



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2024 – 09:18 AM EST

PDB ID : 3K22  
Title : Glucocorticoid Receptor with Bound alaninamide 10 with TIF2 peptide  
Authors : Biggadike, K.B.; McLay, I.M.; Madauss, K.P.; Williams, S.P.; Bledsoe, R.K.  
Deposited on : 2009-09-29  
Resolution : 2.10 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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

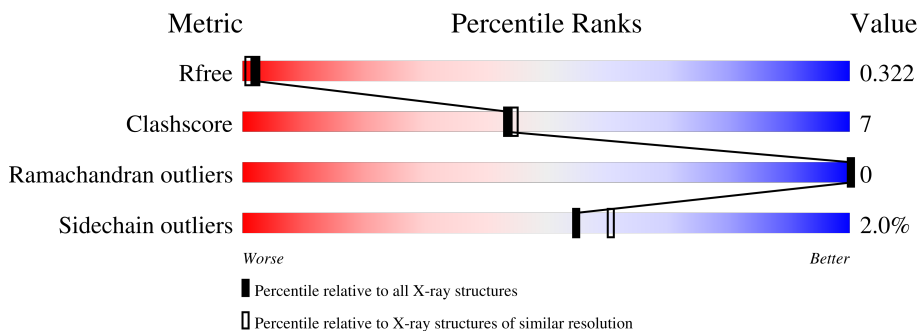
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	259	85% 11% ..
1	B	259	86% 9% ..
2	D	12	75% 25%
2	H	12	92% 8%

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
3	JZS	B	1	-	-	X	-
4	JZR	A	1731	X	-	-	-
4	JZR	B	1731	X	-	-	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4352 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 Glucocorticoid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	250	2017	1306	331	364	16	0	0	0
1	B	250	1979	1289	324	349	17	0	0	0

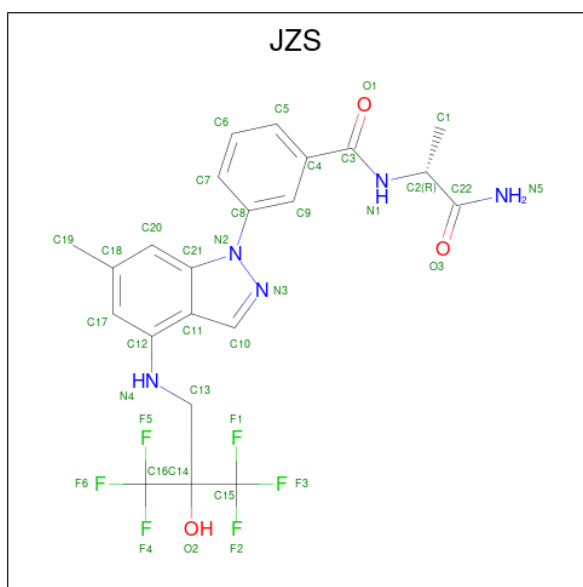
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	519	GLY	-	expression tag	UNP P04150
A	520	SER	-	expression tag	UNP P04150
A	602	TYR	PHE	engineered mutation	UNP P04150
A	638	GLY	CYS	engineered mutation	UNP P04150
B	519	GLY	-	expression tag	UNP P04150
B	520	SER	-	expression tag	UNP P04150
B	602	TYR	PHE	engineered mutation	UNP P04150
B	638	GLY	CYS	engineered mutation	UNP P04150

- Molecule 2 is a protein called Transcriptional Intermediary Factor 2.

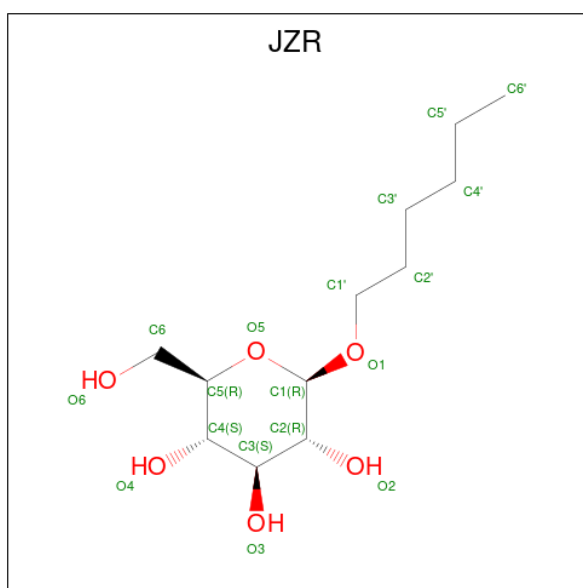
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	H	11	90	58	14	18	0	0	0
2	D	12	96	62	17	17	0	0	0

- Molecule 3 is N-[(1R)-2-amino-1-methyl-2-oxoethyl]-3-(6-methyl-4-[[3,3,3-trifluoro-2-hydroxy-2-(trifluoromethyl)propyl]amino]-1H-indazol-1-yl)benzamide (three-letter code: JZS) (formula: C<sub>22</sub>H<sub>21</sub>F<sub>6</sub>N<sub>5</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
			Total	C	F	N			O	
3	A	1	Total	36	22	6	5	3	0	0
3	B	1	Total	36	22	6	5	3	0	0

- Molecule 4 is hexyl beta-D-glucopyranoside (three-letter code: JZR) (formula:  $C_{12}H_{24}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	O			
4	A	1	Total	18	12	6	0	0
4	B	1	Total	18	12	6	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	B	1	18	12	6	0	0


- Molecule 5 is water.

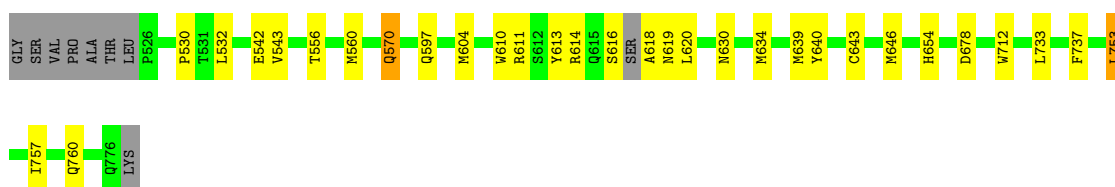
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total	O	0	0
			31	31		
5	B	13	Total	O	0	0
			13	13		

### 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. 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. 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.

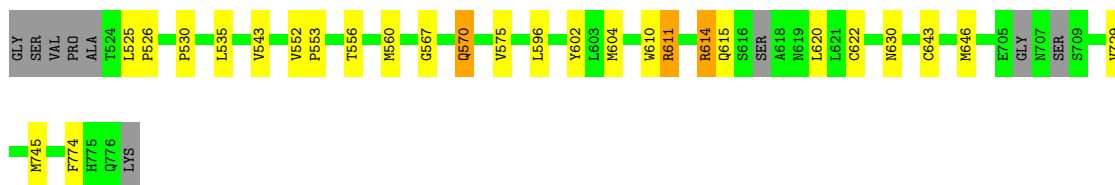
- Molecule 1: Glucocorticoid receptor

Chain A:  85% 11% ..



- Molecule 1: Glucocorticoid receptor

Chain B:  86% 9% ..



- Molecule 2: Transcriptional Intermediary Factor 2

Chain H:  92% 8%



- Molecule 2: Transcriptional Intermediary Factor 2

Chain D:  75% 25%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	127.60Å 127.60Å 78.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.85 – 2.10 19.24 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.85-2.10) 97.0 (19.24-2.10)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.98 (at 2.09Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.211 , 0.255 0.320 , 0.322	Depositor DCC
$R_{free}$ test set	2889 reflections (7.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.9	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.025 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4352	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: JZS, JZR

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	0/2061	0.47	0/2789
1	B	0.35	0/2022	0.46	0/2741
2	D	0.39	0/96	0.52	0/127
2	H	0.38	0/90	0.51	0/119
All	All	0.36	0/4269	0.47	0/5776

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	2017	0	2013	26	1
1	B	1979	0	1949	32	1
2	D	96	0	97	2	0
2	H	90	0	87	0	0
3	A	36	0	21	5	0
3	B	36	0	21	13	0
4	A	18	0	24	1	0
4	B	36	0	48	2	0
5	A	31	0	0	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	13	0	0	0	0
All	All	4352	0	4260	57	1

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 7.

The worst 5 of 57 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:604:MET:HE3	3:B:1:JZS:H9	1.43	0.97
1:A:570:GLN:HG2	3:A:1:JZS:HN5	1.37	0.89
1:B:604:MET:CE	3:B:1:JZS:H9	2.03	0.88
1:A:530:PRO:HB3	1:B:535:LEU:HD12	1.62	0.81
1:A:570:GLN:HG2	3:A:1:JZS:N5	2.02	0.74

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:TRP:NE1	1:B:774:PHE:O[4_565]	2.13	0.07

## 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	246/259 (95%)	237 (96%)	9 (4%)	0	100	100
1	B	243/259 (94%)	239 (98%)	4 (2%)	0	100	100
2	D	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
2	H	9/12 (75%)	9 (100%)	0	0	100	100
All	All	508/542 (94%)	494 (97%)	14 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	220/236 (93%)	216 (98%)	4 (2%)	59	65
1	B	208/236 (88%)	203 (98%)	5 (2%)	49	53
2	D	9/11 (82%)	9 (100%)	0	100	100
2	H	8/11 (73%)	8 (100%)	0	100	100
All	All	445/494 (90%)	436 (98%)	9 (2%)	55	60

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	614	ARG
1	B	615	GLN
1	A	753	LEU
1	B	543	VAL
1	B	570	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	570	GLN
1	A	760	GLN
1	B	588	HIS
1	B	760	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](#)

5 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
4	JZR	B	778	-	18,18,18	0.75	1 (5%)	23,23,23	0.92	1 (4%)
4	JZR	A	1731	-	18,18,18	0.70	1 (5%)	23,23,23	2.11	3 (13%)
4	JZR	B	1731	-	18,18,18	0.73	1 (5%)	23,23,23	2.20	5 (21%)
3	JZS	A	1	-	34,38,38	1.56	7 (20%)	48,59,59	1.38	8 (16%)
3	JZS	B	1	-	34,38,38	1.56	7 (20%)	48,59,59	1.40	8 (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
4	JZR	B	778	-	-	6/9/29/29	0/1/1/1
4	JZR	A	1731	-	1/1/5/5	5/9/29/29	0/1/1/1
4	JZR	B	1731	-	1/1/5/5	5/9/29/29	0/1/1/1
3	JZS	A	1	-	-	1/36/40/40	0/3/3/3
3	JZS	B	1	-	-	0/36/40/40	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	JZS	C9-C8	-4.15	1.37	1.40
3	A	1	JZS	C9-C8	-4.08	1.37	1.40
3	B	1	JZS	C7-C8	-3.65	1.37	1.41
3	A	1	JZS	C7-C8	-3.51	1.37	1.41
3	A	1	JZS	C21-N2	-3.08	1.36	1.40

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1731	JZR	O1-C1-C2	7.34	119.77	108.30
4	B	1731	JZR	O1-C1-C2	6.14	117.89	108.30
4	B	1731	JZR	O5-C1-C2	5.12	121.19	110.35
4	B	1731	JZR	O5-C1-O1	4.42	120.45	109.97
4	A	1731	JZR	O5-C1-C2	4.28	119.40	110.35

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1731	JZR	C1
4	B	1731	JZR	C1

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1731	JZR	O5-C1-O1-C1'
4	B	1731	JZR	O5-C1-O1-C1'
4	B	1731	JZR	C2'-C1'-O1-C1
4	B	778	JZR	C2'-C1'-O1-C1
4	B	778	JZR	O5-C1-O1-C1'

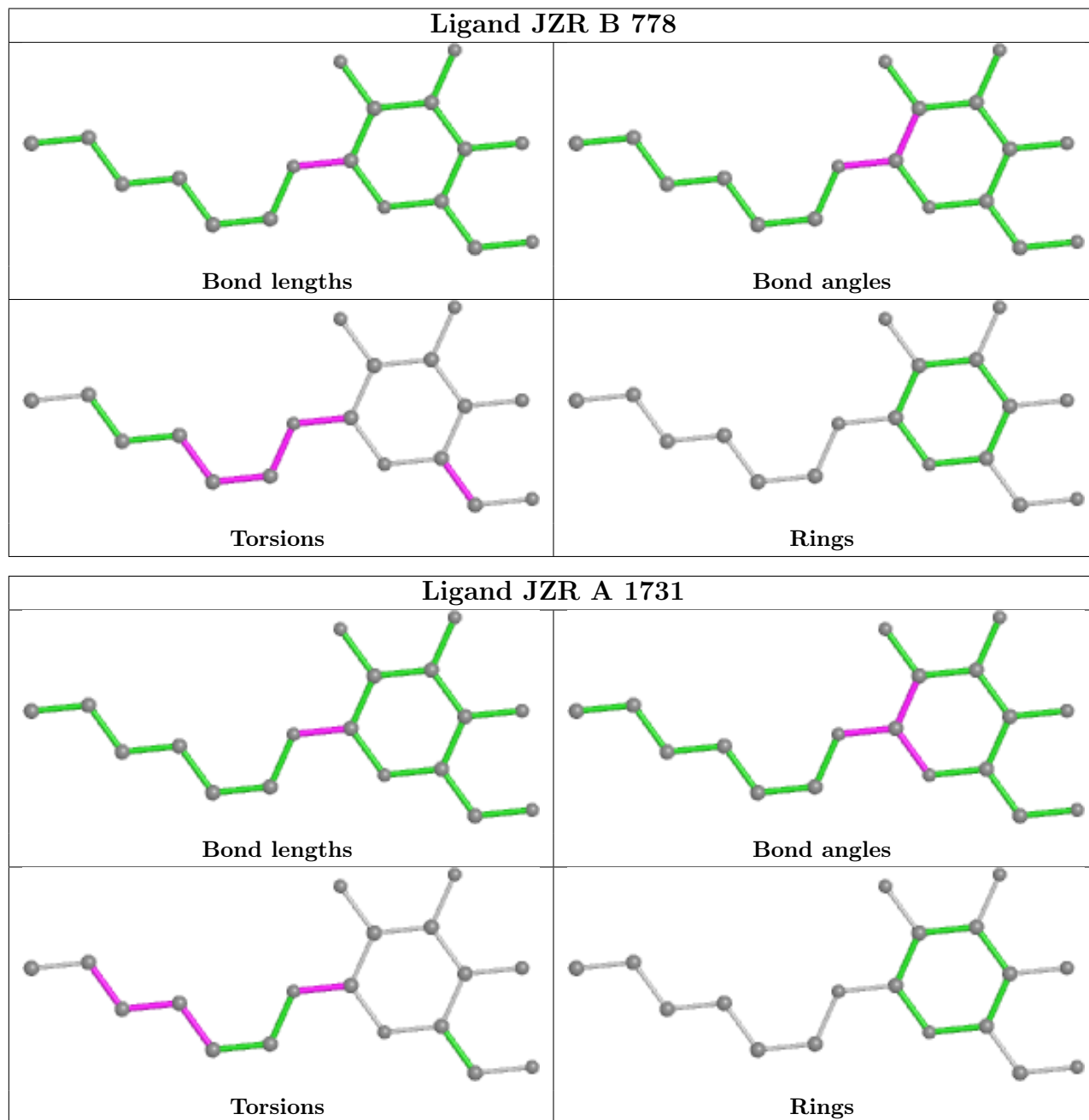
There are no ring outliers.

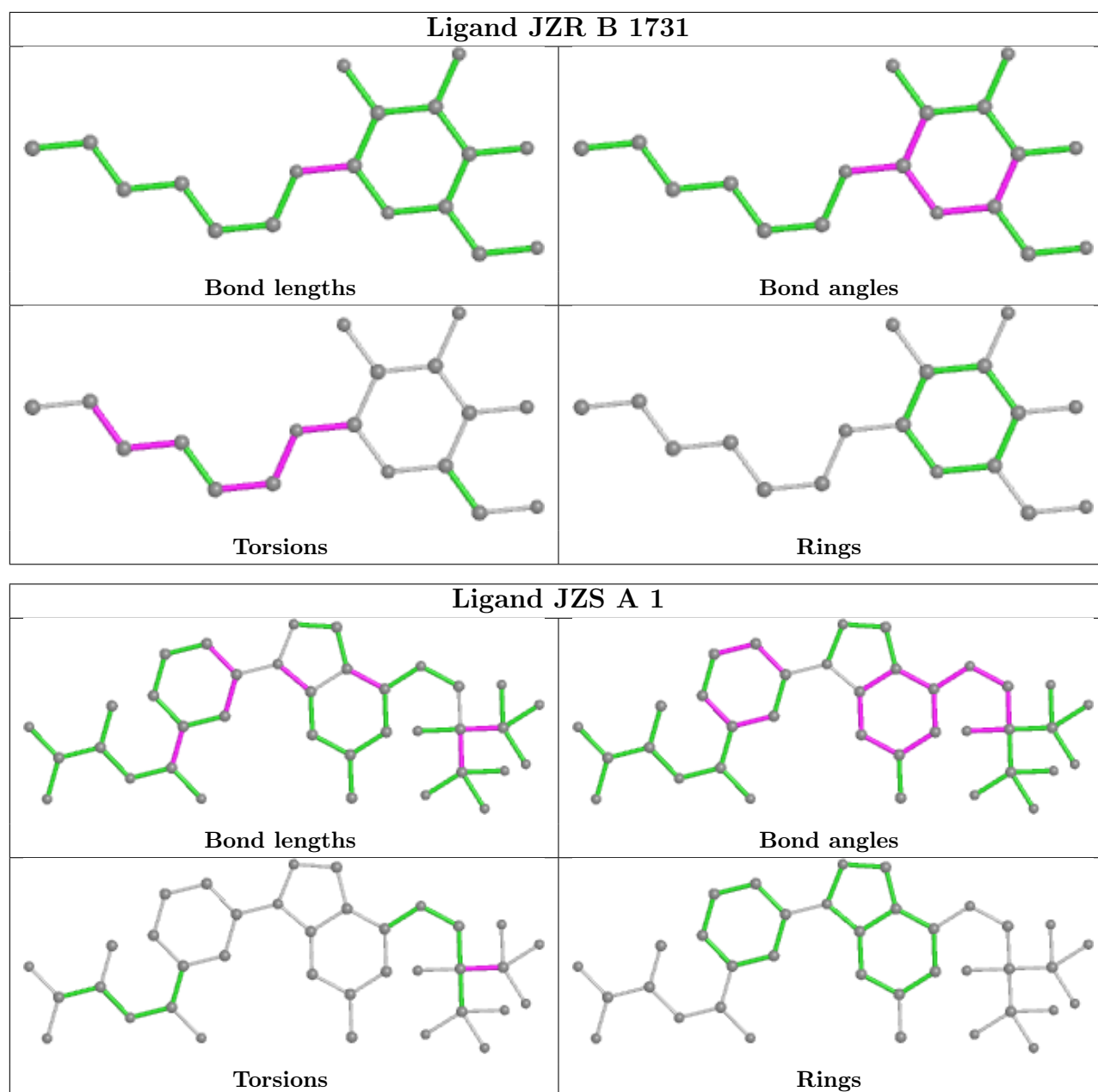
4 monomers are involved in 21 short contacts:

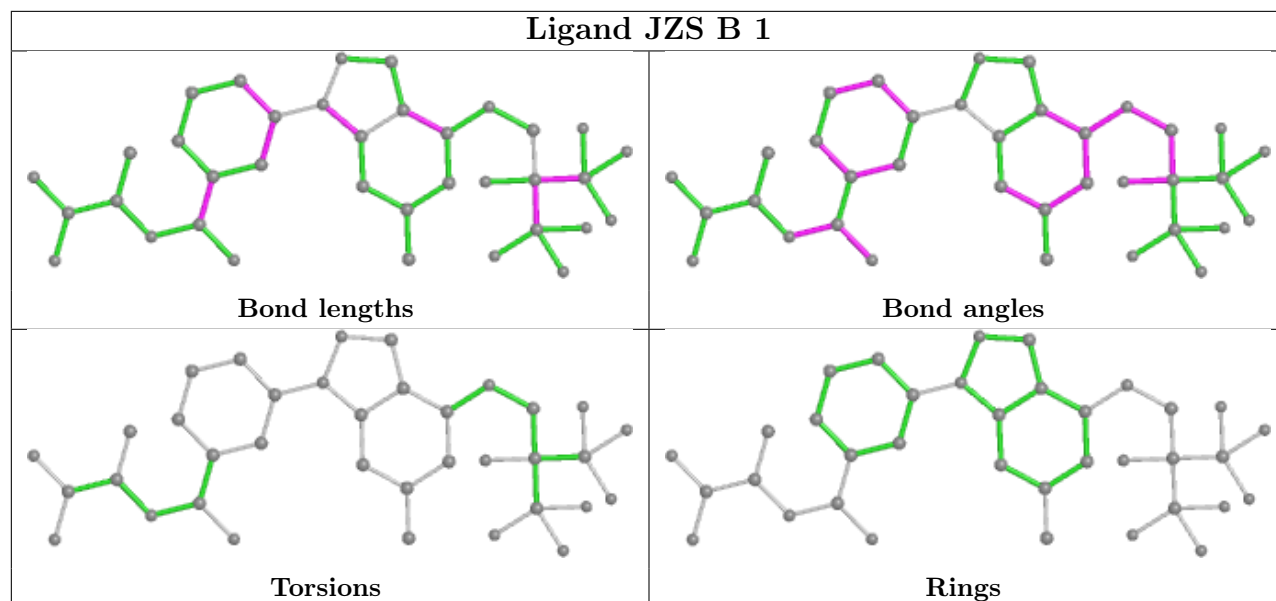
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1731	JZR	1	0
4	B	1731	JZR	2	0
3	A	1	JZS	5	0
3	B	1	JZS	13	0

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

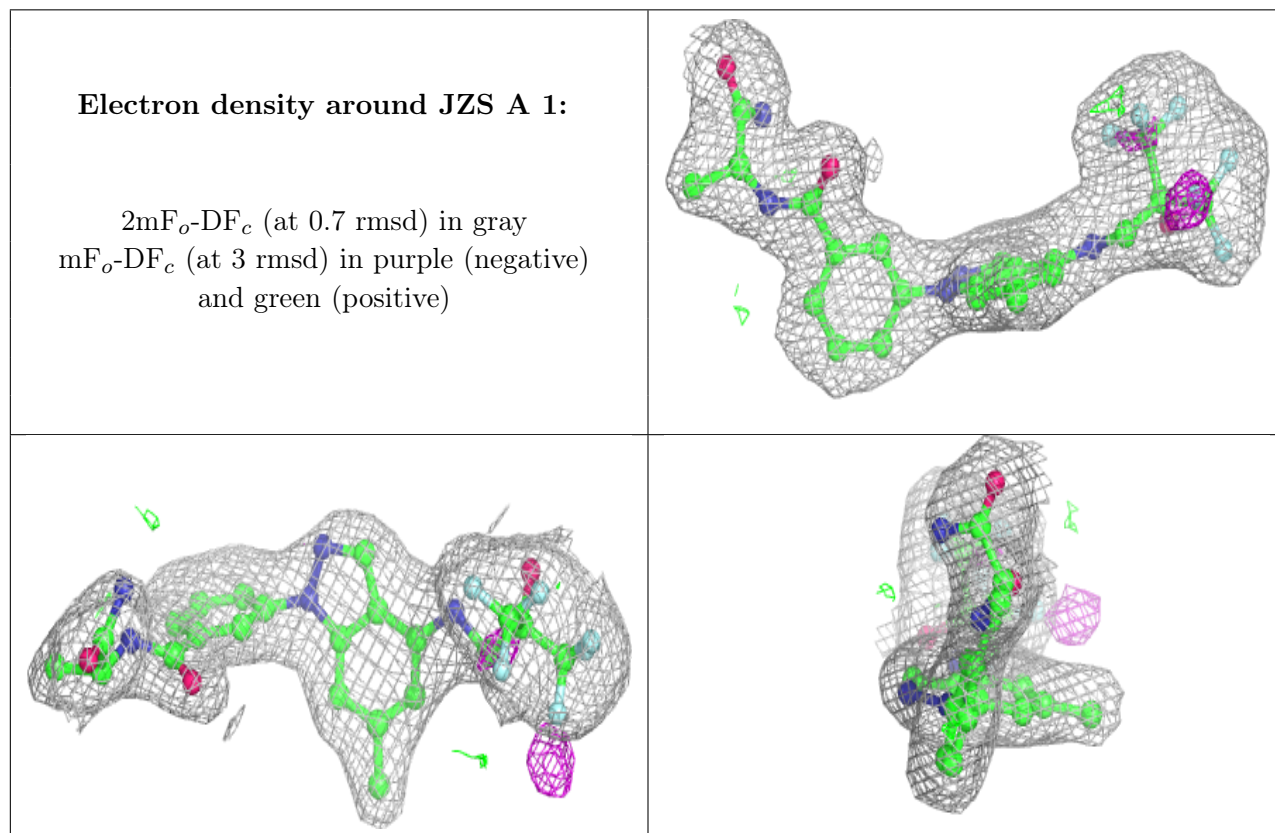
### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

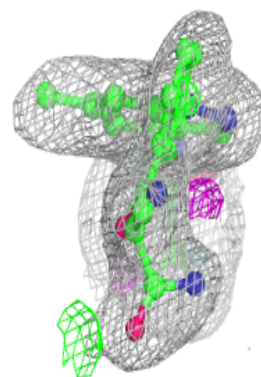
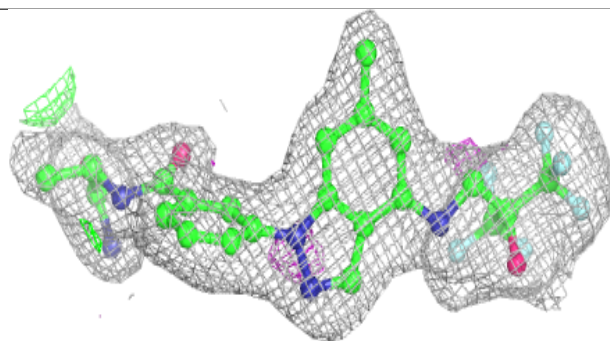
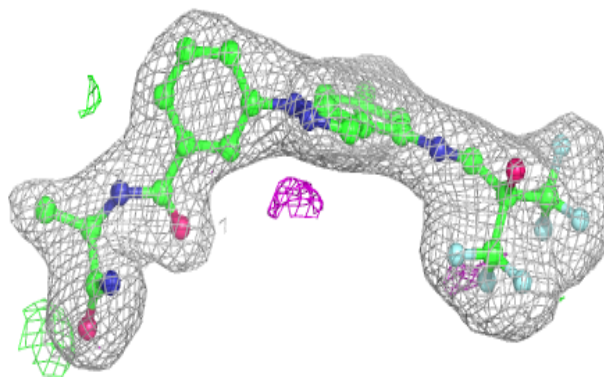
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

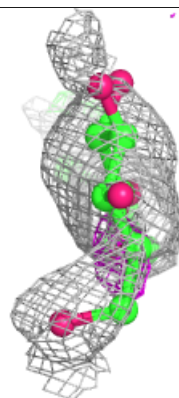
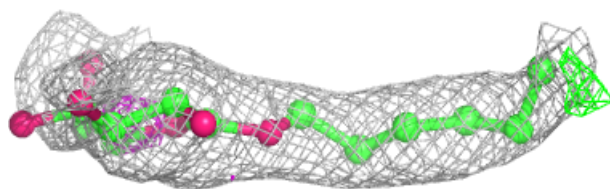
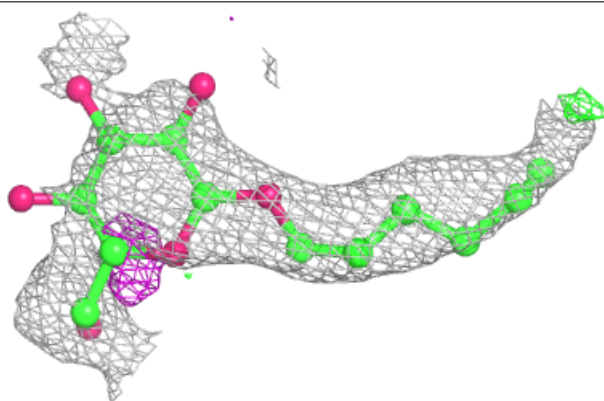


**Electron density around JZS B 1:**

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

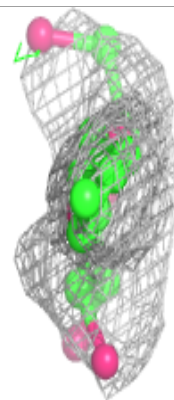
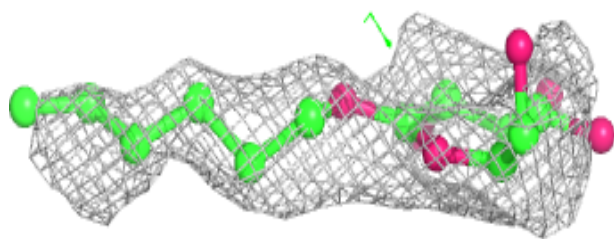
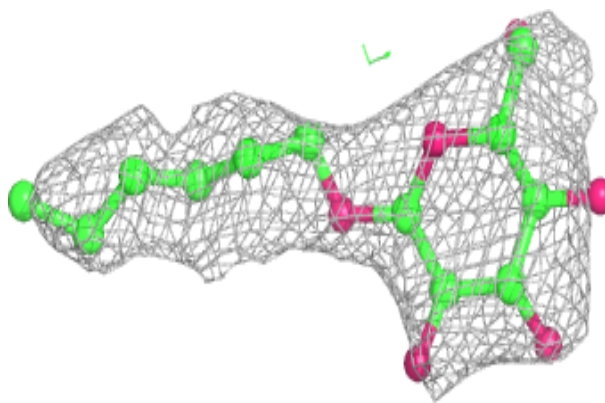
**Electron density around JZR A 1731:**

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

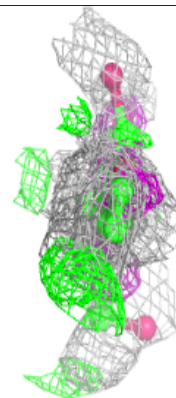
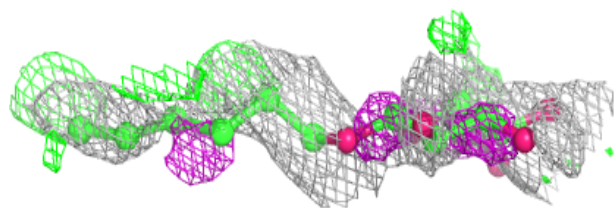
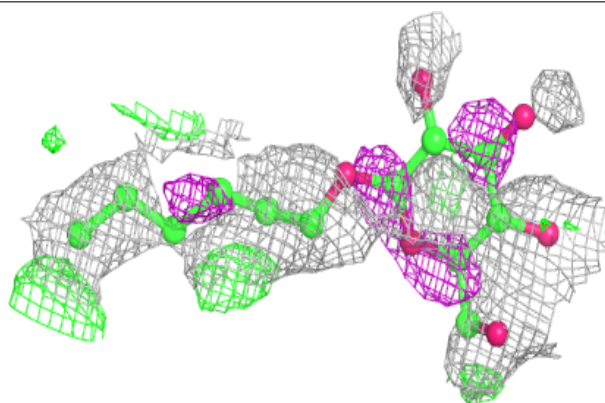


**Electron density around JZR B 1731:**

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

**Electron density around JZR B 778:**

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



## 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.