



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2025 – 10:06 AM EDT

PDB ID : 9NT6 / pdb\_00009nt6  
Title : Crystal structure of ecLacI transcription factor ancestor 4 bound to Beta-met  
hyl-D-galactoside  
Authors : Georgelin, R.L.; Frkic, R.L.; Tan, L.; Kaczmariski, J.; Jackson, C.J.  
Deposited on : 2025-03-18  
Resolution : 1.50 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 : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

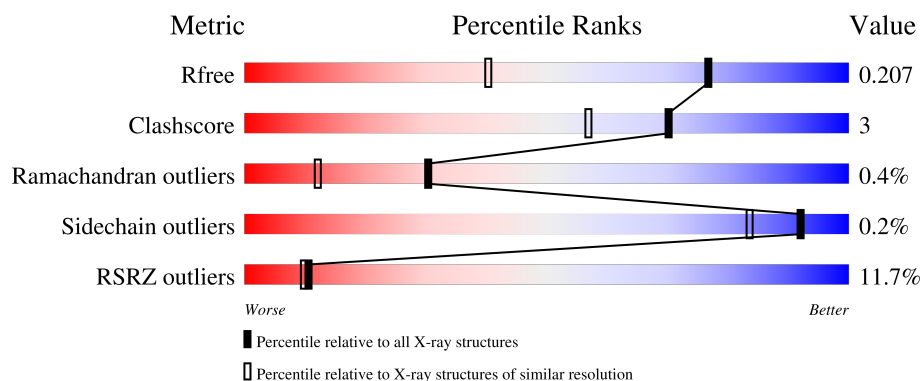
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 1.50 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))
$R_{free}$	164625	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (1.50-1.50)

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	281	 <p>4% 89% 7% .</p>
1	B	281	 <p>19% 90% 9% .</p>

## 2 Entry composition [i](#)

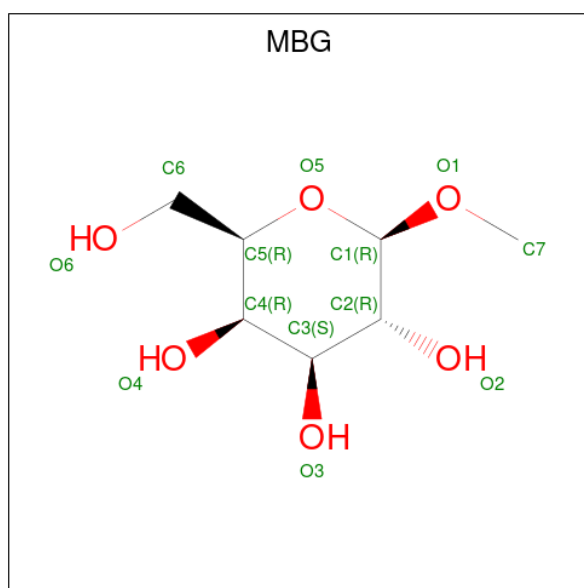
There are 4 unique types of molecules in this entry. The entry contains 4746 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 LacI Transcription Factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	12	0
			2129	1338	380	401	10			
1	B	277	Total	C	N	O	S	0	7	0
			2140	1347	381	402	10			

- Molecule 2 is methyl beta-D-galactopyranoside (CCD ID: MBG) (formula:  $C_7H_{14}O_6$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	1
			26	14	12		
2	B	1	Total	C	O	0	1
			26	14	12		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula:  $C_2H_6O_2$ ).



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

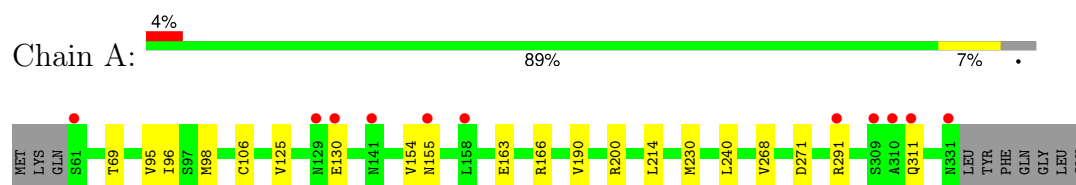
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	234	Total	O	0	0
			234	234		
4	B	175	Total	O	0	0
			175	175		

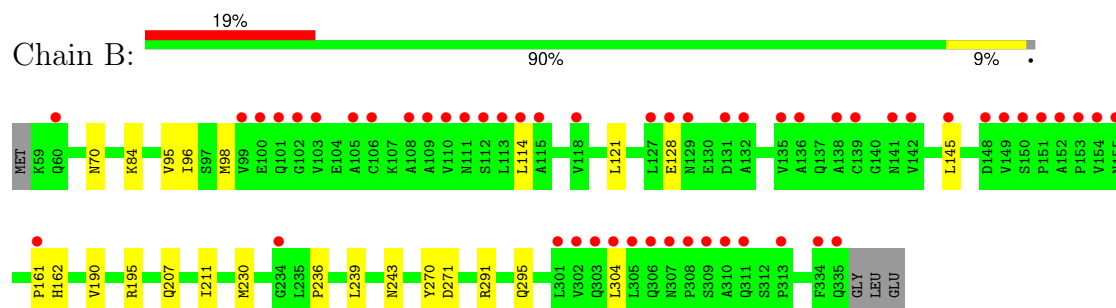
### 3 Residue-property plots [i](#)

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: LacI Transcription Factor



#### • Molecule 1: LacI Transcription Factor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	36.47Å 108.34Å 119.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.34 – 1.50 49.34 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.34-1.50) 99.8 (49.34-1.50)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 1.50Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.176 , 0.208 0.175 , 0.207	Depositor DCC
$R_{free}$ test set	3852 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.2	Xtriage
Anisotropy	0.336	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 35.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4746	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MBG, EDO

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	0.36	0/2165	0.56	0/2956
1	B	0.31	0/2177	0.52	0/2970
All	All	0.34	0/4342	0.54	0/5926

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

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	2129	0	2158	16	0
1	B	2140	0	2171	18	0
2	A	26	0	28	0	0
2	B	26	0	28	0	0
3	A	8	0	12	0	0
3	B	8	0	12	3	0
4	A	234	0	0	3	0
4	B	175	0	0	2	0
All	All	4746	0	4409	29	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 (29) 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:70:ASN:HA	1:B:98[A]:MET:HE3	1.51	0.93
1:B:195:ARG:HE	3:B:402:EDO:H12	1.36	0.91
1:A:95[B]:VAL:HG13	1:B:95:VAL:HG13	1.63	0.79
1:B:114:LEU:HD21	1:B:121:LEU:HD11	1.76	0.67
1:B:291:ARG:O	1:B:295:GLN:HG3	1.99	0.61
1:A:130:GLU:H	1:A:130:GLU:CD	2.12	0.57
1:B:195:ARG:NE	3:B:402:EDO:H12	2.15	0.56
1:A:154:VAL:O	1:A:155:ASN:HB2	2.10	0.51
1:A:190[A]:VAL:HG23	4:A:656:HOH:O	2.09	0.51
1:B:207[A]:GLN:NE2	4:B:501:HOH:O	2.36	0.49
1:A:163[A]:GLU:OE1	1:A:166:ARG:NH2	2.46	0.48
1:B:162:HIS:HD2	4:B:513:HOH:O	1.96	0.48
1:A:154:VAL:HG13	1:A:311:GLN:O	2.13	0.48
1:A:95[B]:VAL:CG1	1:B:95:VAL:HG13	2.41	0.47
1:A:106[B]:CYS:SG	1:A:125:VAL:HG11	2.55	0.47
1:B:161:PRO:HA	3:B:402:EDO:H11	1.96	0.47
1:A:214:LEU:HD21	1:A:230:MET:HB2	1.96	0.47
1:B:211[B]:ILE:HD11	1:B:236:PRO:HB3	1.97	0.46
1:A:200:ARG:HG2	1:A:200:ARG:HH11	1.79	0.46
1:B:230[B]:MET:HE1	1:B:239:LEU:HD13	2.00	0.44
1:B:243:ASN:HA	1:B:270:TYR:O	2.17	0.44
1:B:128:GLU:OE2	1:B:190:VAL:HB	2.17	0.44
1:A:69:THR:HG23	4:A:589:HOH:O	2.18	0.43
1:A:240:LEU:HD23	1:A:268:VAL:HB	2.01	0.43
1:B:145:LEU:HD21	1:B:304:LEU:HD12	2.01	0.43
1:A:69:THR:HG21	4:A:502:HOH:O	2.19	0.42
1:A:96:ILE:HB	1:B:96:ILE:HB	2.02	0.42
1:A:98:MET:O	1:B:84:LYS:HE3	2.20	0.42
1:A:95[B]:VAL:HG13	1:B:95:VAL:CG1	2.44	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	281/281 (100%)	272 (97%)	8 (3%)	1 (0%)	30	12
1	B	282/281 (100%)	270 (96%)	11 (4%)	1 (0%)	30	12
All	All	563/562 (100%)	542 (96%)	19 (3%)	2 (0%)	30	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	271	ASP
1	B	271	ASP

### 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	235/232 (101%)	233 (99%)	2 (1%)	75	57
1	B	235/232 (101%)	235 (100%)	0	100	100
All	All	470/464 (101%)	468 (100%)	2 (0%)	92	79

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	291[A]	ARG
1	A	291[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	229	GLN
1	B	116	GLN
1	B	162	HIS

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Mol	Chain	Res	Type
1	B	314	GLN
1	B	331	ASN

### 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

8 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	$\# Z  > 2$
3	EDO	B	402	-	3,3,3	0.49	0	2,2,2	0.25	0
2	MBG	A	401[B]	-	13,13,13	1.27	2 (15%)	18,18,18	1.22	3 (16%)
3	EDO	A	402	-	3,3,3	0.45	0	2,2,2	0.29	0
3	EDO	B	403	-	3,3,3	0.54	0	2,2,2	0.17	0
2	MBG	B	401[A]	-	13,13,13	1.14	1 (7%)	18,18,18	1.38	4 (22%)
3	EDO	A	403	-	3,3,3	0.38	0	2,2,2	0.36	0
2	MBG	A	401[A]	-	13,13,13	1.23	1 (7%)	18,18,18	1.32	3 (16%)
2	MBG	B	401[B]	-	13,13,13	1.17	1 (7%)	18,18,18	1.21	3 (16%)

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	EDO	B	402	-	-	0/1/1/1	-
2	MBG	A	401[B]	-	-	0/4/24/24	0/1/1/1
3	EDO	A	402	-	-	1/1/1/1	-
3	EDO	B	403	-	-	0/1/1/1	-
2	MBG	B	401[A]	-	-	1/4/24/24	0/1/1/1
3	EDO	A	403	-	-	0/1/1/1	-
2	MBG	A	401[A]	-	-	1/4/24/24	0/1/1/1
2	MBG	B	401[B]	-	-	1/4/24/24	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401[B]	MBG	O5-C1	3.26	1.50	1.41
2	A	401[A]	MBG	O5-C1	3.25	1.50	1.41
2	B	401[B]	MBG	O5-C1	3.25	1.50	1.41
2	B	401[A]	MBG	O5-C1	3.12	1.49	1.41
2	A	401[B]	MBG	O1-C1	-2.32	1.36	1.40

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401[A]	MBG	O1-C1-C2	3.24	111.88	108.14
2	B	401[B]	MBG	O1-C1-C2	3.13	111.75	108.14
2	A	401[A]	MBG	C1-O5-C5	-2.98	107.90	113.72
2	A	401[A]	MBG	C7-O1-C1	2.68	117.33	113.26
2	B	401[A]	MBG	C7-O1-C1	2.59	117.20	113.26
2	A	401[B]	MBG	C1-O5-C5	-2.55	108.75	113.72
2	B	401[A]	MBG	C4-C3-C2	2.46	115.14	110.83
2	A	401[A]	MBG	O1-C1-C2	2.41	110.92	108.14
2	B	401[A]	MBG	C1-O5-C5	-2.36	109.12	113.72
2	A	401[B]	MBG	O1-C1-C2	2.29	110.78	108.14
2	B	401[B]	MBG	C4-C3-C2	2.28	114.82	110.83
2	B	401[B]	MBG	C1-O5-C5	-2.01	109.79	113.72
2	A	401[B]	MBG	C4-C3-C2	2.01	114.36	110.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401[A]	MBG	C2-C1-O1-C7

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Mol	Chain	Res	Type	Atoms
2	B	401[A]	MBG	C2-C1-O1-C7
2	B	401[B]	MBG	C2-C1-O1-C7
3	A	402	EDO	O1-C1-C2-O2

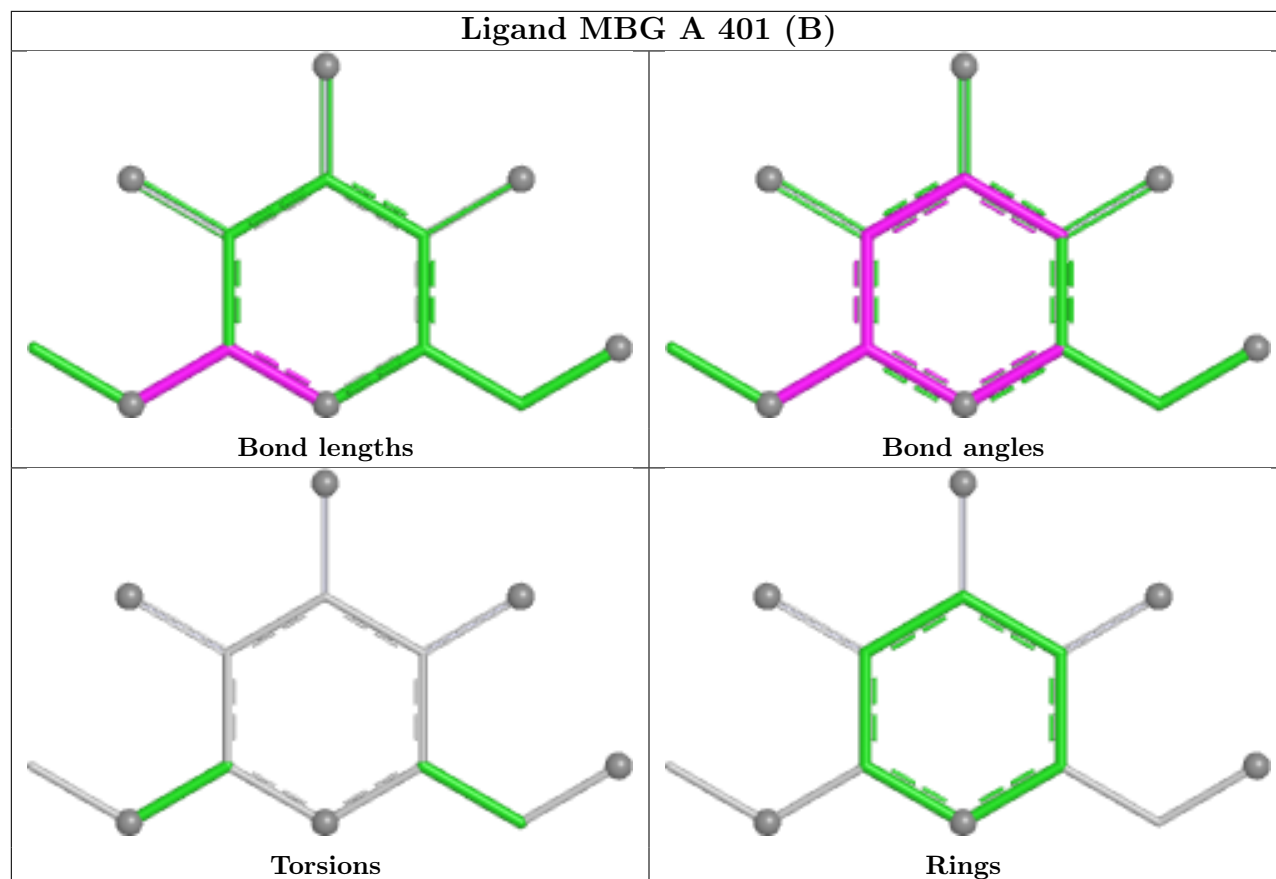
There are no ring outliers.

1 monomer is involved in 3 short contacts:

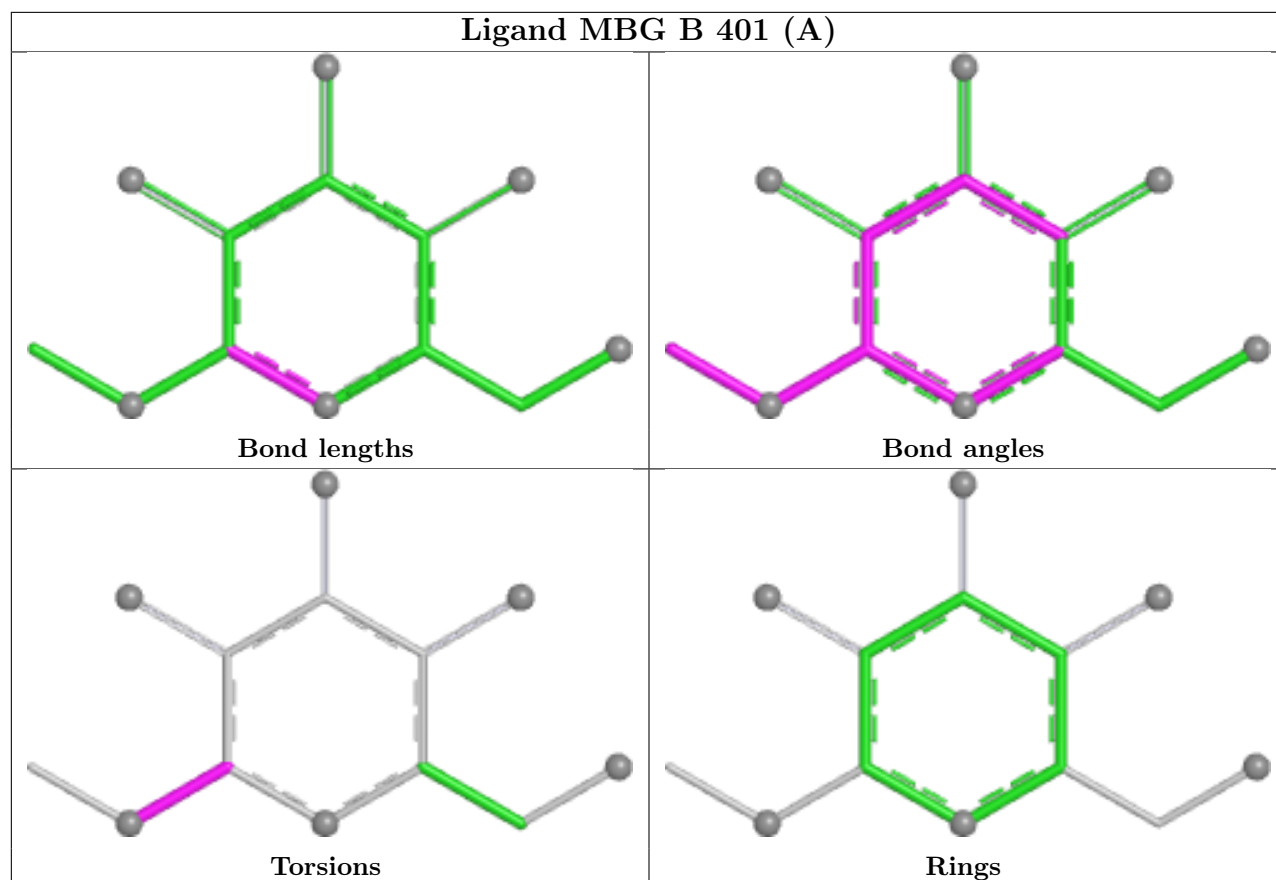
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	402	EDO	3	0

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.

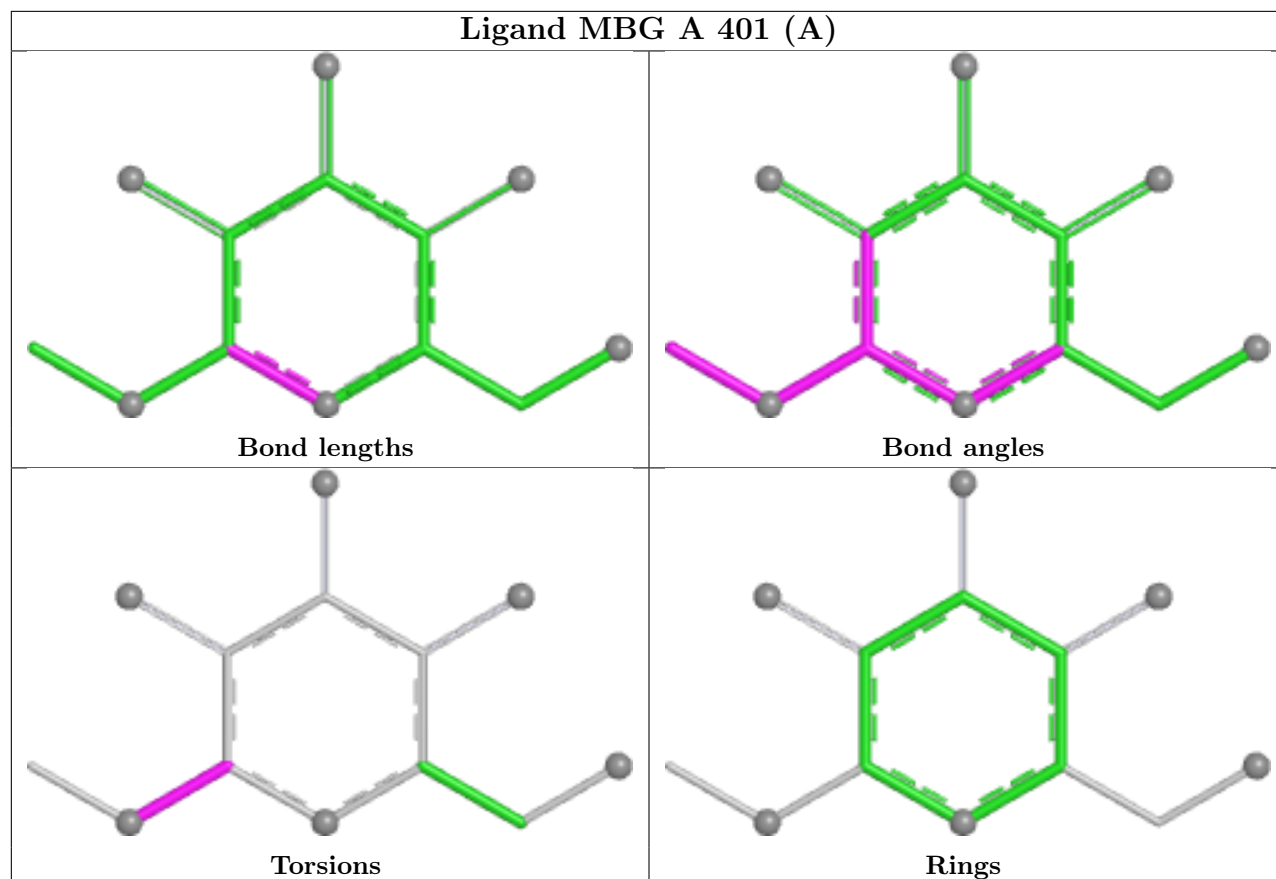
## Ligand MBG A 401 (B)



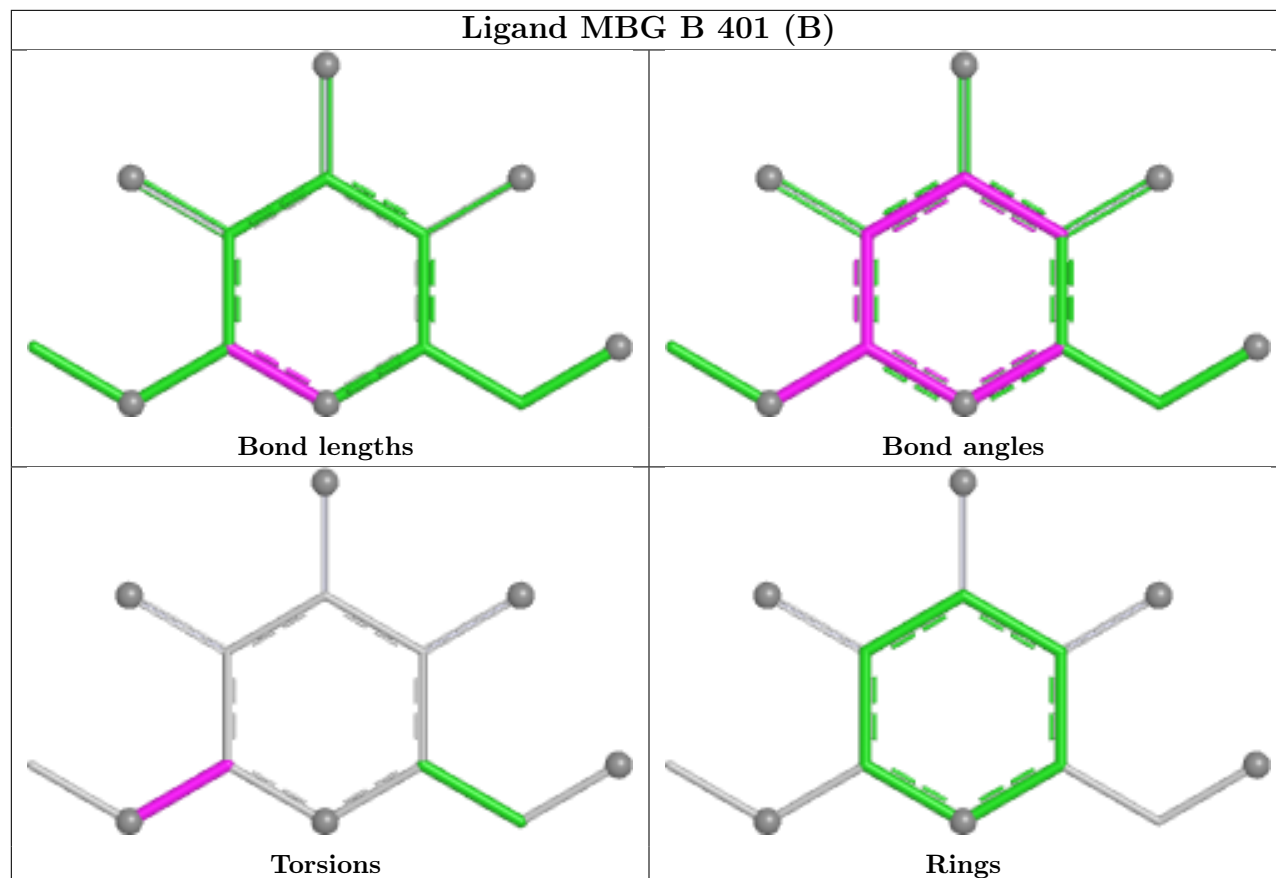
## Ligand MBG B 401 (A)



## Ligand MBG A 401 (A)



## Ligand MBG B 401 (B)



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	271/281 (96%)	0.11	11 (4%) 42 45	7, 18, 42, 74	12 (4%)
1	B	277/281 (98%)	0.65	53 (19%) 4 3	7, 23, 70, 91	7 (2%)
All	All	548/562 (97%)	0.38	64 (11%) 10 10	7, 20, 61, 91	19 (3%)

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	310	ALA	5.1
1	B	154	VAL	4.9
1	B	302	VAL	3.9
1	B	103	VAL	3.8
1	B	99	VAL	3.6
1	B	152	ALA	3.5
1	B	60	GLN	3.5
1	B	113	LEU	3.4
1	B	114	LEU	3.3
1	B	311	GLN	3.3
1	B	305	LEU	3.2
1	B	301	LEU	3.2
1	A	155	ASN	3.1
1	B	313	PRO	3.1
1	A	309	SER	3.1
1	B	309	SER	3.1
1	B	109	ALA	3.1
1	B	141	ASN	3.0
1	B	101	GLN	3.0
1	B	234	GLY	3.0
1	B	308	PRO	3.0
1	B	100	GLU	2.9
1	A	158[A]	LEU	2.9
1	B	138	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	127	LEU	2.9
1	A	141[A]	ASN	2.9
1	B	150	SER	2.8
1	B	335	GLN	2.7
1	B	128	GLU	2.7
1	B	136	ALA	2.7
1	B	149	VAL	2.6
1	B	148	ASP	2.6
1	A	129	ASN	2.6
1	B	102	GLY	2.6
1	B	139	CYS	2.6
1	B	108	ALA	2.6
1	B	118	VAL	2.5
1	B	161	PRO	2.5
1	B	131	ASP	2.5
1	B	307	ASN	2.5
1	B	106	CYS	2.5
1	A	310	ALA	2.5
1	A	61	SER	2.5
1	B	304	LEU	2.5
1	B	142	VAL	2.5
1	A	331	ASN	2.4
1	B	110	VAL	2.4
1	B	115	ALA	2.4
1	A	130	GLU	2.4
1	B	132	ALA	2.3
1	B	151	PRO	2.3
1	B	105	ALA	2.3
1	B	153	PRO	2.3
1	B	135	VAL	2.3
1	B	112	SER	2.3
1	B	111	ASN	2.2
1	B	129	ASN	2.2
1	A	311	GLN	2.2
1	B	334	PHE	2.1
1	A	291[A]	ARG	2.1
1	B	303	GLN	2.1
1	B	145	LEU	2.1
1	B	306	GLN	2.0
1	B	155	ASN	2.0

## 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](#)

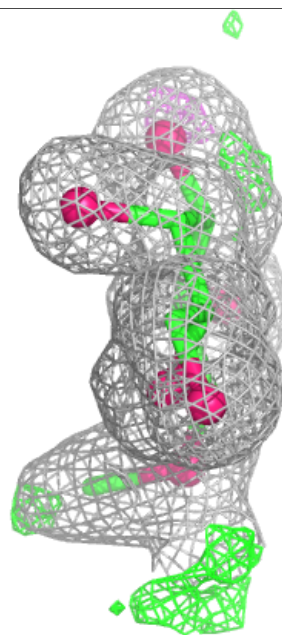
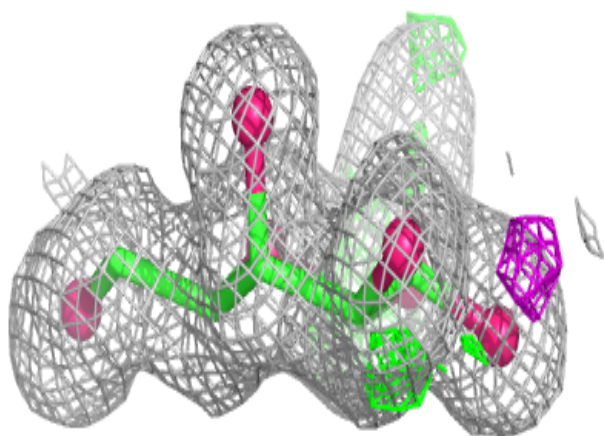
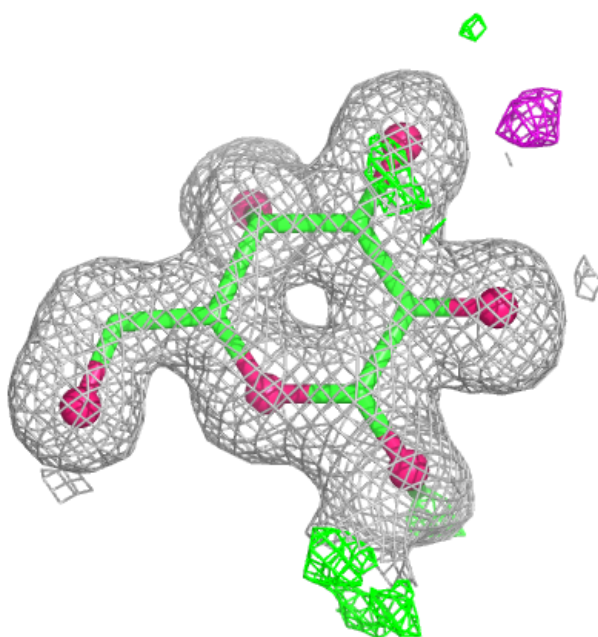
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	EDO	B	402	4/4	0.74	0.20	31,37,40,61	0
3	EDO	B	403	4/4	0.76	0.17	34,46,54,55	0
3	EDO	A	402	4/4	0.83	0.14	38,43,46,59	0
3	EDO	A	403	4/4	0.89	0.12	35,37,45,47	0
2	MBG	A	401[A]	13/13	0.95	0.06	6,13,17,20	13
2	MBG	A	401[B]	13/13	0.95	0.06	12,13,18,22	13
2	MBG	B	401[A]	13/13	0.96	0.06	9,16,22,23	13
2	MBG	B	401[B]	13/13	0.96	0.06	13,16,21,26	13

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.

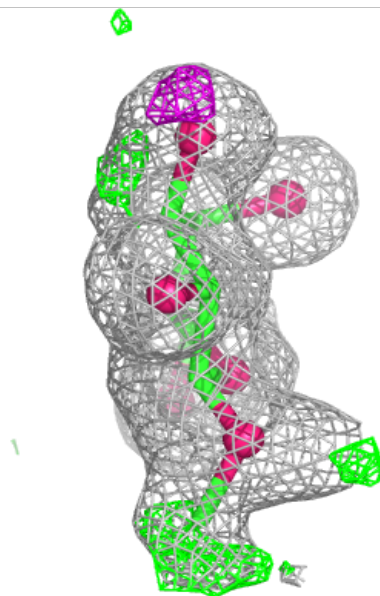
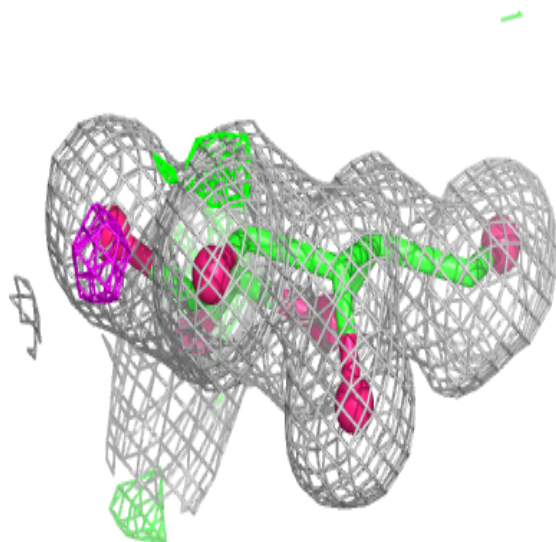
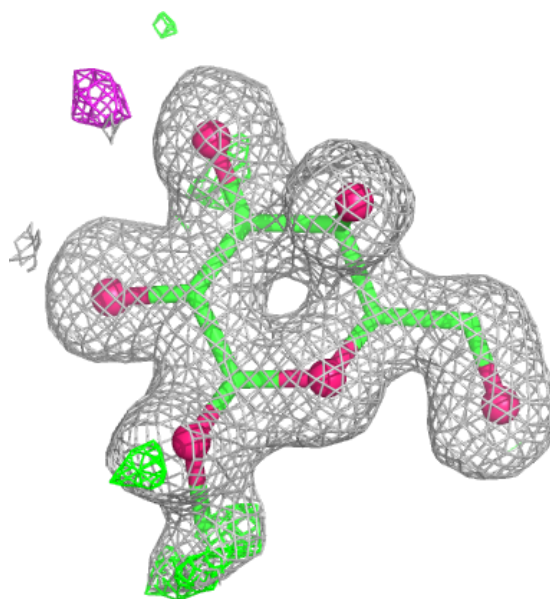
**Electron density around MBG A 401 (A):**

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



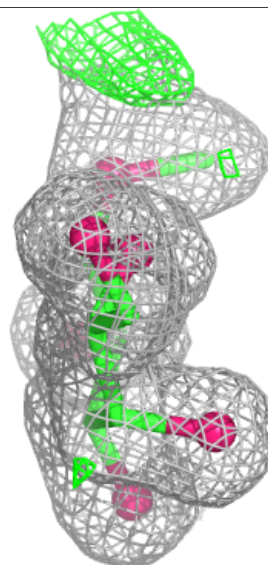
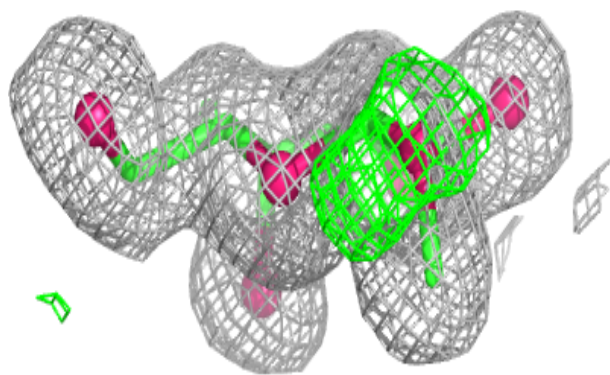
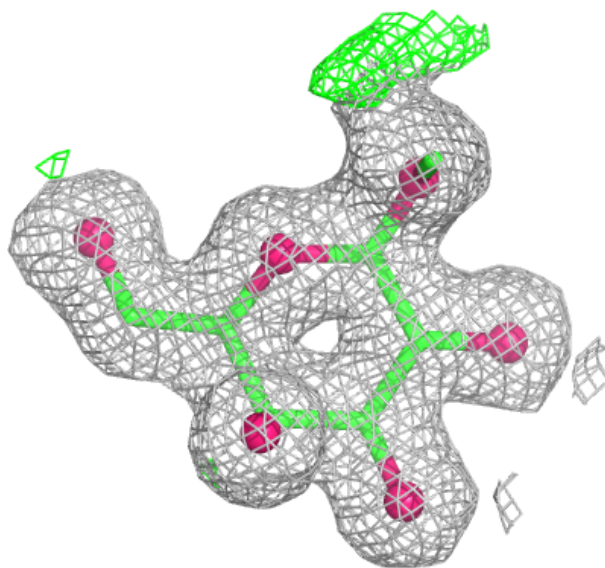
**Electron density around MBG A 401 (B):**

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



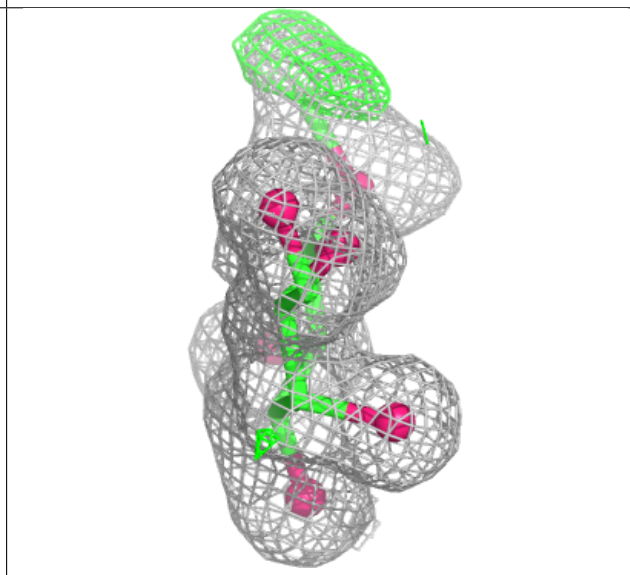
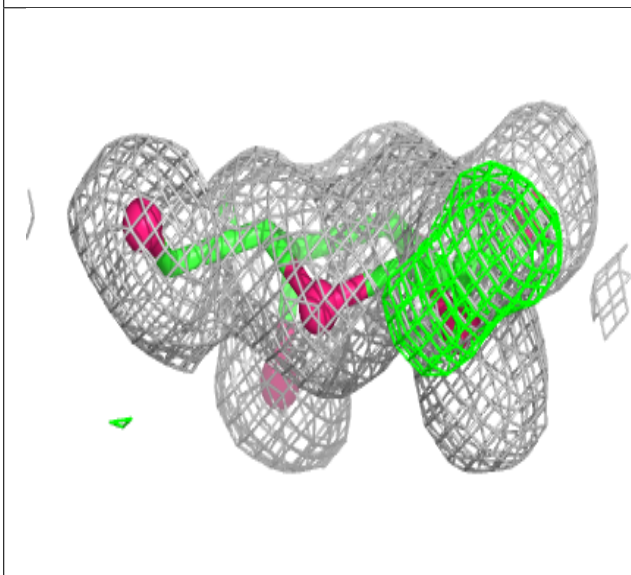
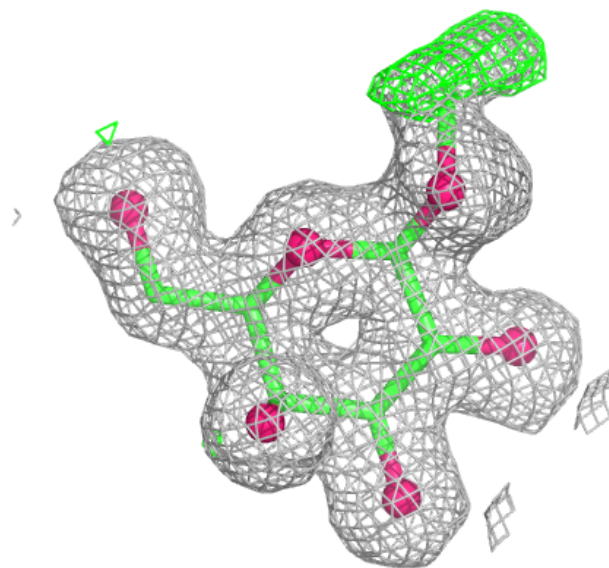
**Electron density around MBG B 401 (A):**

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



**Electron density around MBG B 401 (B):**

$2mF_o-DF_c$  (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.