44	109.24

There are no chirality outliers.

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
9	A	1539	NAG	4	0

## 5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 25 are unknown and 5 are monoatomic - leaving 12 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	$\# Z  > 2$
3	VX	A	1530	1	1,5,6	0.93	0	1,5,8	0.55	0
2	GLY	A	1531	-	1,4,4	0.73	0	0,4,4	0.00	-
4	SO4	A	1532	-	4,4,4	0.32	0	6,6,6	0.57	0
4	SO4	A	1533	-	4,4,4	0.16	0	6,6,6	0.28	0
10	FUC	A	1541	-	10,10,11	0.89	0	14,14,16	2.17	6 (42%)
11	NAG	A	1542	1	14,14,15	1.24	1 (7%)	15,19,21	2.07	6 (40%)
11	NAG	A	1543	-	14,14,15	0.74	0	15,19,21	1.76	4 (26%)
11	NAG	A	1544	1	14,14,15	0.85	0	15,19,21	2.04	1 (6%)
11	NAG	A	1545	-	14,14,15	0.59	0	15,19,21	1.25	2 (13%)
11	NAG	A	1546	-	14,14,15	0.50	0	15,19,21	1.41	2 (13%)
11	NAG	A	1547	-	14,14,15	0.68	0	15,19,21	1.72	3 (20%)
10	FUC	A	1548	-	10,10,11	0.66	0	14,14,16	1.37	2 (14%)

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
3	VX	A	1530	1	-	0/1/3/4	0/0/0/0
2	GLY	A	1531	-	-	0/0/2/2	0/0/0/0
4	SO4	A	1532	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1533	-	-	0/0/0/0	0/0/0/0
10	FUC	A	1541	-	-	0/0/17/20	0/1/1/1
11	NAG	A	1542	1	-	0/6/23/26	0/1/1/1
11	NAG	A	1543	-	-	0/6/23/26	0/1/1/1
11	NAG	A	1544	1	-	0/6/23/26	0/1/1/1
11	NAG	A	1545	-	-	0/6/23/26	0/1/1/1
11	NAG	A	1546	-	-	0/6/23/26	0/1/1/1
11	NAG	A	1547	-	-	0/6/23/26	0/1/1/1
10	FUC	A	1548	-	-	0/0/17/20	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	1542	NAG	C1-C2	3.26	1.57	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	1543	NAG	O7-C7-C8	-2.99	116.58	122.06
11	A	1542	NAG	C3-C4-C5	-2.59	105.68	110.20
11	A	1542	NAG	O7-C7-C8	-2.10	118.21	122.06
11	A	1546	NAG	O7-C7-C8	-2.05	118.31	122.06
10	A	1541	FUC	O5-C5-C4	2.09	113.16	109.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1530	VX	1	0
2	A	1531	GLY	2	0
10	A	1541	FUC	3	0
11	A	1543	NAG	2	0
11	A	1545	NAG	4	0
11	A	1546	NAG	3	0
10	A	1548	FUC	1	0

## 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	527/527 (100%)	0.08	19 (3%) 46 47	22, 37, 66, 91	15 (2%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	255	GLU	4.6
1	A	377	VAL	4.4
1	A	378	ASP	4.2
1	A	54	ASP	4.2
1	A	3	ASP	3.5

### 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
9	NAG	A	1539	14/15	0.97	0.22	0.42	37,50,54,60	0
9	NAG	A	1540	14/15	0.80	0.27	-	67,78,82,82	0

## 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
12	UNX	A	1553	1/1	0.89	0.55	10.51	20,20,20,20	0
12	UNX	A	1555	1/1	0.74	0.40	6.12	41,41,41,41	0
12	UNX	A	1570	1/1	0.83	0.23	4.01	28,28,28,28	0
10	FUC	A	1548	10/11	0.78	0.39	3.09	78,83,85,85	0
5	CA	A	1534	1/1	0.89	0.17	2.73	79,79,79,79	0
11	NAG	A	1546	14/15	0.87	0.31	1.70	101,106,113,113	0
12	UNX	A	1554	1/1	0.96	0.19	1.23	43,43,43,43	0
11	NAG	A	1544	14/15	0.75	0.25	0.50	53,69,76,77	0
3	VX	A	1530	6/7	0.98	0.19	0.21	28,34,49,54	0
4	SO4	A	1532	5/5	0.97	0.14	-0.62	28,29,33,34	5
4	SO4	A	1533	5/5	0.95	0.15	-0.79	68,68,70,71	5
2	GLY	A	1531	5/5	0.96	0.07	-2.73	41,43,45,46	0
12	UNX	A	1557	1/1	0.68	0.21	-	24,24,24,24	0
12	UNX	A	1565	1/1	0.70	0.43	-	31,31,31,31	0
11	NAG	A	1545	14/15	0.76	0.38	-	109,114,115,116	0
12	UNX	A	1556	1/1	0.86	0.16	-	14,14,14,14	0
7	CL	A	1537	1/1	0.94	0.06	-	68,68,68,68	0
12	UNX	A	1549	1/1	0.74	0.19	-	42,42,42,42	0
8	K	A	1538	1/1	0.87	0.12	-	91,91,91,91	1
12	UNX	A	1559	1/1	0.79	0.47	-	35,35,35,35	0
12	UNX	A	1568	1/1	0.87	0.27	-	19,19,19,19	0
12	UNX	A	1569	1/1	0.90	0.38	-	20,20,20,20	0
12	UNX	A	1566	1/1	0.85	0.30	-	34,34,34,34	0
12	UNX	A	1563	1/1	0.92	0.09	-	34,34,34,34	0
12	UNX	A	1558	1/1	0.90	0.36	-	37,37,37,37	0
12	UNX	A	1562	1/1	0.85	0.14	-	28,28,28,28	0
12	UNX	A	1564	1/1	0.66	0.35	-	39,39,39,39	0
12	UNX	A	1572	1/1	0.88	0.26	-	18,18,18,18	0
11	NAG	A	1547	14/15	0.58	0.55	-	126,131,132,132	0
12	UNX	A	1561	1/1	0.55	0.23	-	37,37,37,37	0
7	CL	A	1536	1/1	0.85	0.07	-	81,81,81,81	0
10	FUC	A	1541	10/11	0.84	0.28	-	84,87,88,88	0
11	NAG	A	1543	14/15	0.68	0.32	-	92,99,101,102	0
12	UNX	A	1550	1/1	0.59	0.30	-	23,23,23,23	0
12	UNX	A	1560	1/1	0.83	0.30	-	23,23,23,23	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
11	NAG	A	1542	14/15	0.77	0.26	-	56,65,68,68	0
12	UNX	A	1571	1/1	0.96	0.22	-	28,28,28,28	0
12	UNX	A	1551	1/1	0.28	0.71	-	39,39,39,39	0
12	UNX	A	1552	1/1	0.80	0.72	-	17,17,17,17	0
12	UNX	A	1573	1/1	0.87	0.37	-	32,32,32,32	0
12	UNX	A	1567	1/1	0.92	0.33	-	10,10,10,10	0
6	NA	A	1535	1/1	0.90	0.29	-	42,42,42,42	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.