



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:34 AM UTC

PDB ID : 7UVM / pdb\_00007uvm  
Title : Crystal structure of human ClpP protease in complex with TR-27  
Authors : Mabanglo, M.F.; Houry, W.A.  
Deposited on : 2022-05-02  
Resolution : 2.19 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

<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)  
Xtrriage (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

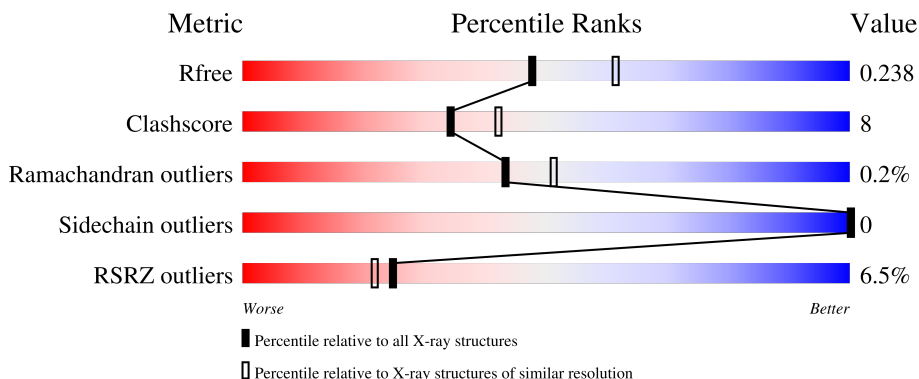
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.19 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.



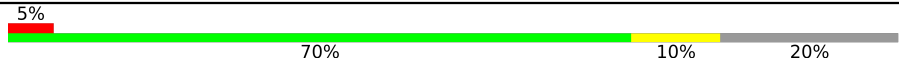

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	221	 4% 66% 12% 21%
1	B	221	 4% 71% 7% 22%
1	C	221	 5% 64% 14% 22%
1	D	221	 5% 71% 7% 21%
1	E	221	 6% 70% 9% 21%

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Mol	Chain	Length	Quality of chain
1	F	221	 5% 70% 10% 20%
1	G	221	 6% 68% 10% 21%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 20131 atoms, of which 9967 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.

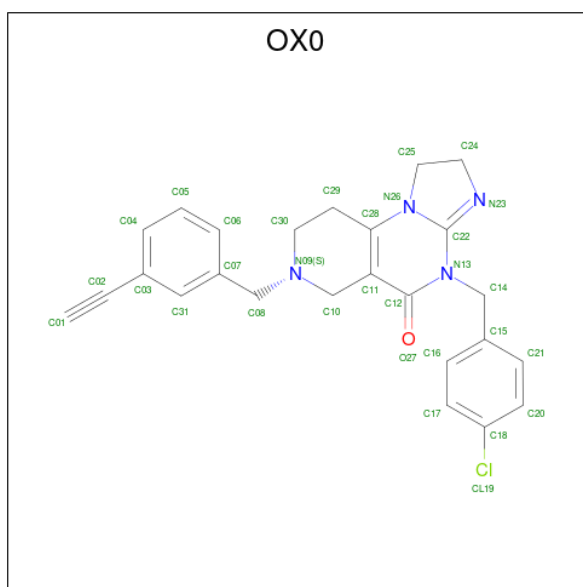
- Molecule 1 is a protein called ATP-dependent Clp protease proteolytic subunit, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	174	2756	867	1398	232	246	13	0	0	0
1	B	173	2732	861	1387	228	243	13	0	0	0
1	C	173	2742	864	1389	231	245	13	0	0	0
1	D	175	2771	872	1406	233	247	13	0	0	0
1	E	175	2761	869	1403	230	246	13	0	0	0
1	F	177	2806	882	1424	235	251	14	0	1	0
1	G	174	2757	867	1399	232	246	13	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	57	SER	-	cloning artifact	UNP Q16740
B	57	SER	-	cloning artifact	UNP Q16740
C	57	SER	-	cloning artifact	UNP Q16740
D	57	SER	-	cloning artifact	UNP Q16740
E	57	SER	-	cloning artifact	UNP Q16740
F	57	SER	-	cloning artifact	UNP Q16740
G	57	SER	-	cloning artifact	UNP Q16740

- Molecule 2 is (10R)-4-[(4-chlorophenyl)methyl]-7-[(3-ethynylphenyl)methyl]-2,4,6,7,8,9-hexahydroimidazo[1,2-a]pyrido[3,4-e]pyrimidin-5(1H)-one (CCD ID: OX0) (formula: C<sub>25</sub>H<sub>23</sub>ClN<sub>4</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Cl	H	N			O
2	A	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		
2	B	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		
2	C	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		
2	D	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		
2	E	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		
2	F	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		
2	G	1	Total	C	Cl	H	N	O	0	0
			54	25	1	23	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	52	Total	O	0	0
			52	52		
3	B	62	Total	O	0	0
			62	62		
3	C	64	Total	O	0	0
			64	64		
3	D	70	Total	O	0	0
			70	70		
3	E	63	Total	O	0	0
			63	63		

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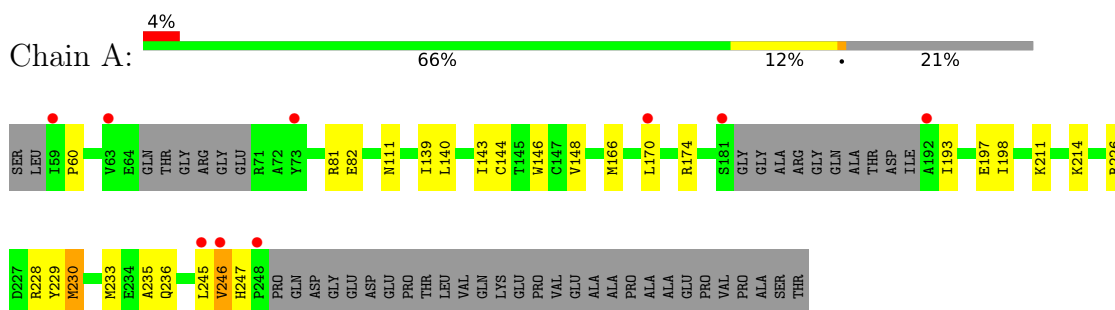
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	F	63	Total 63	O 63	0	0
3	G	54	Total 54	O 54	0	0

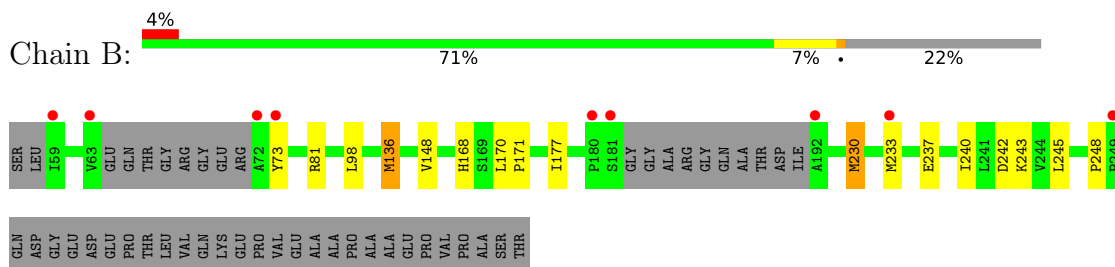
### 3 Residue-property plots [i](#)

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.

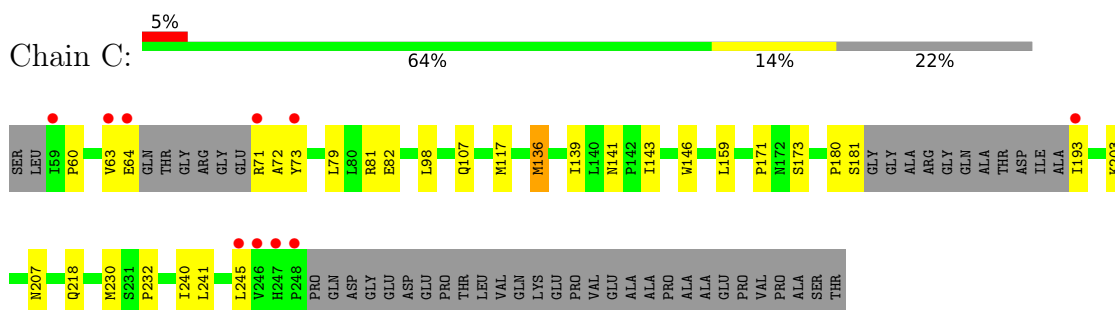
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



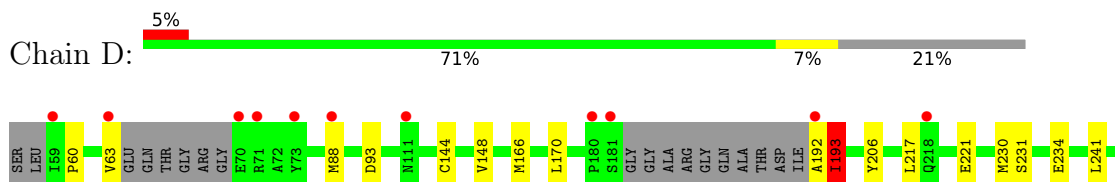
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

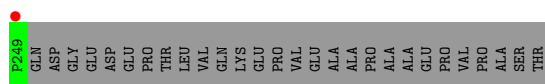


- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

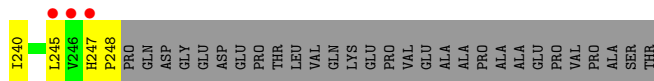


- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial

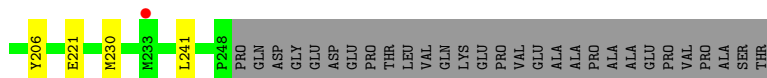




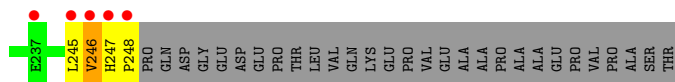
- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



- Molecule 1: ATP-dependent Clp protease proteolytic subunit, mitochondrial



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.15Å 153.72Å 105.10Å 90.00° 117.76° 90.00°	Depositor
Resolution (Å)	29.40 – 2.19 29.40 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.40-2.19) 99.2 (29.40-2.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.29 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.197 , 0.237 0.199 , 0.238	Depositor DCC
$R_{free}$ test set	2000 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.2	Xtrriage
Anisotropy	0.171	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 33.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20131	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.13% 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: OX0

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	0.59	1/1382 (0.1%)	0.74	1/1868 (0.1%)
1	B	0.64	1/1370 (0.1%)	0.74	1/1854 (0.1%)
1	C	0.60	0/1377	0.79	1/1861 (0.1%)
1	D	0.61	0/1390	0.78	2/1880 (0.1%)
1	E	0.64	1/1381 (0.1%)	0.76	0/1867
1	F	0.67	1/1409 (0.1%)	0.78	2/1904 (0.1%)
1	G	0.60	1/1382 (0.1%)	0.81	3/1868 (0.2%)
All	All	0.62	5/9691 (0.1%)	0.77	10/13102 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	136	MET	CG-SD	12.31	2.11	1.80
1	B	136	MET	CG-SD	9.38	2.04	1.80
1	A	246	VAL	C-N	5.68	1.40	1.32
1	G	136	MET	CG-SD	5.64	1.94	1.80
1	E	176	MET	SD-CE	-5.30	1.66	1.79

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	110	SER	CA-C-N	6.91	131.75	120.63
1	G	110	SER	C-N-CA	6.91	131.75	120.63
1	D	193	ILE	N-CA-C	5.91	121.63	109.34
1	F	230	MET	CB-CG-SD	-5.61	95.87	112.70
1	C	136	MET	CB-CG-SD	-5.45	96.36	112.70

There are no chirality outliers.

There are no planarity outliers.

## 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	1358	1398	1398	21	0
1	B	1345	1387	1386	22	0
1	C	1353	1389	1393	33	0
1	D	1365	1406	1405	18	0
1	E	1358	1403	1401	28	0
1	F	1382	1424	1423	27	0
1	G	1358	1399	1398	19	0
2	A	31	23	0	1	0
2	B	31	23	0	1	0
2	C	31	23	0	1	0
2	D	31	23	0	0	0
2	E	31	23	0	1	0
2	F	31	23	0	0	0
2	G	31	23	0	0	0
3	A	52	0	0	0	0
3	B	62	0	0	1	0
3	C	64	0	0	2	0
3	D	70	0	0	2	0
3	E	63	0	0	1	0
3	F	63	0	0	1	0
3	G	54	0	0	0	0
All	All	10164	9967	9804	149	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 149 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:B:136:MET:CG	1:B:136:MET:SD	2.04	1.46
1:F:136:MET:CG	1:F:136:MET:SD	2.11	1.39
1:E:163:THR:OG1	1:E:166:MET:HE2	1.45	1.15
1:E:148:VAL:HG12	1:E:170:LEU:HD12	1.23	1.08
1:E:163:THR:OG1	1:E:166:MET:CE	2.02	1.08

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	168/221 (76%)	161 (96%)	7 (4%)	0	100	100
1	B	167/221 (76%)	163 (98%)	4 (2%)	0	100	100
1	C	167/221 (76%)	163 (98%)	4 (2%)	0	100	100
1	D	169/221 (76%)	165 (98%)	3 (2%)	1 (1%)	21	23
1	E	167/221 (76%)	162 (97%)	5 (3%)	0	100	100
1	F	172/221 (78%)	169 (98%)	3 (2%)	0	100	100
1	G	168/221 (76%)	161 (96%)	6 (4%)	1 (1%)	21	23
All	All	1178/1547 (76%)	1144 (97%)	32 (3%)	2 (0%)	43	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	193	ILE
1	G	246	VAL

#### 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	151/185 (82%)	151 (100%)	0	100	100
1	B	150/185 (81%)	150 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	151/185 (82%)	151 (100%)	0	100	100
1	D	152/185 (82%)	152 (100%)	0	100	100
1	E	151/185 (82%)	151 (100%)	0	100	100
1	F	154/185 (83%)	154 (100%)	0	100	100
1	G	151/185 (82%)	151 (100%)	0	100	100
All	All	1060/1295 (82%)	1060 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	204	GLN
1	G	172	ASN
1	C	137	GLN
1	C	178	HIS
1	C	218	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

7 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
2	OX0	B	301	-	35,35,35	7.03	18 (51%)	43,50,50	1.99	13 (30%)
2	OX0	G	301	-	35,35,35	7.06	17 (48%)	43,50,50	2.29	13 (30%)
2	OX0	D	301	-	35,35,35	6.87	16 (45%)	43,50,50	2.26	13 (30%)
2	OX0	E	301	-	35,35,35	7.03	16 (45%)	43,50,50	2.25	13 (30%)
2	OX0	F	301	-	35,35,35	6.99	16 (45%)	43,50,50	2.19	14 (32%)
2	OX0	C	301	-	35,35,35	7.14	17 (48%)	43,50,50	2.38	17 (39%)
2	OX0	A	301	-	35,35,35	7.21	17 (48%)	43,50,50	2.31	11 (25%)

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	OX0	B	301	-	-	2/10/25/25	0/5/5/5
2	OX0	G	301	-	-	0/10/25/25	0/5/5/5
2	OX0	D	301	-	-	0/10/25/25	0/5/5/5
2	OX0	E	301	-	-	0/10/25/25	0/5/5/5
2	OX0	F	301	-	-	0/10/25/25	0/5/5/5
2	OX0	C	301	-	-	0/10/25/25	0/5/5/5
2	OX0	A	301	-	-	0/10/25/25	0/5/5/5

The worst 5 of 117 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	OX0	C22-N23	34.77	1.55	1.28
2	A	301	OX0	C22-N23	34.68	1.55	1.28
2	E	301	OX0	C22-N23	33.95	1.54	1.28
2	B	301	OX0	C22-N23	33.93	1.54	1.28
2	G	301	OX0	C22-N23	33.82	1.54	1.28

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	OX0	C24-C25-N26	7.88	106.99	101.30
2	G	301	OX0	C29-C30-N09	7.86	118.20	111.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	OX0	C24-C25-N26	7.51	106.73	101.30
2	C	301	OX0	C29-C30-N09	6.75	117.22	111.19
2	B	301	OX0	C29-C30-N09	6.39	116.89	111.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

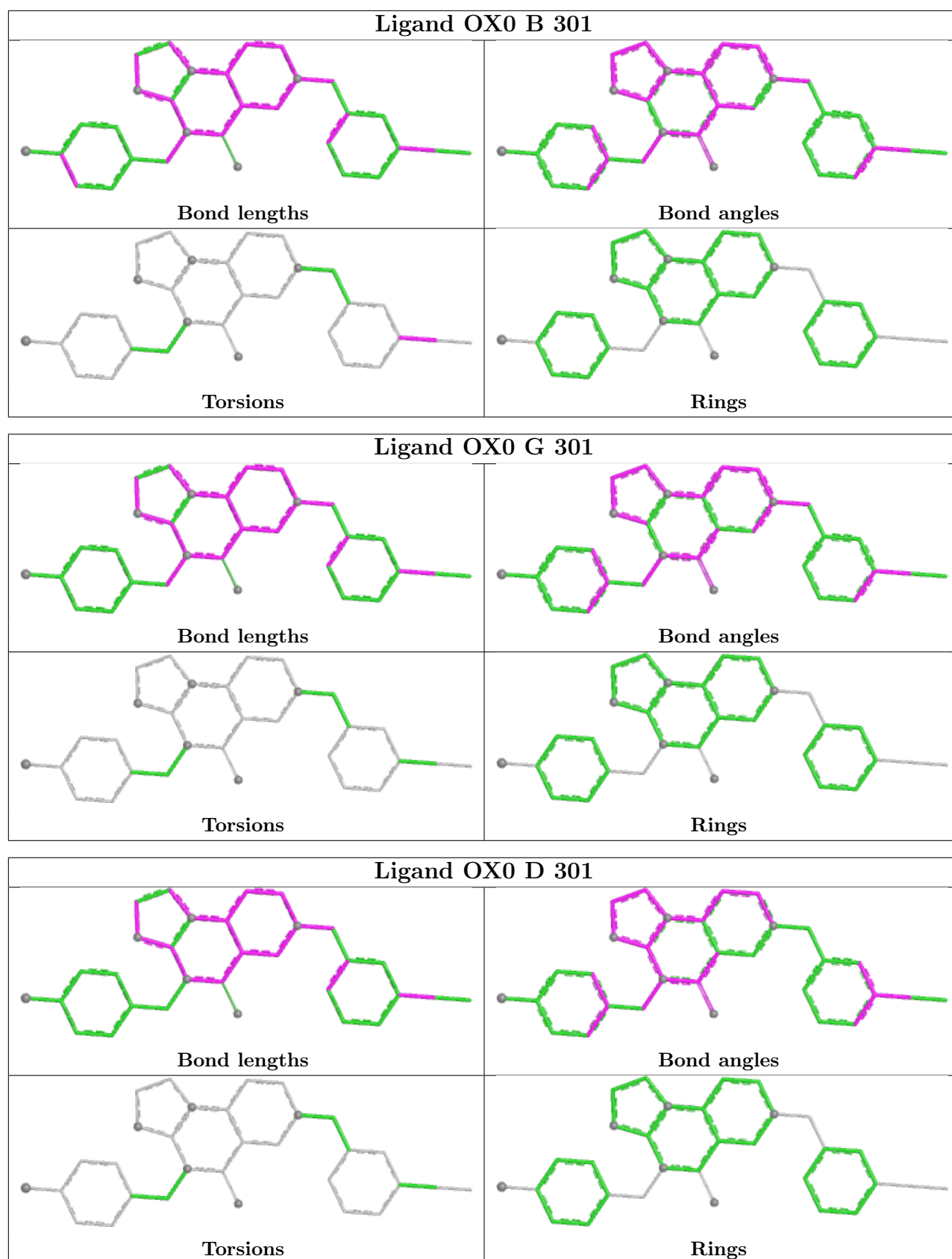
Mol	Chain	Res	Type	Atoms
2	B	301	OX0	C01-C02-C03-C31
2	B	301	OX0	C01-C02-C03-C04

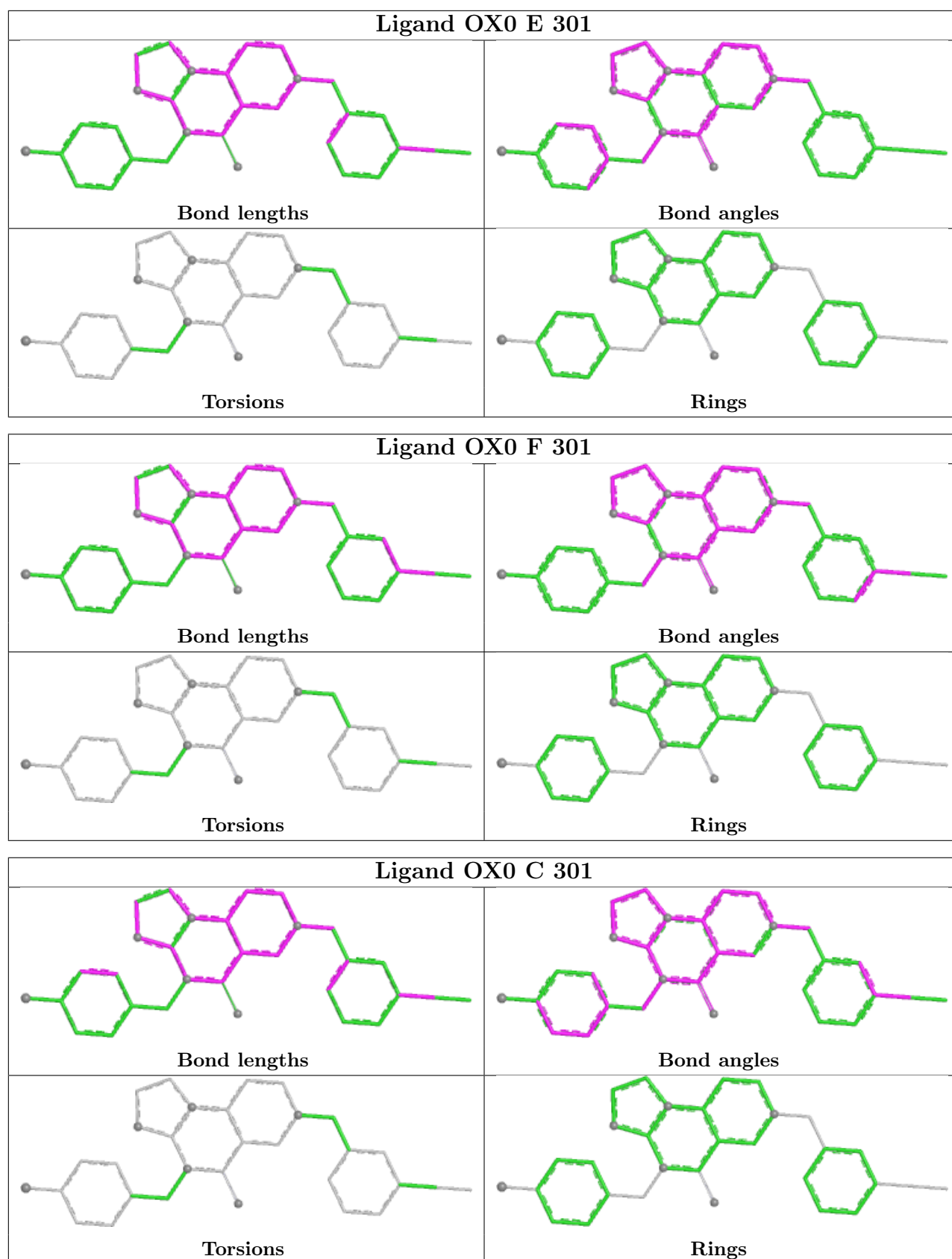
There are no ring outliers.

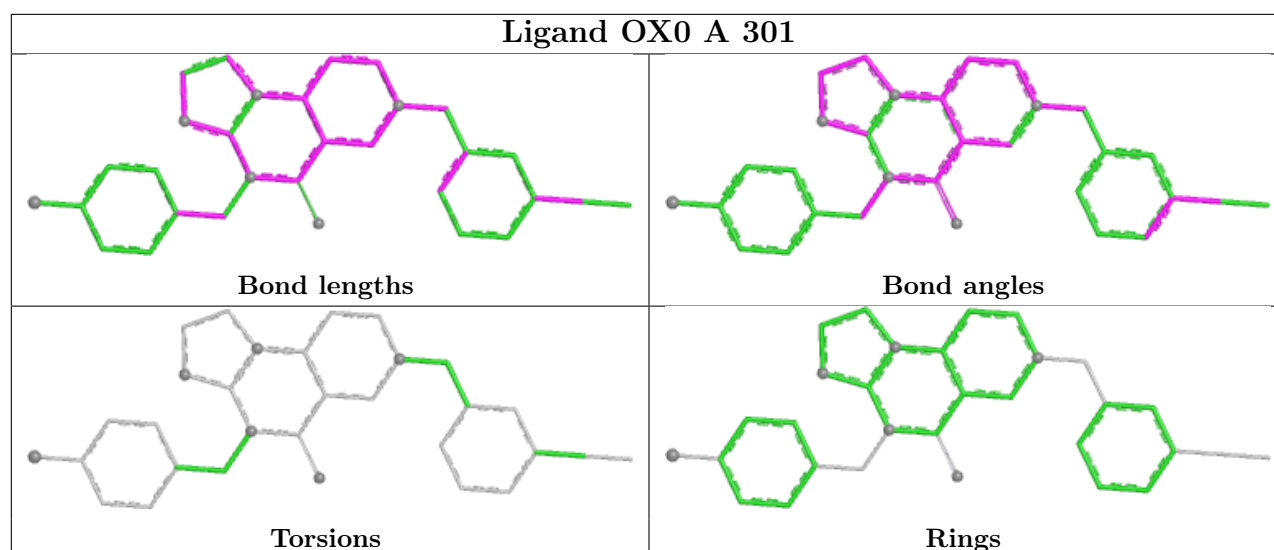
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	OX0	1	0
2	E	301	OX0	1	0
2	C	301	OX0	1	0
2	A	301	OX0	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	174/221 (78%)	0.32	9 (5%) 33 29	33, 45, 80, 99	0
1	B	173/221 (78%)	0.13	9 (5%) 33 29	30, 41, 69, 84	0
1	C	173/221 (78%)	0.26	10 (5%) 29 25	30, 42, 71, 121	0
1	D	175/221 (79%)	0.26	12 (6%) 23 20	31, 41, 73, 106	0
1	E	175/221 (79%)	0.28	13 (7%) 20 18	33, 42, 76, 107	0
1	F	177/221 (80%)	0.17	12 (6%) 23 20	23, 41, 84, 106	1 (0%)
1	G	174/221 (78%)	0.26	14 (8%) 18 16	34, 45, 70, 128	0
All	All	1221/1547 (78%)	0.24	79 (6%) 25 22	23, 43, 75, 128	1 (0%)

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	72	ALA	5.9
1	C	73	TYR	5.6
1	C	246	VAL	4.9
1	D	73	TYR	4.9
1	E	63	VAL	4.9

### 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](#)

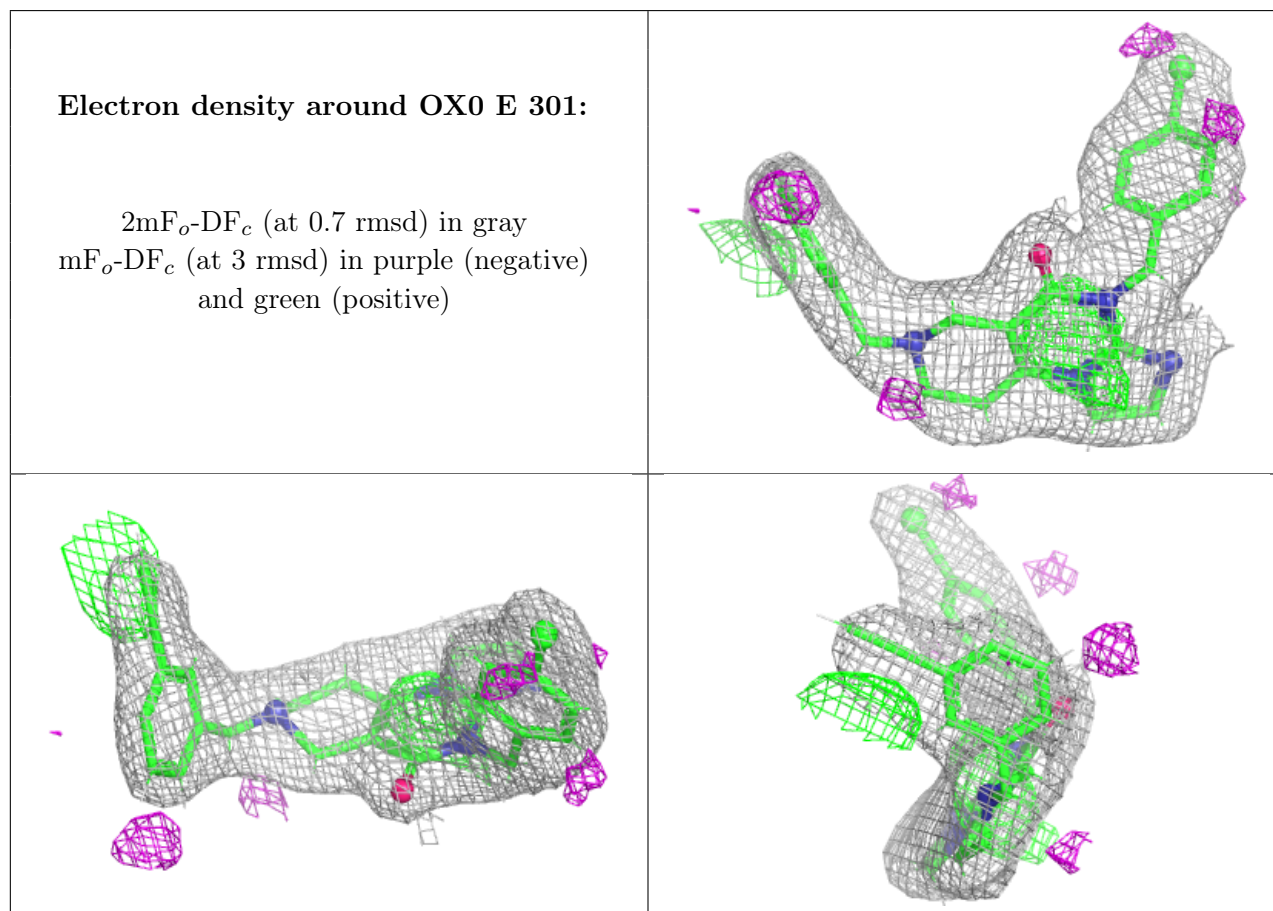
There are no oligosaccharides in this entry.

## 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.

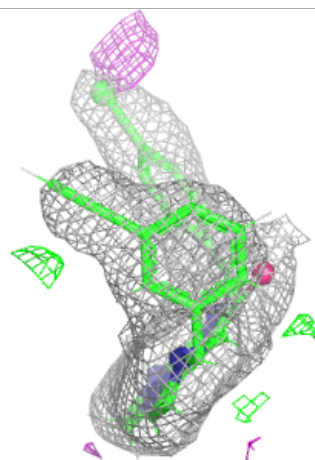
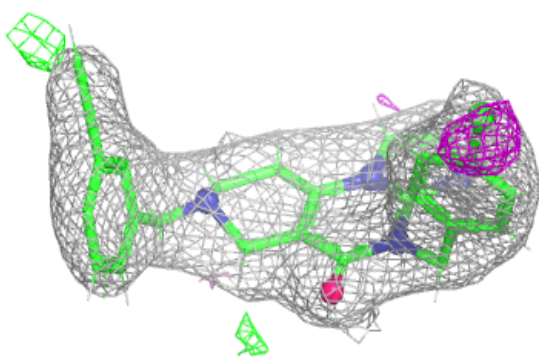
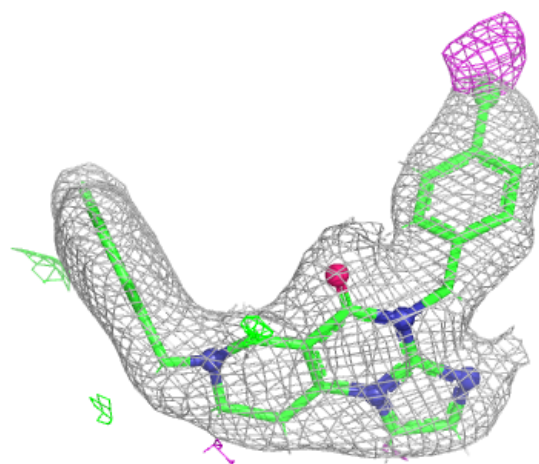
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	OX0	E	301	31/31	0.90	0.12	33,42,51,65	0
2	OX0	A	301	31/31	0.91	0.12	41,50,63,71	0
2	OX0	F	301	31/31	0.91	0.12	35,44,54,64	0
2	OX0	C	301	31/31	0.92	0.11	34,42,55,65	0
2	OX0	D	301	31/31	0.92	0.10	34,43,56,59	0
2	OX0	G	301	31/31	0.92	0.10	35,43,54,68	0
2	OX0	B	301	31/31	0.93	0.11	34,44,55,65	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.



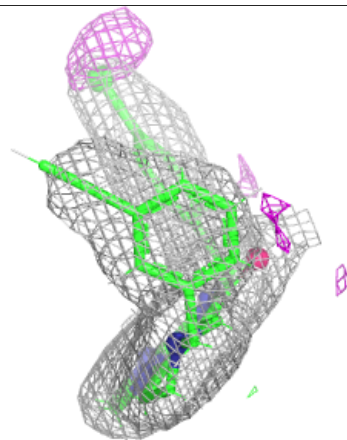
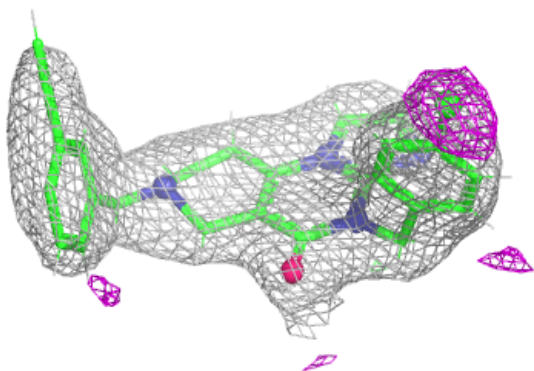
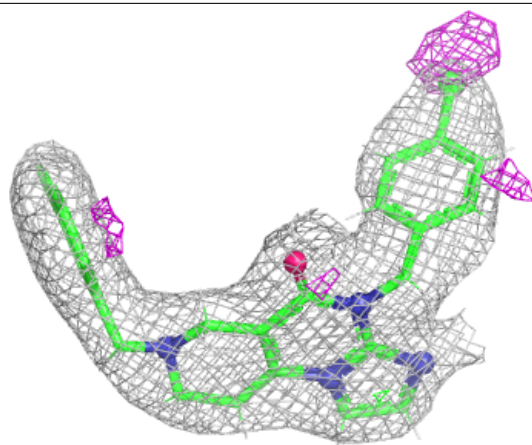
**Electron density around OX0 A 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



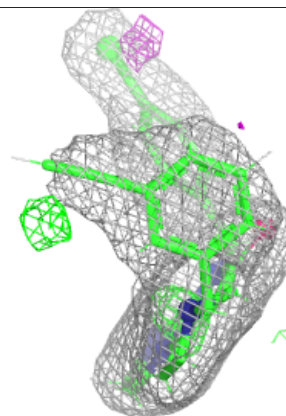
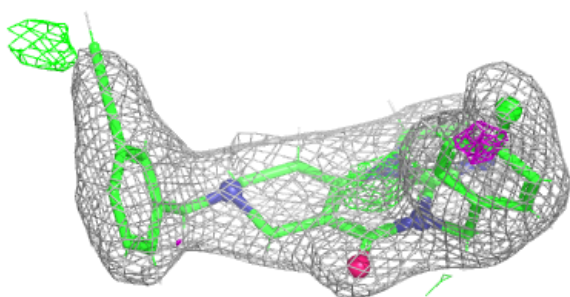
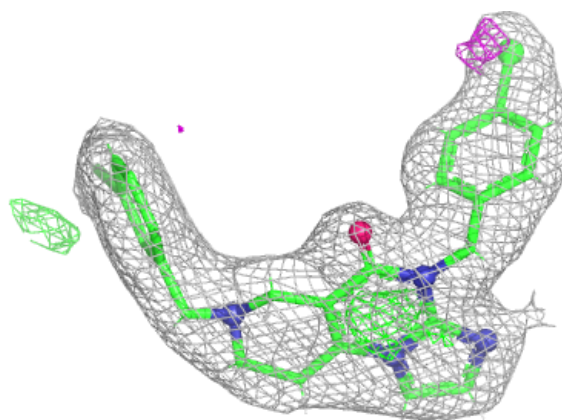
**Electron density around OX0 F 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

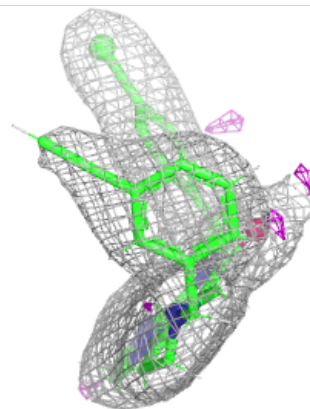
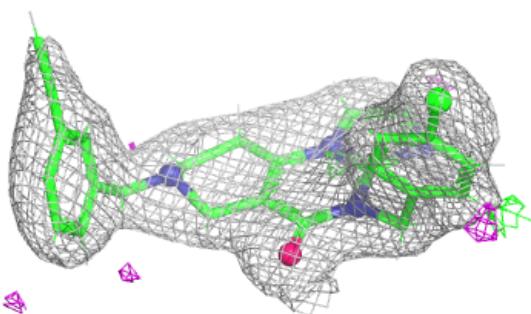
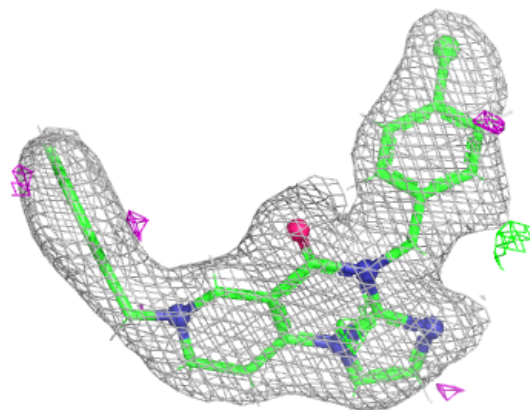


**Electron density around OX0 C 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

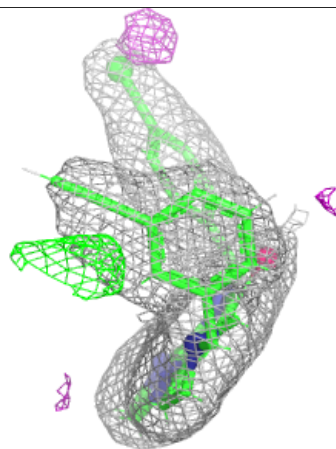
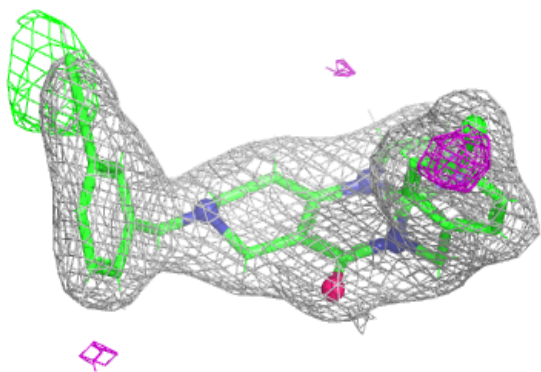
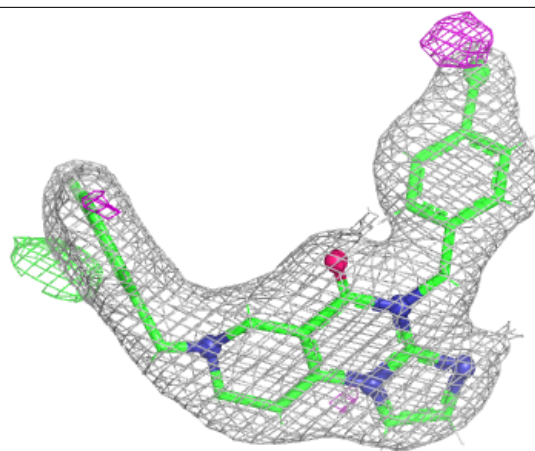
**Electron density around OX0 D 301:**

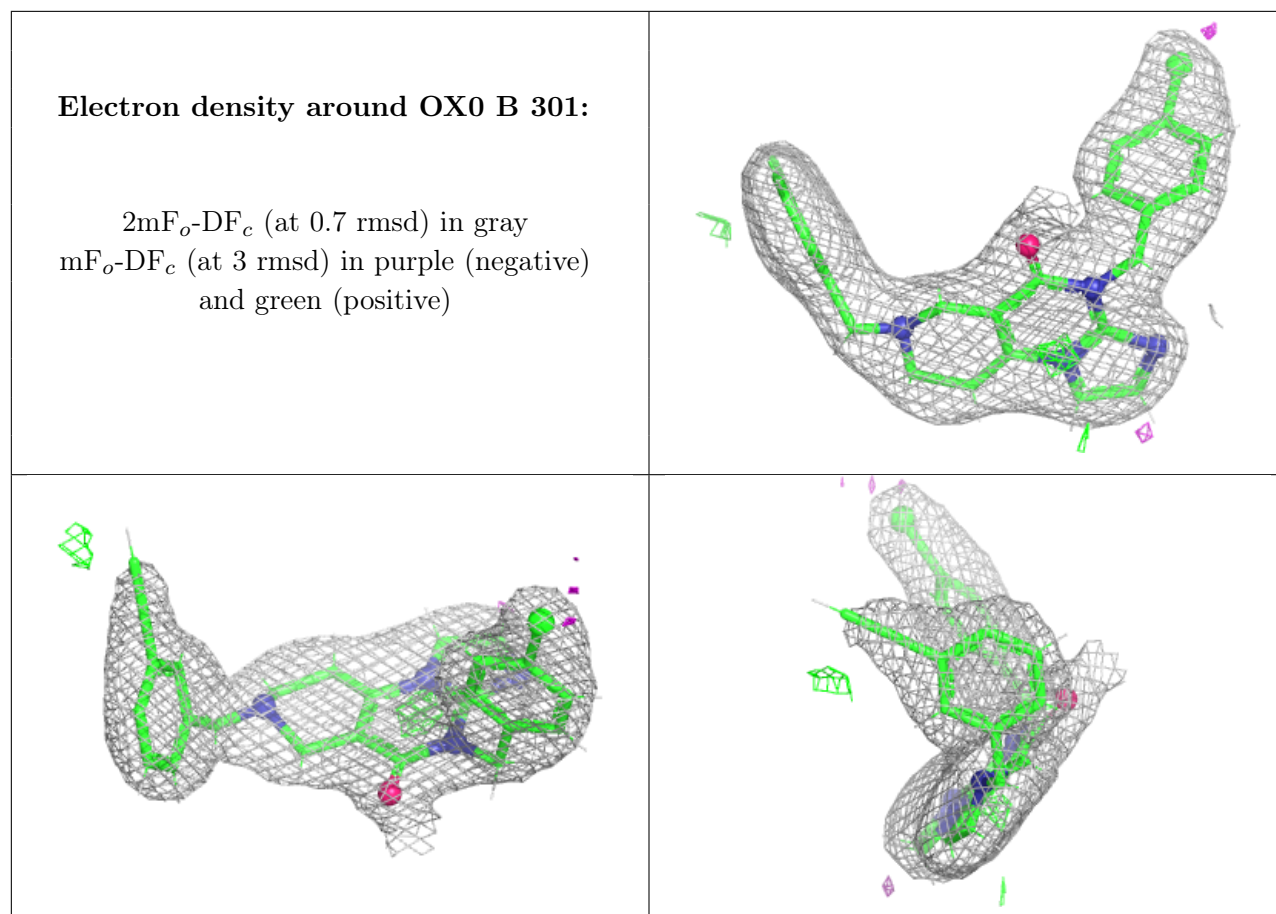
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around OX0 G 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.