



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2024 – 09:57 AM EST

PDB ID : 1JKX  
Title : Unexpected formation of an epoxide-derived multisubstrate adduct inhibitor on the active site of GAR transformylase  
Authors : Greasley, S.E.; Marsilje, T.H.; Cai, H.; Baker, S.; Benkovic, S.J.; Boger, D.L.; Wilson, I.A.  
Deposited on : 2001-07-13  
Resolution : 1.60 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 : 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

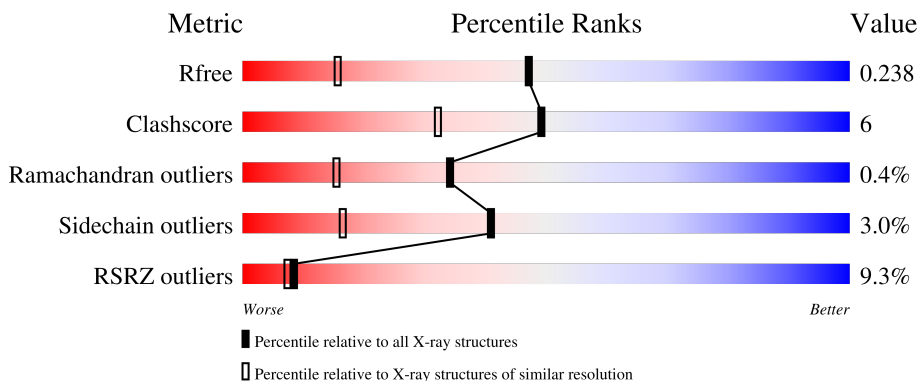
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	212	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 90%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">2%      90%      8%      .</p>
1	B	212	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">5%      88%      9%      ..</p>
1	C	212	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">8%      84%      13%      ..</p>
1	D	212	<div style="display: flex; align-items: center;"> <div style="width: 22%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 77%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 19%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">22%      77%      19%      ..</p>

## 2 Entry composition [i](#)

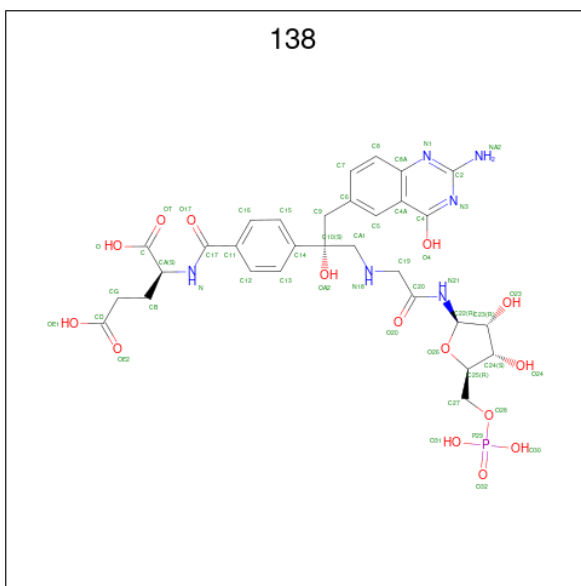
There are 3 unique types of molecules in this entry. The entry contains 7283 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	209	Total 1617	C 1024	N 287	O 301	S 5	0	0	0
1	B	209	Total 1617	C 1024	N 287	O 301	S 5	0	0	0
1	C	209	Total 1617	C 1024	N 287	O 301	S 5	0	0	0
1	D	209	Total 1617	C 1024	N 287	O 301	S 5	0	0	0

- Molecule 2 is N-[5'-O-PHOSPHONO-RIBOFURANOSYL]-2-[2-HYDROXY-2-[4-[GLUTAMIC ACID]-N-CARBONYLPHENYL]-3-[2-AMINO-4-HYDROXY-QUINAZOLIN-6-YL]-PROPANYLAMINO]-ACETAMIDE (three-letter code: 138) (formula: C<sub>30</sub>H<sub>37</sub>N<sub>6</sub>O<sub>15</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 52	C 30	N 6	O 15	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			52	30	6	15	1		
2	C	1	Total	C	N	O	P	0	0
			52	30	6	15	1		
2	D	1	Total	C	N	O	P	0	0
			52	30	6	15	1		

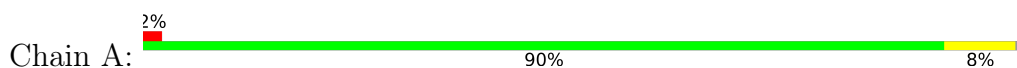
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	172	Total	O	0	0
			172	172		
3	B	181	Total	O	0	0
			181	181		
3	C	146	Total	O	0	0
			146	146		
3	D	108	Total	O	0	0
			108	108		

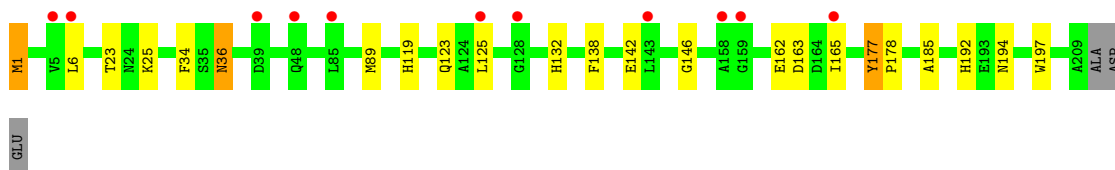
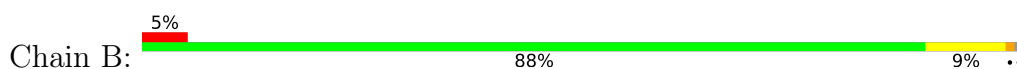
### 3 Residue-property plots [i](#)

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.

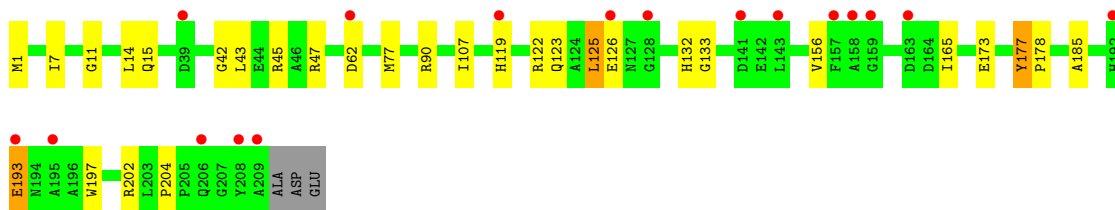
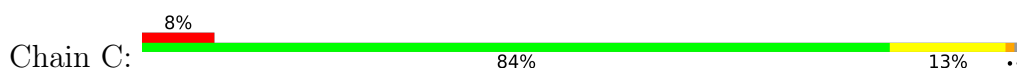
- Molecule 1: PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE



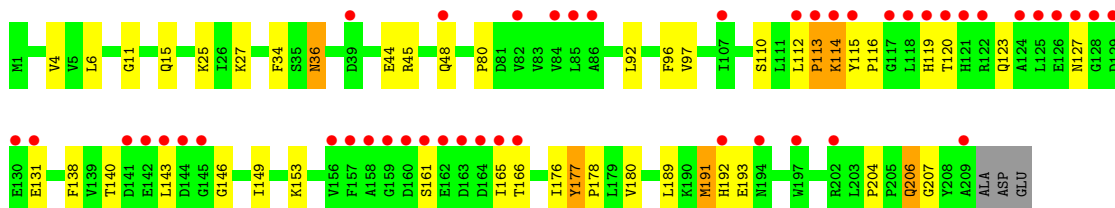
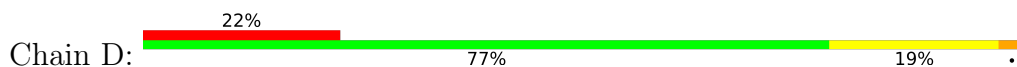
- Molecule 1: PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE



- Molecule 1: PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE



- Molecule 1: PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.14Å 56.01Å 76.13Å 80.83° 71.71° 83.69°	Depositor
Resolution (Å)	30.00 – 1.60 27.59 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.4 (30.00-1.60) 94.6 (27.59-1.60)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 1.60Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.221 , 0.243 0.215 , 0.238	Depositor DCC
$R_{free}$ test set	10690 reflections (10.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtrriage
Anisotropy	0.339	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 44.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7283	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% 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:  
138

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	0.31	0/1654	0.58	0/2248
1	B	0.32	0/1654	0.58	0/2248
1	C	0.28	0/1654	0.56	0/2248
1	D	0.28	0/1654	0.54	0/2248
All	All	0.30	0/6616	0.56	0/8992

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	1617	0	1592	14	0
1	B	1617	0	1592	21	0
1	C	1617	0	1592	16	0
1	D	1617	0	1592	31	0
2	A	52	0	34	1	0
2	B	52	0	34	1	0
2	C	52	0	34	1	0
2	D	52	0	34	1	0
3	A	172	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	181	0	0	2	0
3	C	146	0	0	3	0
3	D	108	0	0	2	0
All	All	7283	0	6504	78	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 6.

All (78) 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:D:36:ASN:HD22	1:D:36:ASN:H	1.27	0.80
1:B:36:ASN:H	1:B:36:ASN:HD22	1.30	0.79
1:D:44:GLU:O	1:D:48:GLN:HG2	1.82	0.79
1:D:206:GLN:NE2	1:D:206:GLN:H	1.81	0.78
1:C:122:ARG:O	1:C:126:GLU:HG2	1.92	0.69
1:D:119:HIS:O	1:D:123:GLN:HG3	1.93	0.68
1:D:115:TYR:N	1:D:116:PRO:HD3	2.12	0.65
1:C:77:MET:HE3	3:C:3255:HOH:O	1.97	0.64
1:D:206:GLN:H	1:D:206:GLN:HE21	1.43	0.63
1:D:161:SER:O	1:D:165:ILE:HG22	2.00	0.62
1:B:125:LEU:HD21	1:B:165:ILE:HG13	1.82	0.62
1:D:206:GLN:HE21	1:D:206:GLN:N	1.98	0.61
1:B:125:LEU:HD11	1:B:162:GLU:HA	1.83	0.60
1:D:15:GLN:HE21	1:D:45:ARG:HH11	1.50	0.60
1:B:6:LEU:HD22	1:B:34:PHE:HB2	1.83	0.59
1:A:1:MET:H1	1:B:1:MET:H1	1.49	0.59
1:C:156:VAL:HG22	1:C:165:ILE:HD11	1.87	0.56
1:B:192:HIS:HD2	3:B:2239:HOH:O	1.88	0.56
1:C:15:GLN:HE21	1:C:45:ARG:HH11	1.54	0.56
1:A:1:MET:N	1:B:1:MET:N	2.53	0.55
1:C:107:ILE:HD11	1:C:173:GLU:HG2	1.89	0.55
1:D:6:LEU:HD22	1:D:34:PHE:HB2	1.90	0.54
1:D:165:ILE:HG23	1:D:166:THR:N	2.23	0.54
1:A:149:ILE:HD13	1:A:189:LEU:HD21	1.89	0.53
1:B:142:GLU:OE2	1:B:194:ASN:HB3	2.09	0.52
1:B:192:HIS:HE1	3:B:2277:HOH:O	1.92	0.52
1:D:165:ILE:HG23	1:D:166:THR:H	1.77	0.50
1:A:1:MET:H1	1:B:1:MET:N	2.08	0.50
1:D:177:TYR:HB3	1:D:178:PRO:HD3	1.94	0.49
1:C:177:TYR:HB3	1:C:178:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:HIS:O	1:C:123:GLN:HG3	2.13	0.48
1:D:110:SER:HB3	1:D:120:THR:HB	1.95	0.48
1:D:192:HIS:O	1:D:193:GLU:HB2	2.14	0.48
1:D:27:LYS:HE3	3:D:4284:HOH:O	2.14	0.47
1:C:197:TRP:CE2	1:C:202:ARG:HG3	2.49	0.47
1:C:1:MET:HE2	1:C:185:ALA:HB2	1.97	0.47
1:D:11:GLY:HA2	3:D:4224:HOH:O	2.15	0.47
1:B:119:HIS:O	1:B:123:GLN:HG3	2.15	0.47
1:D:113:PRO:O	1:D:114:LYS:C	2.53	0.47
1:A:1:MET:HE1	1:A:185:ALA:HA	1.97	0.46
1:D:176:ILE:O	1:D:180:VAL:HG23	2.15	0.46
1:A:15:GLN:HE21	1:A:45:ARG:HH11	1.63	0.46
1:B:89:MET:HA	2:B:2221:138:H15	1.97	0.46
1:B:1:MET:HE2	1:B:185:ALA:HB2	1.97	0.46
1:D:115:TYR:N	1:D:115:TYR:CD2	2.79	0.46
1:D:140:THR:HG21	1:D:191:MET:CE	2.46	0.46
1:D:131:GLU:OE2	1:D:153:LYS:HD3	2.16	0.45
1:A:1:MET:H2	1:B:1:MET:H2	1.64	0.45
1:B:138:PHE:O	1:B:146:GLY:HA3	2.17	0.45
1:C:125:LEU:HD12	1:C:125:LEU:HA	1.90	0.44
1:D:36:ASN:H	1:D:36:ASN:ND2	2.07	0.44
1:B:177:TYR:HB3	1:B:178:PRO:HD3	1.99	0.43
1:A:90:ARG:O	2:A:1221:138:H8	2.18	0.43
1:D:97:VAL:HG21	2:D:4221:138:NA2	2.34	0.43
1:D:138:PHE:O	1:D:146:GLY:HA3	2.19	0.43
1:D:112:LEU:HA	1:D:113:PRO:C	2.39	0.43
1:C:11:GLY:HA2	3:C:3224:HOH:O	2.17	0.43
1:B:192:HIS:HB2	1:B:197:TRP:NE1	2.33	0.43
1:A:1:MET:HE2	1:A:185:ALA:HB2	2.01	0.43
1:A:119:HIS:O	1:A:123:GLN:HG3	2.18	0.43
1:D:4:VAL:HG23	1:D:80:PRO:HB3	2.02	0.42
1:C:43:LEU:O	1:C:47:ARG:HG3	2.19	0.42
1:A:114:LYS:HG2	1:A:115:TYR:CD2	2.55	0.42
1:B:132:HIS:HD2	1:B:165:ILE:HG22	1.84	0.42
1:D:92:LEU:HD13	1:D:96:PHE:CE1	2.54	0.42
1:B:36:ASN:HD22	1:B:36:ASN:N	2.05	0.42
1:C:204:PRO:HB2	3:C:3299:HOH:O	2.19	0.42
1:A:7:ILE:CD1	1:A:42:GLY:HA3	2.50	0.41
1:A:177:TYR:HB3	1:A:178:PRO:HD3	2.01	0.41
1:D:149:ILE:HD13	1:D:189:LEU:HD21	2.02	0.41
1:C:7:ILE:CD1	1:C:42:GLY:HA3	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:113:PRO:O	1:D:114:LYS:O	2.37	0.41
1:C:90:ARG:O	2:C:3221:138:H8	2.21	0.41
1:C:132:HIS:CG	1:C:133:GLY:H	2.39	0.41
1:D:204:PRO:HG2	1:D:207:GLY:O	2.21	0.40
1:A:69:ARG:NH2	3:A:1339:HOH:O	2.54	0.40
1:B:36:ASN:H	1:B:36:ASN:ND2	2.09	0.40
1:B:23:THR:OG1	1:B:25:LYS:HG3	2.21	0.40

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	207/212 (98%)	206 (100%)	1 (0%)	0	100	100
1	B	207/212 (98%)	203 (98%)	4 (2%)	0	100	100
1	C	207/212 (98%)	202 (98%)	4 (2%)	1 (0%)	29	11
1	D	207/212 (98%)	199 (96%)	6 (3%)	2 (1%)	15	3
All	All	828/848 (98%)	810 (98%)	15 (2%)	3 (0%)	34	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	193	GLU
1	D	113	PRO
1	D	114	LYS

### 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	169/171 (99%)	165 (98%)	4 (2%)	49	24
1	B	169/171 (99%)	165 (98%)	4 (2%)	49	24
1	C	169/171 (99%)	164 (97%)	5 (3%)	41	16
1	D	169/171 (99%)	162 (96%)	7 (4%)	30	9
All	All	676/684 (99%)	656 (97%)	20 (3%)	41	16

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLU
1	A	177	TYR
1	A	192	HIS
1	A	193	GLU
1	B	1	MET
1	B	36	ASN
1	B	163	ASP
1	B	177	TYR
1	C	14	LEU
1	C	62	ASP
1	C	125	LEU
1	C	177	TYR
1	C	193	GLU
1	D	25	LYS
1	D	36	ASN
1	D	127	ASN
1	D	143	LEU
1	D	177	TYR
1	D	191	MET
1	D	206	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	99	HIS
1	B	15	GLN

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Mol	Chain	Res	Type
1	B	36	ASN
1	B	192	HIS
1	B	201	GLN
1	C	15	GLN
1	D	15	GLN
1	D	36	ASN
1	D	192	HIS
1	D	206	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](#)

4 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	138	B	2221	-	54,55,55	2.95	23 (42%)	73,80,80	2.07	13 (17%)
2	138	C	3221	-	54,55,55	3.06	23 (42%)	73,80,80	2.05	13 (17%)
2	138	D	4221	-	54,55,55	3.18	25 (46%)	73,80,80	2.06	13 (17%)
2	138	A	1221	-	54,55,55	3.03	23 (42%)	73,80,80	2.06	13 (17%)

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	138	B	2221	-	-	7/45/61/61	0/4/4/4
2	138	C	3221	-	-	8/45/61/61	0/4/4/4
2	138	D	4221	-	-	8/45/61/61	0/4/4/4
2	138	A	1221	-	-	9/45/61/61	0/4/4/4

All (94) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4221	138	O17-C17	10.39	1.44	1.23
2	A	1221	138	O17-C17	10.38	1.44	1.23
2	B	2221	138	O17-C17	10.36	1.44	1.23
2	C	3221	138	O17-C17	10.25	1.44	1.23
2	D	4221	138	C10-C14	7.58	1.59	1.53
2	A	1221	138	C10-C14	7.17	1.59	1.53
2	D	4221	138	CA1-N18	7.05	1.55	1.46
2	C	3221	138	C10-C14	6.84	1.59	1.53
2	B	2221	138	C9-C10	6.75	1.64	1.54
2	C	3221	138	CA1-N18	6.67	1.55	1.46
2	A	1221	138	C9-C10	6.58	1.64	1.54
2	A	1221	138	C2-NA2	6.48	1.46	1.33
2	D	4221	138	C2-NA2	6.46	1.46	1.33
2	A	1221	138	CA1-N18	6.46	1.54	1.46
2	C	3221	138	C2-NA2	6.41	1.46	1.33
2	D	4221	138	C9-C10	6.39	1.63	1.54
2	C	3221	138	C9-C10	6.21	1.63	1.54
2	B	2221	138	C2-NA2	6.15	1.46	1.33
2	B	2221	138	CA1-N18	6.08	1.54	1.46
2	B	2221	138	C10-C14	5.97	1.58	1.53
2	D	4221	138	C15-C14	4.91	1.47	1.39
2	C	3221	138	C15-C14	4.79	1.46	1.39
2	A	1221	138	C15-C14	4.68	1.46	1.39
2	D	4221	138	C13-C14	4.64	1.46	1.39
2	C	3221	138	C13-C14	4.56	1.46	1.39
2	B	2221	138	C13-C14	4.52	1.46	1.39
2	B	2221	138	C15-C14	4.50	1.46	1.39
2	A	1221	138	C13-C14	4.27	1.46	1.39
2	D	4221	138	C2-N3	4.11	1.42	1.35
2	A	1221	138	C2-N3	3.86	1.42	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4221	138	C12-C11	3.80	1.45	1.39
2	C	3221	138	C2-N3	3.77	1.42	1.35
2	B	2221	138	C2-N3	3.74	1.42	1.35
2	D	4221	138	C7-C6	3.72	1.46	1.38
2	D	4221	138	C8-C7	3.71	1.44	1.36
2	D	4221	138	C9-C6	3.70	1.57	1.51
2	C	3221	138	C8-C7	3.70	1.44	1.36
2	C	3221	138	C12-C11	3.65	1.45	1.39
2	C	3221	138	C7-C6	3.64	1.46	1.38
2	B	2221	138	C12-C11	3.62	1.45	1.39
2	A	1221	138	O-C	3.54	1.42	1.30
2	A	1221	138	C8-C7	3.53	1.44	1.36
2	A	1221	138	C7-C6	3.50	1.46	1.38
2	B	2221	138	O-C	3.43	1.41	1.30
2	B	2221	138	C7-C6	3.40	1.46	1.38
2	C	3221	138	O-C	3.38	1.41	1.30
2	C	3221	138	C9-C6	3.36	1.57	1.51
2	D	4221	138	O-C	3.36	1.41	1.30
2	D	4221	138	C5-C6	3.36	1.45	1.37
2	B	2221	138	C8-C7	3.35	1.43	1.36
2	A	1221	138	C8A-N1	3.32	1.43	1.37
2	D	4221	138	C8A-N1	3.27	1.42	1.37
2	A	1221	138	C12-C11	3.26	1.44	1.39
2	C	3221	138	C8A-N1	3.18	1.42	1.37
2	B	2221	138	C5-C6	3.12	1.44	1.37
2	C	3221	138	C5-C6	3.10	1.44	1.37
2	D	4221	138	O4-C4	2.99	1.43	1.28
2	C	3221	138	O4-C4	2.87	1.42	1.28
2	D	4221	138	C12-C13	2.84	1.43	1.38
2	A	1221	138	C9-C6	2.84	1.56	1.51
2	A	1221	138	C5-C6	2.82	1.44	1.37
2	B	2221	138	C8A-N1	2.78	1.42	1.37
2	C	3221	138	C12-C13	2.77	1.43	1.38
2	B	2221	138	C9-C6	2.71	1.56	1.51
2	A	1221	138	O4-C4	2.66	1.41	1.28
2	B	2221	138	C12-C13	2.66	1.43	1.38
2	B	2221	138	O4-C4	2.62	1.41	1.28
2	C	3221	138	P29-O32	-2.62	1.42	1.50
2	D	4221	138	C16-C11	2.60	1.43	1.39
2	B	2221	138	P29-O32	-2.55	1.42	1.50
2	A	1221	138	C16-C11	2.52	1.43	1.39
2	D	4221	138	C22-N21	2.50	1.46	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4221	138	P29-O32	-2.49	1.42	1.50
2	D	4221	138	C15-C16	2.46	1.43	1.38
2	D	4221	138	C4A-C8A	2.45	1.46	1.42
2	C	3221	138	C16-C11	2.39	1.43	1.39
2	D	4221	138	C4-N3	2.38	1.42	1.36
2	A	1221	138	C12-C13	2.37	1.43	1.38
2	A	1221	138	C4-N3	2.34	1.42	1.36
2	C	3221	138	C4A-C8A	2.32	1.46	1.42
2	A	1221	138	CA1-C10	2.27	1.56	1.53
2	A	1221	138	P29-O32	-2.27	1.43	1.50
2	C	3221	138	CA1-C10	2.26	1.56	1.53
2	C	3221	138	C22-N21	2.25	1.46	1.43
2	D	4221	138	CB-CA	2.22	1.58	1.53
2	C	3221	138	C4-N3	2.21	1.42	1.36
2	B	2221	138	C16-C11	2.21	1.43	1.39
2	D	4221	138	CA1-C10	2.18	1.56	1.53
2	B	2221	138	C4A-C8A	2.17	1.46	1.42
2	B	2221	138	CB-CA	2.13	1.58	1.53
2	B	2221	138	CA1-C10	2.09	1.56	1.53
2	A	1221	138	C4A-C8A	2.05	1.45	1.42
2	A	1221	138	C15-C16	2.05	1.42	1.38
2	B	2221	138	C4-N3	2.03	1.41	1.36

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1221	138	C10-CA1-N18	-8.44	100.39	112.91
2	D	4221	138	C10-CA1-N18	-8.43	100.40	112.91
2	B	2221	138	C10-CA1-N18	-8.36	100.51	112.91
2	C	3221	138	C10-CA1-N18	-8.11	100.88	112.91
2	A	1221	138	C4-C4A-C8A	7.05	119.32	114.73
2	B	2221	138	C4-C4A-C8A	6.77	119.14	114.73
2	D	4221	138	C4-C4A-C8A	6.76	119.14	114.73
2	C	3221	138	C4-C4A-C8A	6.72	119.11	114.73
2	C	3221	138	O17-C17-C11	-5.91	110.40	120.94
2	D	4221	138	O17-C17-C11	-5.68	110.80	120.94
2	B	2221	138	O17-C17-C11	-5.68	110.81	120.94
2	A	1221	138	O17-C17-C11	-5.50	111.12	120.94
2	D	4221	138	N1-C2-N3	-5.49	119.91	127.22
2	B	2221	138	N1-C2-N3	-5.48	119.91	127.22
2	C	3221	138	N1-C2-N3	-5.44	119.96	127.22
2	A	1221	138	N1-C2-N3	-5.39	120.03	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2221	138	O26-C22-C23	-5.24	100.72	106.23
2	A	1221	138	O26-C22-C23	-4.97	101.00	106.23
2	D	4221	138	O26-C22-C23	-4.95	101.03	106.23
2	C	3221	138	O26-C22-C23	-4.69	101.30	106.23
2	D	4221	138	CG-CB-CA	3.53	119.76	113.16
2	B	2221	138	CG-CB-CA	3.49	119.67	113.16
2	C	3221	138	C11-C17-N	3.39	123.56	117.06
2	B	2221	138	C11-C17-N	3.38	123.55	117.06
2	D	4221	138	C11-C17-N	3.23	123.26	117.06
2	A	1221	138	C11-C17-N	3.23	123.25	117.06
2	C	3221	138	CG-CB-CA	3.22	119.18	113.16
2	A	1221	138	C4A-C8A-N1	-3.09	119.53	122.81
2	C	3221	138	C4A-C8A-N1	-3.00	119.63	122.81
2	B	2221	138	C4A-C8A-N1	-2.88	119.76	122.81
2	D	4221	138	C4A-C8A-N1	-2.87	119.77	122.81
2	B	2221	138	CA1-C10-C14	-2.83	103.77	110.84
2	A	1221	138	CB-CG-CD	2.75	119.81	112.51
2	A	1221	138	O30-P29-O28	-2.74	99.43	106.73
2	D	4221	138	O30-P29-O28	-2.72	99.50	106.73
2	C	3221	138	CA1-C10-C14	-2.69	104.11	110.84
2	C	3221	138	O30-P29-O28	-2.64	99.71	106.73
2	A	1221	138	CA1-C10-C14	-2.47	104.68	110.84
2	B	2221	138	O30-P29-O28	-2.45	100.22	106.73
2	B	2221	138	CB-CG-CD	2.40	118.89	112.51
2	C	3221	138	CB-CG-CD	2.34	118.71	112.51
2	D	4221	138	CA1-C10-C14	-2.33	105.03	110.84
2	D	4221	138	O28-P29-O32	2.31	112.96	106.47
2	A	1221	138	O28-P29-O32	2.24	112.77	106.47
2	D	4221	138	CB-CG-CD	2.22	118.40	112.51
2	C	3221	138	O28-P29-O32	2.21	112.68	106.47
2	B	2221	138	O4-C4-C4A	2.21	121.70	116.72
2	A	1221	138	CG-CB-CA	2.15	117.17	113.16
2	A	1221	138	O4-C4-C4A	2.15	121.56	116.72
2	D	4221	138	O4-C4-C4A	2.14	121.53	116.72
2	C	3221	138	O4-C4-C4A	2.11	121.48	116.72
2	B	2221	138	O28-P29-O32	2.11	112.38	106.47

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1221	138	O20-C20-N21-C22

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Mol	Chain	Res	Type	Atoms
2	B	2221	138	O26-C22-N21-C20
2	B	2221	138	C27-O28-P29-O31
2	B	2221	138	O20-C20-N21-C22
2	C	3221	138	O26-C22-N21-C20
2	C	3221	138	C27-O28-P29-O31
2	C	3221	138	O20-C20-N21-C22
2	D	4221	138	O26-C22-N21-C20
2	D	4221	138	O20-C20-N21-C22
2	C	3221	138	C19-C20-N21-C22
2	A	1221	138	CA1-C10-C14-C15
2	C	3221	138	CA1-C10-C14-C15
2	D	4221	138	CA1-C10-C14-C15
2	B	2221	138	C19-C20-N21-C22
2	D	4221	138	C19-C20-N21-C22
2	B	2221	138	CA1-C10-C14-C15
2	A	1221	138	O26-C22-N21-C20
2	C	3221	138	C27-O28-P29-O30
2	D	4221	138	C27-O28-P29-O31
2	A	1221	138	OE2-CD-CG-CB
2	B	2221	138	O26-C25-C27-O28
2	C	3221	138	O26-C25-C27-O28
2	D	4221	138	O26-C25-C27-O28
2	A	1221	138	OE1-CD-CG-CB
2	A	1221	138	O26-C25-C27-O28
2	A	1221	138	C27-O28-P29-O31
2	D	4221	138	OE1-CD-CG-CB
2	D	4221	138	OE2-CD-CG-CB
2	A	1221	138	C10-CA1-N18-C19
2	B	2221	138	C10-CA1-N18-C19
2	C	3221	138	C10-CA1-N18-C19
2	A	1221	138	C19-C20-N21-C22

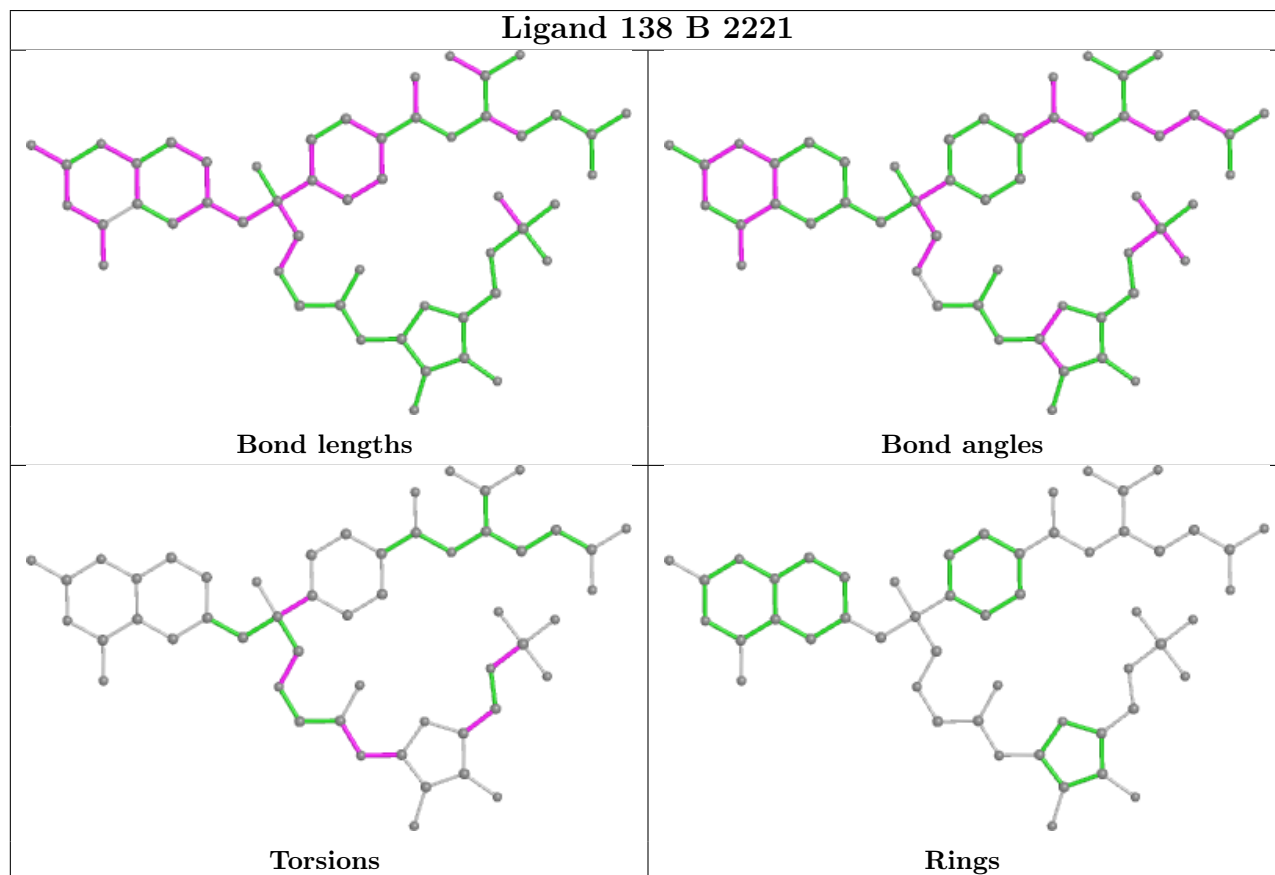
There are no ring outliers.

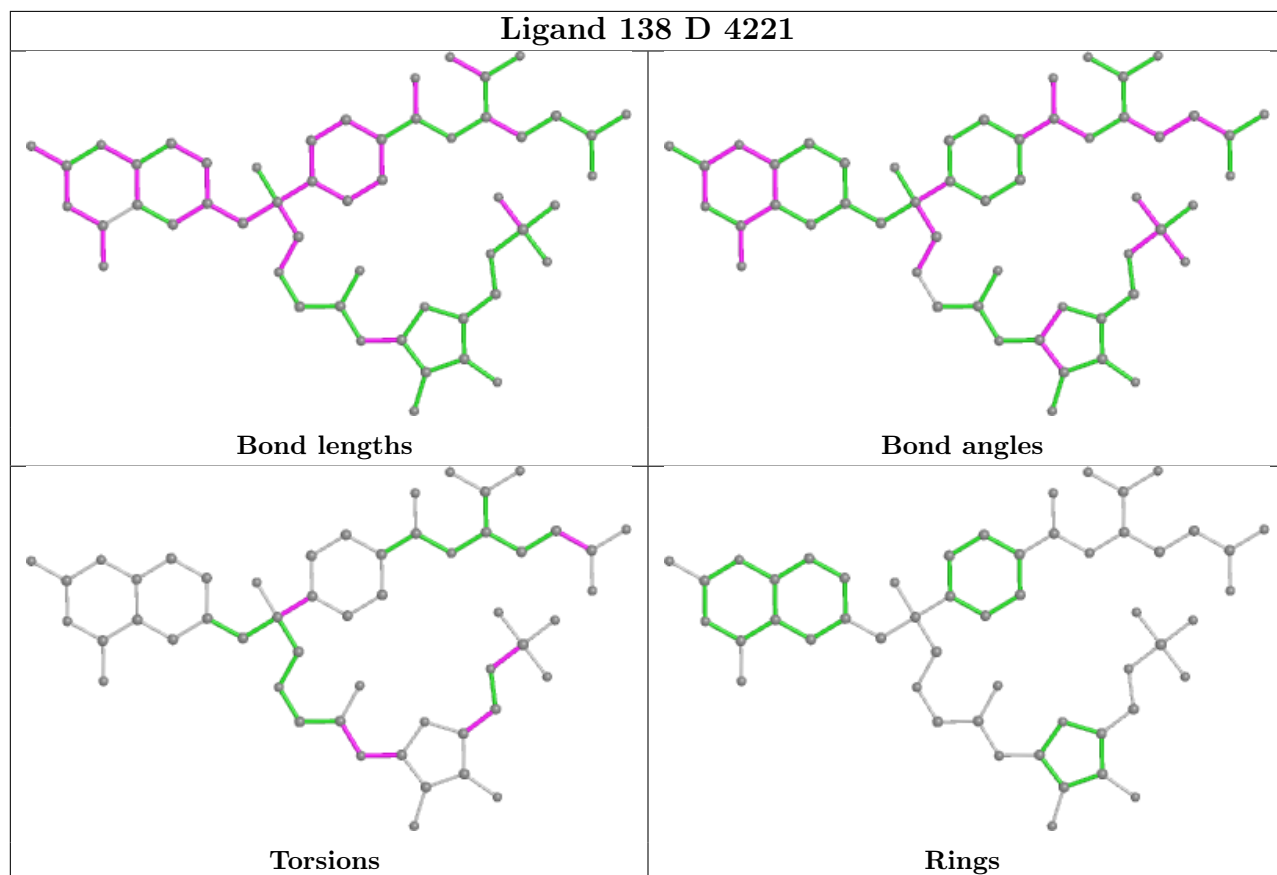
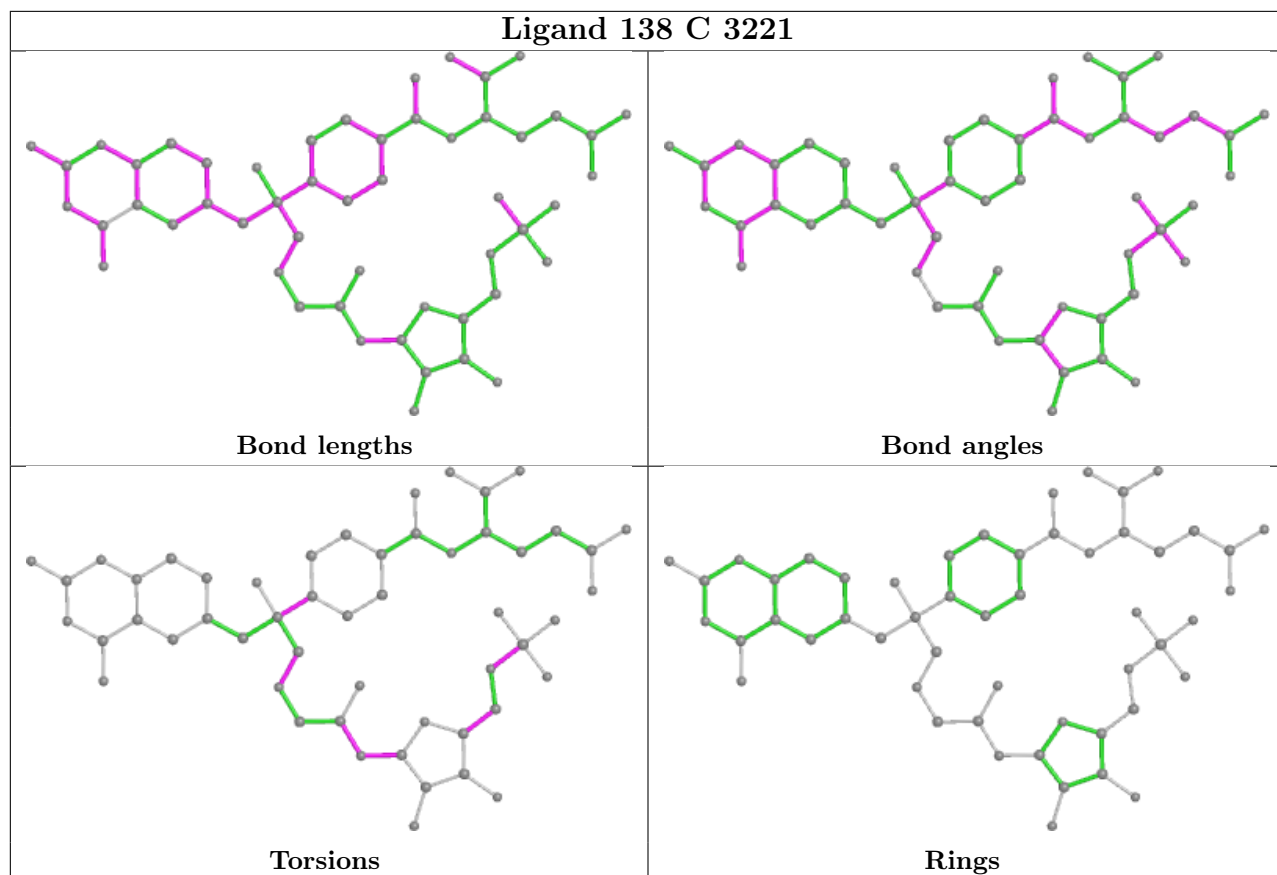
4 monomers are involved in 4 short contacts:

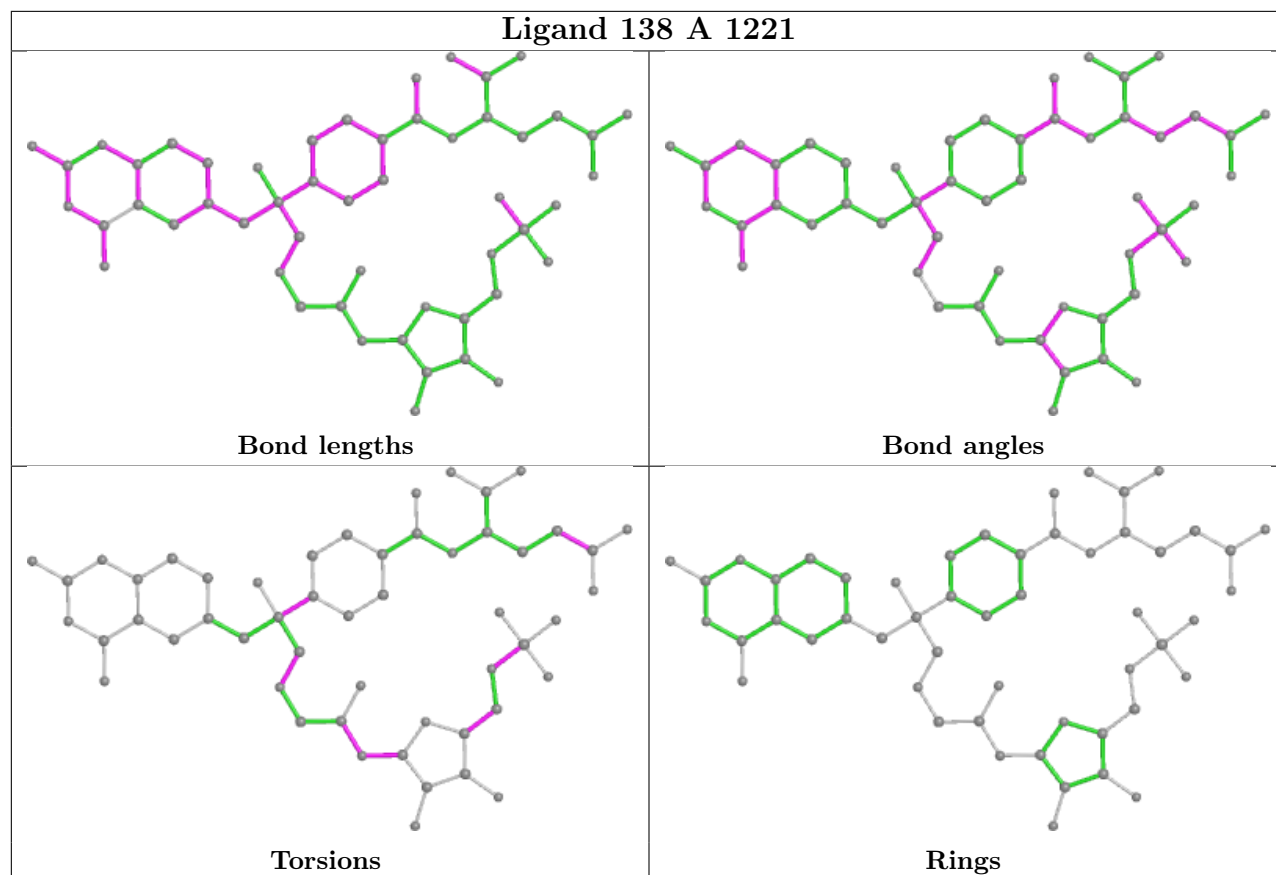
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2221	138	1	0
2	C	3221	138	1	0
2	D	4221	138	1	0
2	A	1221	138	1	0

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

### 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	209/212 (98%)	0.12	4 (1%) 66 65	9, 17, 29, 39	0
1	B	209/212 (98%)	0.24	11 (5%) 26 24	10, 17, 33, 39	0
1	C	209/212 (98%)	0.47	17 (8%) 12 10	16, 24, 38, 48	0
1	D	209/212 (98%)	1.02	46 (22%) 0 0	15, 26, 46, 54	0
All	All	836/848 (98%)	0.46	78 (9%) 8 7	9, 21, 41, 54	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	143	LEU	8.4
1	D	118	LEU	5.9
1	D	159	GLY	5.8
1	D	125	LEU	5.3
1	C	193	GLU	4.9
1	D	161	SER	4.9
1	B	158	ALA	4.8
1	D	141	ASP	4.6
1	B	159	GLY	4.6
1	D	113	PRO	4.6
1	D	115	TYR	4.5
1	D	158	ALA	4.3
1	C	159	GLY	4.2
1	D	163	ASP	4.1
1	C	143	LEU	4.0
1	B	125	LEU	3.9
1	D	39	ASP	3.9
1	D	142	GLU	3.8
1	D	122	ARG	3.8
1	C	209	ALA	3.8
1	D	126	GLU	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	114	LYS	3.7
1	D	120	THR	3.6
1	D	165	ILE	3.5
1	C	192	HIS	3.4
1	B	39	ASP	3.4
1	D	127	ASN	3.3
1	D	121	HIS	3.3
1	D	128	GLY	3.3
1	D	164	ASP	3.2
1	A	192	HIS	3.2
1	A	209	ALA	3.1
1	D	197	TRP	3.0
1	C	157	PHE	3.0
1	C	126	GLU	3.0
1	D	131	GLU	3.0
1	D	112	LEU	3.0
1	D	119	HIS	2.9
1	D	162	GLU	2.9
1	A	125	LEU	2.9
1	D	209	ALA	2.9
1	D	85	LEU	2.9
1	D	84	VAL	2.8
1	D	130	GLU	2.8
1	D	156	VAL	2.8
1	D	166	THR	2.7
1	C	158	ALA	2.7
1	D	202	ARG	2.7
1	B	143	LEU	2.7
1	C	62	ASP	2.5
1	D	194	ASN	2.5
1	B	85	LEU	2.5
1	C	119	HIS	2.4
1	D	124	ALA	2.4
1	D	48	GLN	2.4
1	D	192	HIS	2.3
1	B	6	LEU	2.3
1	D	129	ASP	2.3
1	D	144	ASP	2.2
1	D	145	GLY	2.2
1	C	195	ALA	2.2
1	C	206	GLN	2.2
1	A	107	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	160	ASP	2.2
1	D	86	ALA	2.2
1	B	128	GLY	2.1
1	C	128	GLY	2.1
1	B	165	ILE	2.1
1	C	39	ASP	2.1
1	C	208	TYR	2.1
1	B	5	VAL	2.1
1	D	117	GLY	2.1
1	D	107	ILE	2.1
1	D	157	PHE	2.0
1	B	48	GLN	2.0
1	D	82	VAL	2.0
1	C	141	ASP	2.0
1	C	163	ASP	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](#)

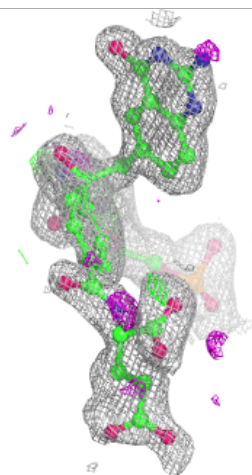
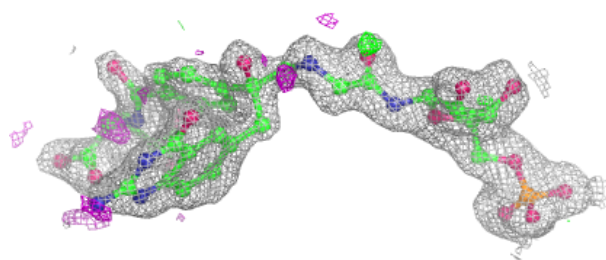
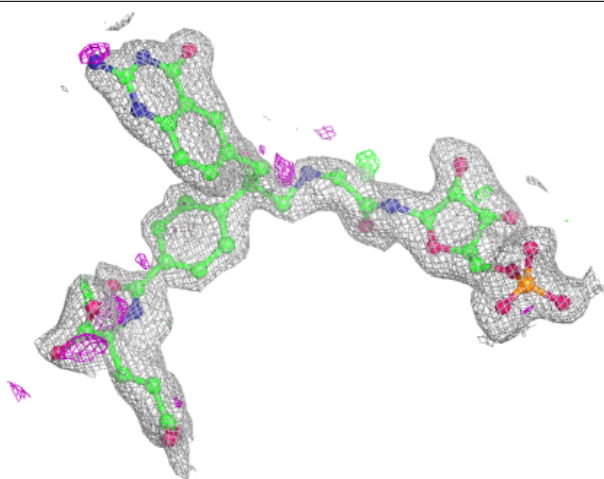
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q < 0.9
2	138	D	4221	52/52	0.86	0.16	26,31,43,46	0
2	138	C	3221	52/52	0.89	0.13	19,24,39,44	0
2	138	B	2221	52/52	0.93	0.12	14,18,40,44	0
2	138	A	1221	52/52	0.94	0.13	10,16,39,44	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 138 D 4221:**

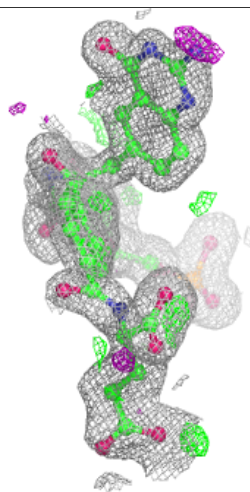
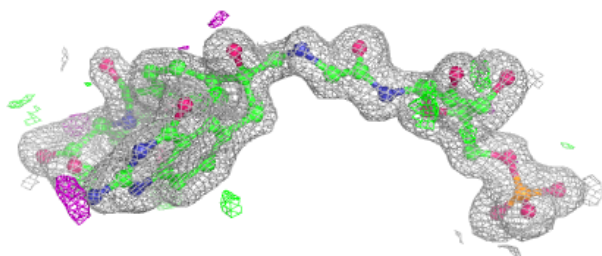
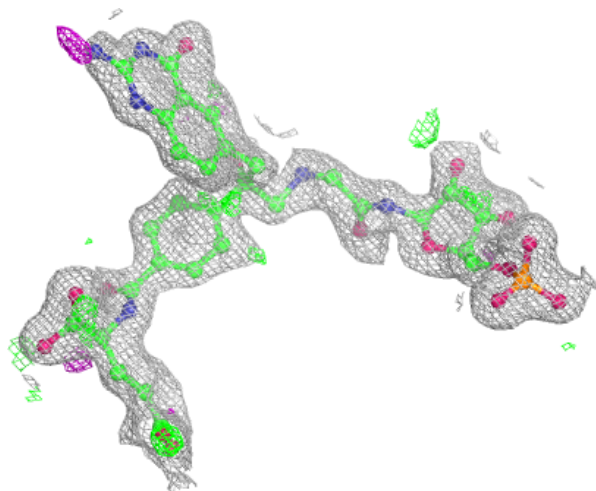
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





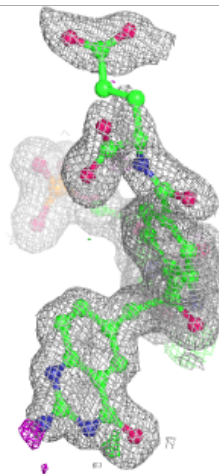
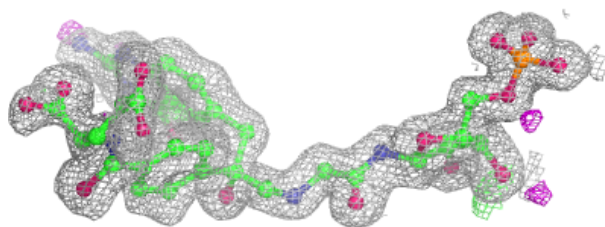
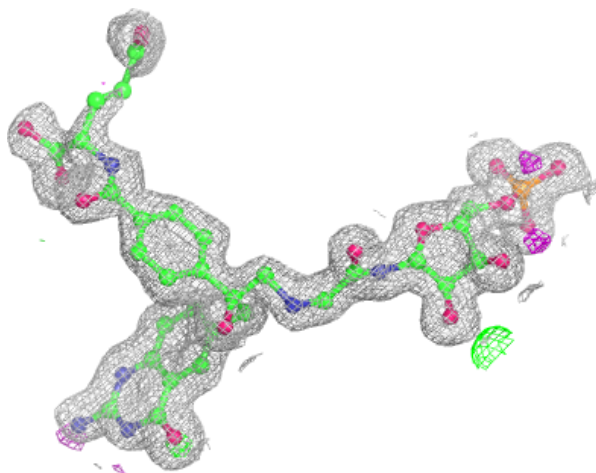
**Electron density around 138 C 3221:**

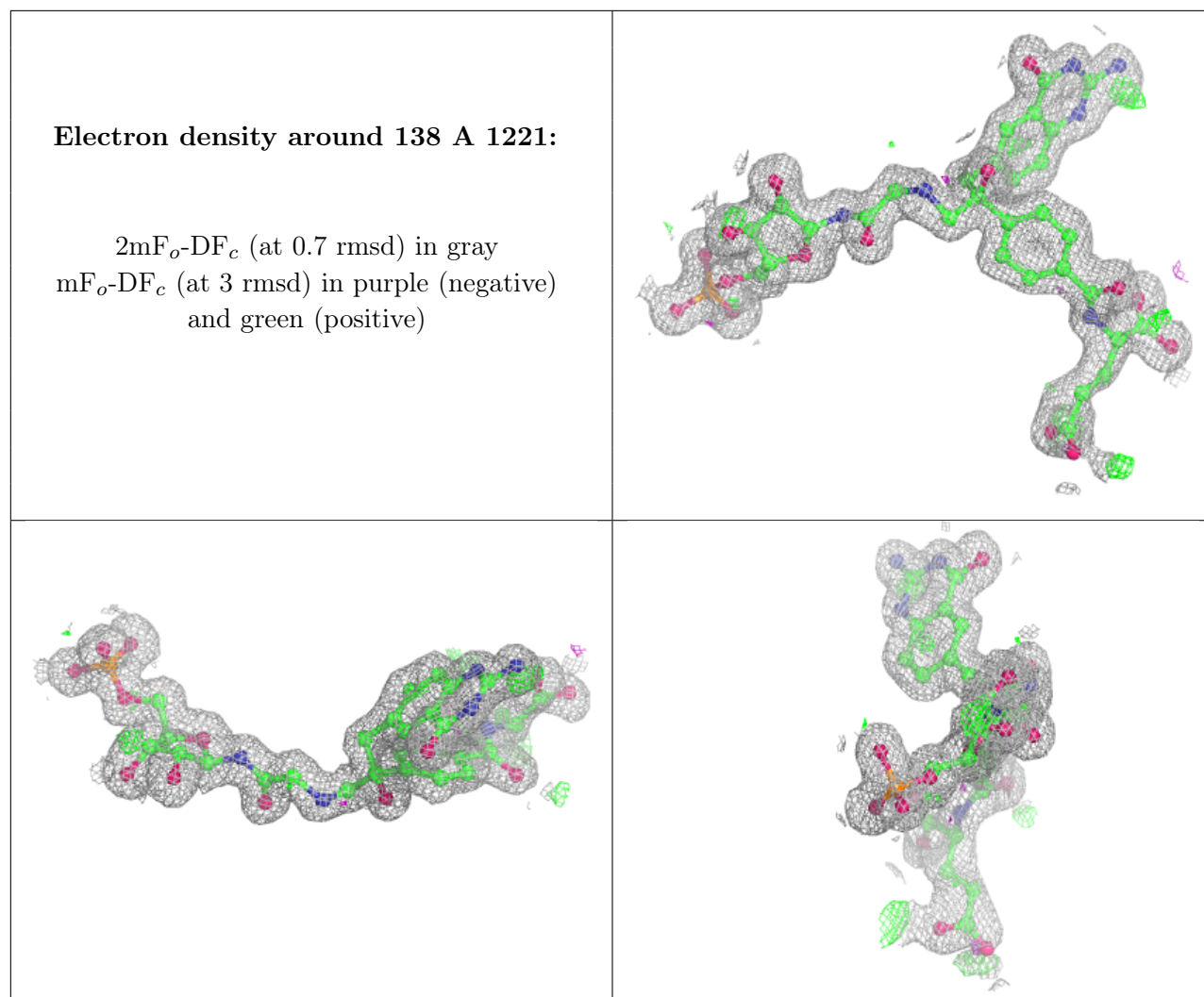
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 138 B 2221:**

$2mF_o-DF_c$  (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.