



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 02:20 PM EDT

PDB ID : 6YN9  
Title : MALT1(329-728) in complex with a sulfonamide containing compound  
Authors : Renatus, M.  
Deposited on : 2020-04-11  
Resolution : 2.56 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 : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
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) : 2.37.1

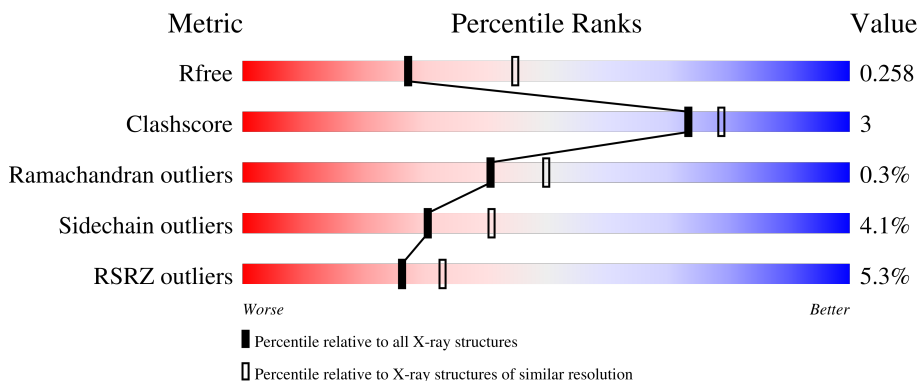
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.56 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	1279 (2.58-2.54)
Clashscore	141614	1327 (2.58-2.54)
Ramachandran outliers	138981	1312 (2.58-2.54)
Sidechain outliers	138945	1312 (2.58-2.54)
RSRZ outliers	127900	1269 (2.58-2.54)

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	404	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 2943 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.

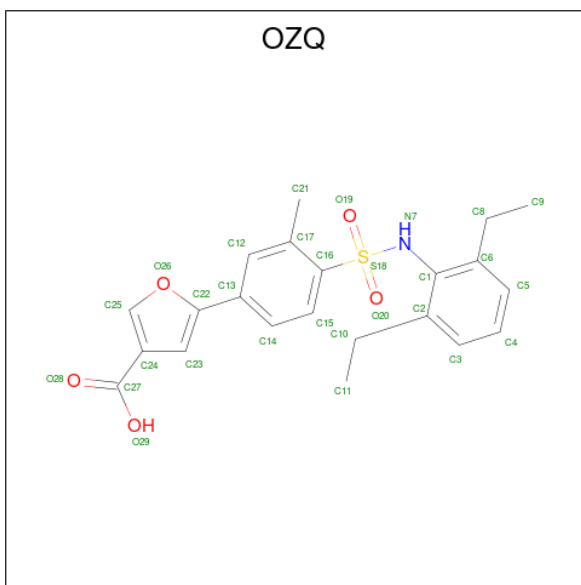
- Molecule 1 is a protein called Mucosa-associated lymphoid tissue lymphoma translocation protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	359	2848	1828	460	540	20	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	GLY	-	expression tag	UNP Q9UDY8
A	326	PRO	-	expression tag	UNP Q9UDY8
A	327	GLY	-	expression tag	UNP Q9UDY8
A	328	SER	-	expression tag	UNP Q9UDY8

- Molecule 2 is 5-[4-[(2,6-diethylphenyl)sulfamoyl]-3-methyl-phenyl]furan-3-carboxylic acid (three-letter code: OZQ) (formula: C<sub>22</sub>H<sub>23</sub>NO<sub>5</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	29	22	1	5	1	0	0

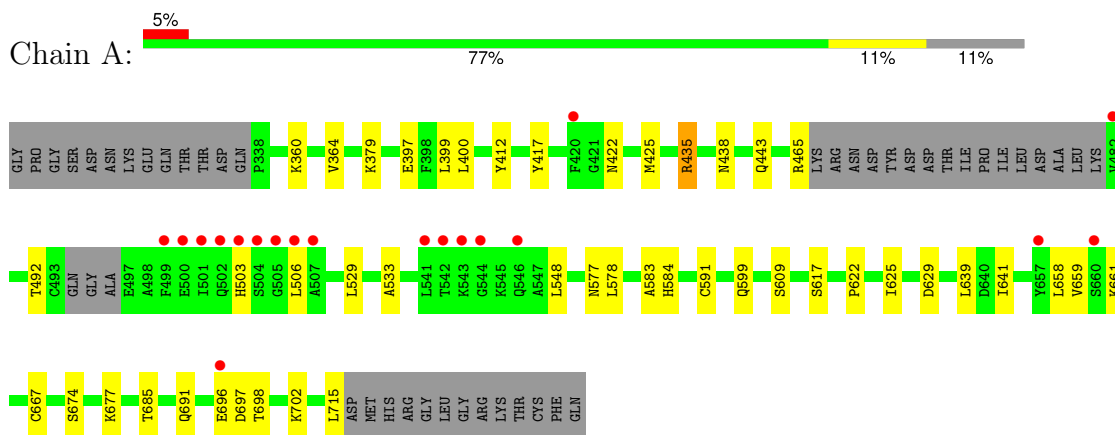
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	66	Total	O	0	0
			66	66		

### 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: Mucosa-associated lymphoid tissue lymphoma translocation protein 1



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.39Å 70.12Å 56.74Å 90.00° 91.64° 90.00°	Depositor
Resolution (Å)	56.06 – 2.56 56.06 – 2.56	Depositor EDS
% Data completeness (in resolution range)	99.2 (56.06-2.56) 99.2 (56.06-2.56)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 2.55Å)	Xtrriage
Refinement program	BUSTER 2.11.7 (6-FEB-2020)	Depositor
R, $R_{free}$	0.202 , 0.251 0.208 , 0.258	Depositor DCC
$R_{free}$ test set	577 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.5	Xtrriage
Anisotropy	0.180	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 38.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.039 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2943	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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: OZQ

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	0.37	0/2900	0.59	0/3919

There are no bond length outliers.

There are no bond angle outliers.

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	2848	0	2873	19	0
2	A	29	0	0	1	0
3	A	66	0	0	0	0
All	All	2943	0	2873	19	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.

All (19) 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:435:ARG:HG3	1:A:438:ASN:HD22	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:ASN:HD22	1:A:443:GLN:HG3	1.57	0.69
1:A:583:ALA:HB2	1:A:715:LEU:HD21	1.81	0.62
1:A:622:PRO:HD2	1:A:625:ILE:HD12	1.82	0.61
1:A:465:ARG:HE	1:A:492:THR:HG21	1.66	0.60
1:A:364:VAL:HG21	1:A:506:LEU:HB3	1.85	0.58
1:A:685:THR:HG21	1:A:702:LYS:HE3	1.89	0.54
1:A:397:GLU:HG2	2:A:801:OZQ:C21	2.40	0.52
1:A:379:LYS:HE3	1:A:577:ASN:ND2	2.25	0.51
1:A:674:SER:HB2	1:A:677:LYS:HD2	1.95	0.49
1:A:584:HIS:HE1	1:A:609:SER:OG	1.95	0.48
1:A:639:LEU:HB3	1:A:641:ILE:HD12	1.97	0.47
1:A:422:ASN:HD22	1:A:443:GLN:CG	2.28	0.46
1:A:691:GLN:HG2	1:A:698:THR:HG22	1.99	0.45
1:A:412:TYR:CD2	1:A:425:MET:HG2	2.52	0.44
1:A:591:CYS:HB3	1:A:599:GLN:HE21	1.82	0.43
1:A:533:ALA:HB2	1:A:548:LEU:HD23	2.02	0.41
1:A:617:SER:HB2	1:A:667:CYS:SG	2.61	0.41
1:A:639:LEU:HB3	1:A:641:ILE:CD1	2.50	0.41

There are no symmetry-related clashes.

## 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	353/404 (87%)	343 (97%)	9 (2%)	1 (0%)	<span style="border: 1px solid red; padding: 2px;">41</span> <span style="border: 1px solid gray; padding: 2px;">50</span>

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	659	VAL



### 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	319/357 (89%)	306 (96%)	13 (4%)	30 41

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	360	LYS
1	A	399	LEU
1	A	400	LEU
1	A	417	TYR
1	A	435	ARG
1	A	503	HIS
1	A	529	LEU
1	A	578	LEU
1	A	629	ASP
1	A	658	LEU
1	A	661	LYS
1	A	696	GLU
1	A	697	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	352	ASN
1	A	422	ASN
1	A	438	ASN
1	A	485	ASN
1	A	508	ASN
1	A	565	GLN
1	A	577	ASN
1	A	579	GLN
1	A	584	HIS
1	A	599	GLN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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
2	OZQ	A	801	-	28,31,31	1.90	7 (25%)	38,45,45	1.82	8 (21%)

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	OZQ	A	801	-	-	0/19/23/23	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	OZQ	C23-C22	-4.41	1.33	1.38
2	A	801	OZQ	O28-C27	3.65	1.33	1.22
2	A	801	OZQ	C25-C24	-3.53	1.32	1.37
2	A	801	OZQ	C13-C22	2.94	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	OZQ	O29-C27	-2.92	1.21	1.30
2	A	801	OZQ	S18-N7	2.71	1.67	1.63
2	A	801	OZQ	O20-S18	2.27	1.46	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	OZQ	C16-S18-N7	-4.90	101.53	107.30
2	A	801	OZQ	O20-S18-O19	-4.88	113.59	119.52
2	A	801	OZQ	C17-C16-S18	3.13	124.79	122.02
2	A	801	OZQ	C1-N7-S18	3.00	127.17	121.89
2	A	801	OZQ	O19-S18-N7	2.95	113.93	106.74
2	A	801	OZQ	C12-C17-C16	2.91	118.98	116.99
2	A	801	OZQ	C15-C16-C17	-2.69	118.73	121.17
2	A	801	OZQ	C2-C1-N7	2.00	121.36	119.02

There are no chirality outliers.

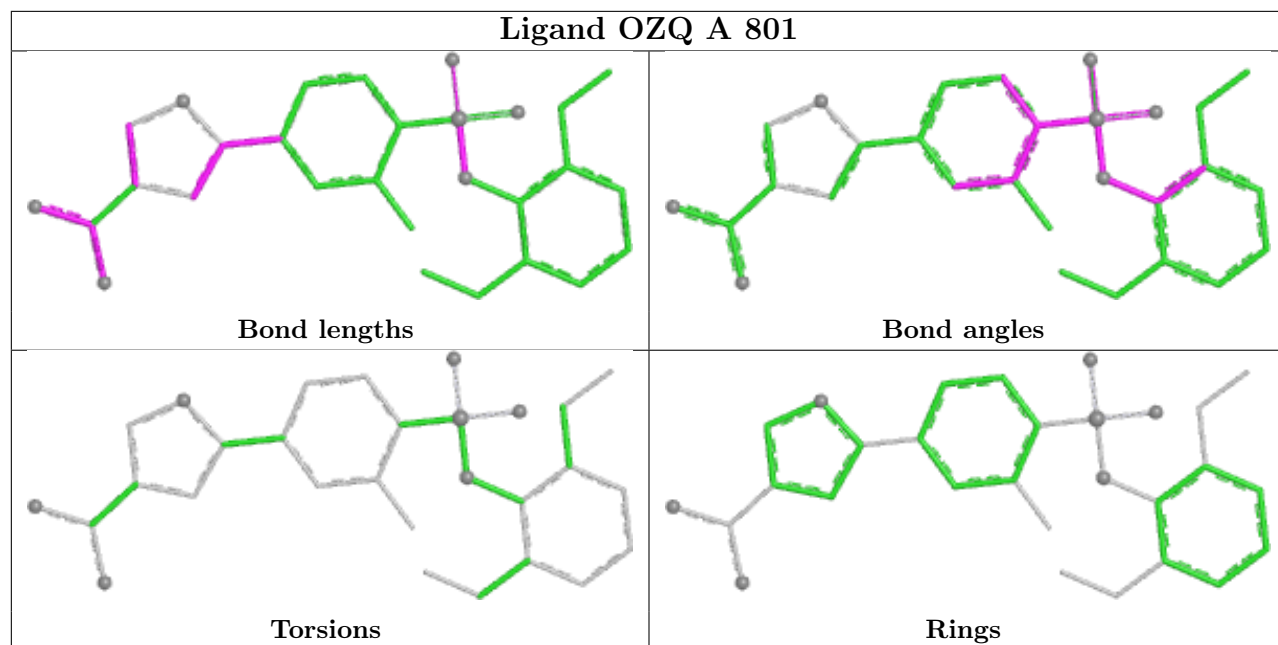
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	OZQ	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	359/404 (88%)	0.16	19 (5%) 26 33	23, 41, 75, 101	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	501	ILE	6.2
1	A	505	GLY	5.2
1	A	544	GLY	4.8
1	A	502	GLN	4.6
1	A	506	LEU	4.6
1	A	504	SER	4.4
1	A	507	ALA	4.3
1	A	542	THR	4.1
1	A	500	GLU	4.0
1	A	696	GLU	3.7
1	A	541	LEU	3.7
1	A	660	SER	3.6
1	A	503	HIS	3.3
1	A	482	VAL	3.1
1	A	546	GLN	3.1
1	A	499	PHE	3.1
1	A	657	TYR	2.8
1	A	420	PHE	2.5
1	A	543	LYS	2.4

### 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](#)

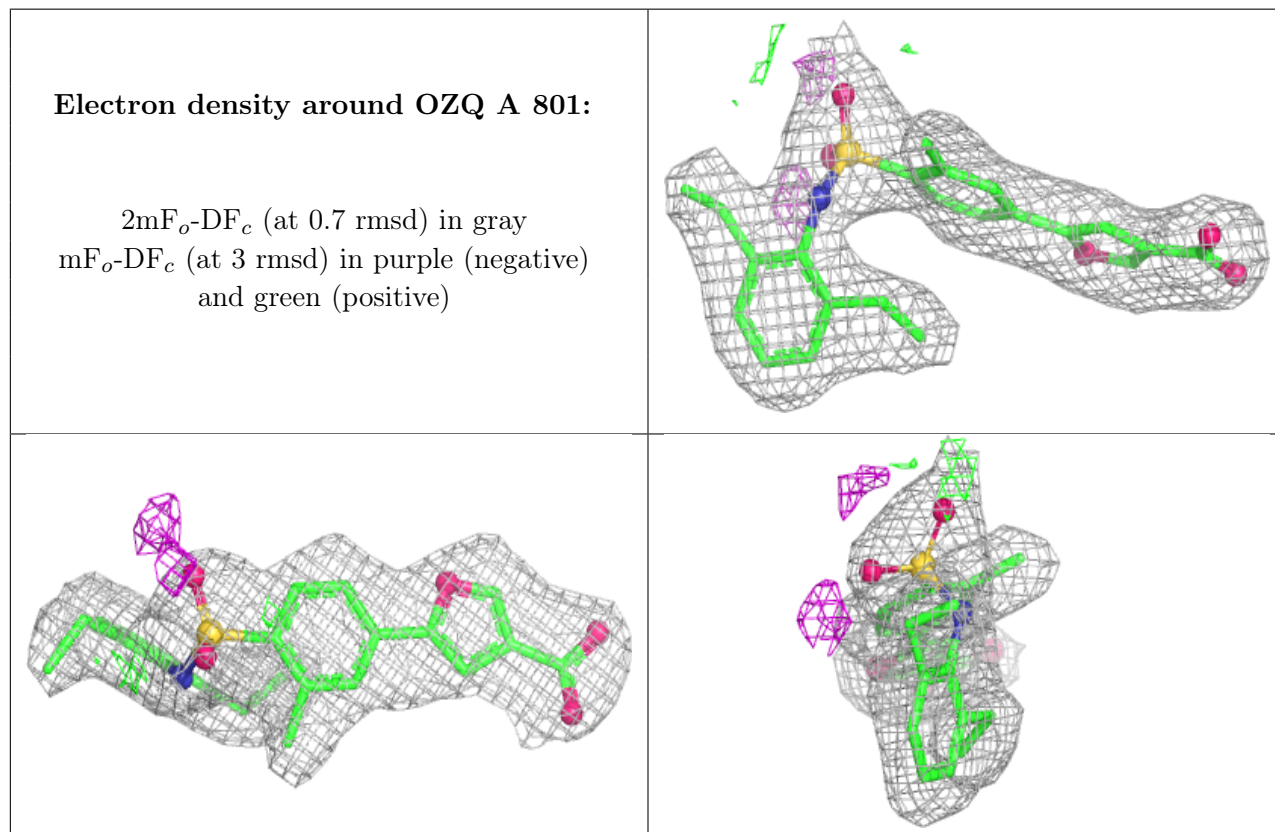
There are no monosaccharides in this entry.

### 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	OZQ	A	801	29/29	0.96	0.14	28,31,32,33	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.