



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 07:46 AM EDT

PDB ID : 5DHQ  
Title : Crystal structure of NAD kinase 1 from *Listeria monocytogenes* in complex with a novel inhibitor  
Authors : Gelin, M.; Paoletti, J.; Assairi, L.; Huteau, V.; Pochet, S.; Labesse, G.  
Deposited on : 2015-08-31  
Resolution : 2.29 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 : 2.37.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

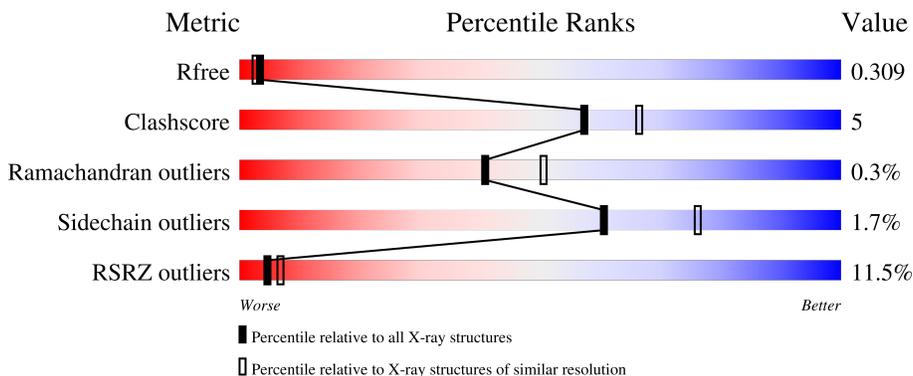
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.29 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 <sub>free</sub>	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	272	
1	B	272	
1	C	272	
1	D	272	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 8483 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 NAD kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	263	2070	1324	347	390	9	0	1	0
1	B	260	2069	1328	347	385	9	0	0	0
1	C	260	2016	1294	339	374	9	0	0	0
1	D	253	1966	1257	337	364	8	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

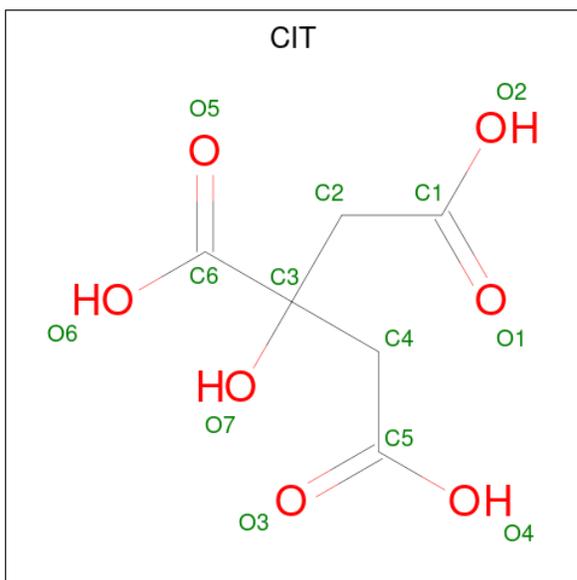
Chain	Residue	Modelled	Actual	Comment	Reference
A	265	LEU	-	expression tag	UNP Q8Y8D7
A	266	GLU	-	expression tag	UNP Q8Y8D7
A	267	HIS	-	expression tag	UNP Q8Y8D7
A	268	HIS	-	expression tag	UNP Q8Y8D7
A	269	HIS	-	expression tag	UNP Q8Y8D7
A	270	HIS	-	expression tag	UNP Q8Y8D7
A	271	HIS	-	expression tag	UNP Q8Y8D7
A	272	HIS	-	expression tag	UNP Q8Y8D7
B	265	LEU	-	expression tag	UNP Q8Y8D7
B	266	GLU	-	expression tag	UNP Q8Y8D7
B	267	HIS	-	expression tag	UNP Q8Y8D7
B	268	HIS	-	expression tag	UNP Q8Y8D7
B	269	HIS	-	expression tag	UNP Q8Y8D7
B	270	HIS	-	expression tag	UNP Q8Y8D7
B	271	HIS	-	expression tag	UNP Q8Y8D7
B	272	HIS	-	expression tag	UNP Q8Y8D7
C	265	LEU	-	expression tag	UNP Q8Y8D7
C	266	GLU	-	expression tag	UNP Q8Y8D7
C	267	HIS	-	expression tag	UNP Q8Y8D7
C	268	HIS	-	expression tag	UNP Q8Y8D7
C	269	HIS	-	expression tag	UNP Q8Y8D7

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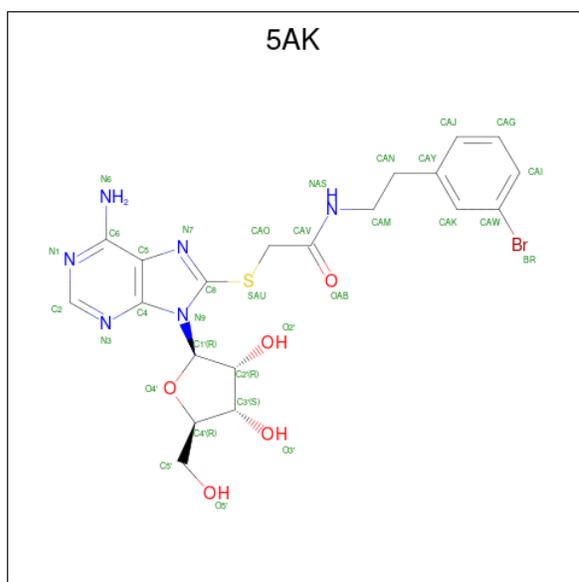
Chain	Residue	Modelled	Actual	Comment	Reference
C	270	HIS	-	expression tag	UNP Q8Y8D7
C	271	HIS	-	expression tag	UNP Q8Y8D7
C	272	HIS	-	expression tag	UNP Q8Y8D7
D	265	LEU	-	expression tag	UNP Q8Y8D7
D	266	GLU	-	expression tag	UNP Q8Y8D7
D	267	HIS	-	expression tag	UNP Q8Y8D7
D	268	HIS	-	expression tag	UNP Q8Y8D7
D	269	HIS	-	expression tag	UNP Q8Y8D7
D	270	HIS	-	expression tag	UNP Q8Y8D7
D	271	HIS	-	expression tag	UNP Q8Y8D7
D	272	HIS	-	expression tag	UNP Q8Y8D7

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



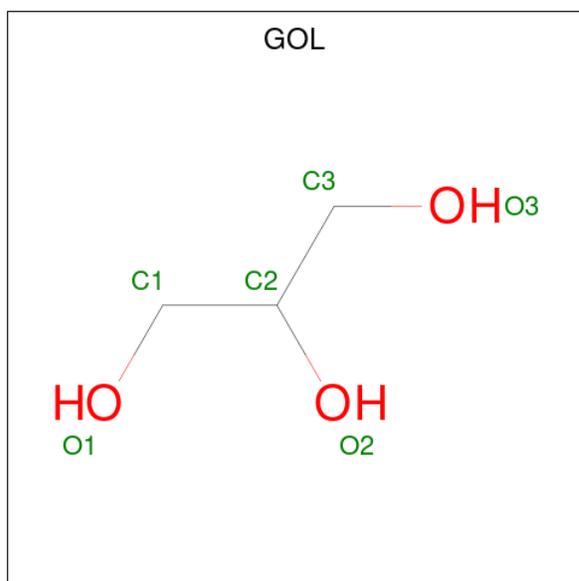
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf		
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is 8-[(2-{[2-(3-bromophenyl)ethyl]amino}-2-oxoethyl)sulfanyl]adenosine (three-letter code: 5AK) (formula: C<sub>20</sub>H<sub>23</sub>BrN<sub>6</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	Br	C	N	O			S
3	A	1	Total 33	Br 1	C 20	N 6	O 5	S 1	0	0
3	B	1	Total 33	Br 1	C 20	N 6	O 5	S 1	0	0
3	C	1	Total 33	Br 1	C 20	N 6	O 5	S 1	0	0
3	D	1	Total 33	Br 1	C 20	N 6	O 5	S 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

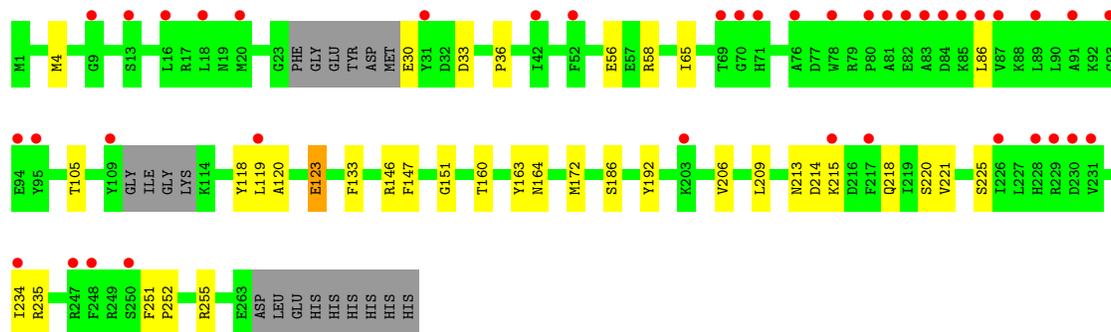


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	56	Total	O	0	0
			56	56		
5	B	36	Total	O	0	0
			36	36		
5	C	63	Total	O	0	0
			63	63		
5	D	43	Total	O	0	0
			43	43		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.79Å 119.18Å 67.21Å 90.00° 99.91° 90.00°	Depositor
Resolution (Å)	44.29 – 2.29 44.29 – 2.29	Depositor EDS
% Data completeness (in resolution range)	89.9 (44.29-2.29) 90.1 (44.29-2.29)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.56 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.260 , 0.311 0.262 , 0.309	Depositor DCC
$R_{free}$ test set	1273 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.9	Xtrriage
Anisotropy	0.149	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 56.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.016 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8483	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.24% 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: GOL, CIT, 5AK

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	0.20	0/2125	0.35	0/2876
1	B	0.21	0/2117	0.35	0/2858
1	C	0.20	0/2065	0.35	0/2795
1	D	0.21	0/2013	0.36	0/2728
All	All	0.21	0/8320	0.35	0/11257

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	2070	0	1990	12	0
1	B	2069	0	2022	24	0
1	C	2016	0	1923	20	0
1	D	1966	0	1876	19	0
2	A	13	0	5	0	0
2	B	13	0	5	0	0
3	A	33	0	0	2	0
3	B	33	0	0	2	0
3	C	33	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	33	0	0	4	0
4	C	6	0	8	0	0
5	A	56	0	0	0	0
5	B	36	0	0	1	0
5	C	63	0	0	4	0
5	D	43	0	0	1	0
All	All	8483	0	7829	79	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 5.

All (79) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:ILE:HD13	1:A:90:LEU:HD22	1.77	0.67
1:D:160:THR:HG21	1:D:172:MET:HG2	1.81	0.62
1:C:188:ASN:ND2	5:C:401:HOH:O	2.35	0.59
1:C:125:THR:OG1	1:C:220:SER:OG	2.19	0.59
1:B:24:PHE:HD1	1:B:29:MET:HG3	1.69	0.58
1:D:30:GLU:N	5:D:402:HOH:O	2.36	0.58
1:D:218:GLN:OE1	1:D:225:SER:OG	2.20	0.57
1:C:24:PHE:HB3	1:C:29:MET:HB2	1.87	0.57
1:B:125:THR:OG1	1:B:220:SER:OG	2.22	0.56
1:B:38:ILE:HD13	1:B:90:LEU:HD22	1.85	0.56
1:D:65:ILE:HG21	1:D:86:LEU:HD21	1.88	0.56
3:B:302:5AK:C2'	3:B:302:5AK:SAU	2.93	0.55
1:D:213:ASN:O	1:D:215:LYS:N	2.39	0.55
1:D:36:PRO:HD2	1:D:58:ARG:HE	1.74	0.53
1:B:104:LYS:HB2	1:B:239:SER:HB2	1.92	0.52
1:B:138:VAL:HB	1:B:208:SER:HB3	1.91	0.52
1:A:108:LYS:NZ	1:A:115:GLU:OE1	2.42	0.52
1:C:79:ARG:HG3	1:C:80:PRO:HD2	1.92	0.51
1:A:261:PHE:O	1:C:193:ARG:NH2	2.43	0.51
1:D:252:PRO:HD2	1:D:255:ARG:HD3	1.93	0.50
1:B:96:GLN:N	5:B:407:HOH:O	2.45	0.49
1:B:33:ASP:O	1:B:55:TYR:OH	2.27	0.49
1:B:209:LEU:HB2	1:B:234:ILE:HB	1.95	0.49
1:C:215:LYS:NZ	5:C:404:HOH:O	2.40	0.49
1:D:4:MET:HG3	1:D:33:ASP:HA	1.95	0.49
1:C:229:ARG:NH2	5:C:407:HOH:O	2.46	0.48
1:B:49:LEU:HD23	1:B:121:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:MET:HE1	1:C:178:ALA:HB3	1.96	0.48
1:D:123:GLU:OE2	3:D:301:5AK:O2'	2.32	0.47
1:A:82:GLU:OE1	1:A:249:ARG:NH2	2.47	0.47
1:B:218:GLN:NE2	1:B:225:SER:OG	2.30	0.47
1:C:5:ILE:HG12	1:C:40:ILE:HB	1.96	0.47
1:D:209:LEU:HB2	1:D:234:ILE:HB	1.97	0.46
1:A:34:VAL:HG12	1:A:35:GLU:HG3	1.96	0.46
1:D:56:GLU:HB3	1:D:119:LEU:HD12	1.97	0.46
1:D:120:ALA:HB2	1:D:221:VAL:HG13	1.97	0.46
1:B:218:GLN:HE21	1:B:225:SER:HG	1.61	0.45
1:B:106:THR:HB	1:B:235:ARG:HB2	1.97	0.45
1:A:210:GLN:HA	1:A:211:PRO:HD3	1.84	0.45
1:B:173:HIS:HA	1:B:174:PRO:HD3	1.85	0.44
1:D:160:THR:HA	1:D:164:ASN:HB3	1.99	0.44
1:C:189:ASN:C	1:C:191:VAL:H	2.21	0.44
1:A:218:GLN:NE2	1:A:225:SER:OG	2.37	0.44
1:C:27:TYR:N	5:C:410:HOH:O	2.51	0.44
1:B:133:PHE:CD2	1:B:151:GLY:HA2	2.53	0.43
1:C:49:LEU:HD23	1:C:222:ASP:HB3	1.99	0.43
1:B:160:THR:HA	1:B:164:ASN:HB3	2.00	0.43
1:C:226:ILE:HG13	1:C:228:HIS:CE1	2.53	0.43
1:D:146:ARG:HG2	1:D:192:TYR:HD1	1.83	0.43
1:B:7:SER:HB2	1:B:17:ARG:HD2	2.00	0.42
1:D:206:VAL:HG11	1:D:235:ARG:NH2	2.34	0.42
1:A:133:PHE:CD2	1:A:151:GLY:HA2	2.54	0.42
1:B:188:ASN:OD1	1:B:194:THR:N	2.47	0.42
1:D:220:SER:HA	1:D:225:SER:HA	2.01	0.42
3:D:301:5AK:SAU	3:D:301:5AK:C2'	3.08	0.42
3:A:302:5AK:NAS	3:A:302:5AK:CAJ	2.76	0.42
3:A:302:5AK:N6	1:C:150:ASP:OD1	2.53	0.42
1:A:146:ARG:HG2	1:A:192:TYR:HD1	1.84	0.42
1:C:63:ALA:HB1	1:C:246:ALA:HB2	2.01	0.42
3:D:301:5AK:CAV	3:D:301:5AK:CAJ	2.97	0.42
1:A:119:LEU:HD11	1:A:241:LYS:HD2	2.01	0.42
1:C:137:VAL:HB	1:C:145:GLU:HG2	2.02	0.42
1:D:147:PHE:CE2	1:D:186:SER:HB2	2.55	0.42
1:C:77:ASP:OD2	1:C:247:ARG:NH1	2.53	0.41
1:B:210:GLN:HA	1:B:211:PRO:HD3	1.84	0.41
1:B:105:THR:HB	1:B:118:TYR:HB2	2.01	0.41
1:B:128:SER:HB3	1:B:133:PHE:HB2	2.03	0.41
1:C:90:LEU:HB3	1:C:248:PHE:HZ	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:105:THR:HB	1:D:118:TYR:HB2	2.03	0.41
1:B:78:TRP:CD2	1:B:86:LEU:HD21	2.56	0.41
1:B:123:GLU:OE1	3:B:302:5AK:O2'	2.38	0.41
1:B:128:SER:OG	1:B:131:GLY:O	2.31	0.41
1:C:189:ASN:O	1:C:191:VAL:N	2.51	0.41
1:A:146:ARG:HG2	1:A:192:TYR:CD1	2.56	0.41
1:B:139:ILE:O	1:B:142:ILE:HG22	2.20	0.41
1:D:133:PHE:CD2	1:D:151:GLY:HA2	2.56	0.41
1:A:1:MET:HB2	1:A:29:MET:SD	2.61	0.40
1:C:123:GLU:OE1	3:C:301:5AK:O2'	2.39	0.40
3:D:301:5AK:CAJ	3:D:301:5AK:NAS	2.83	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	260/272 (96%)	247 (95%)	12 (5%)	1 (0%)	34	42
1	B	252/272 (93%)	233 (92%)	19 (8%)	0	100	100
1	C	254/272 (93%)	232 (91%)	21 (8%)	1 (0%)	34	42
1	D	247/272 (91%)	231 (94%)	15 (6%)	1 (0%)	34	42
All	All	1013/1088 (93%)	943 (93%)	67 (7%)	3 (0%)	41	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	190	ARG
1	D	214	ASP
1	A	130	GLY

### 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	221/237 (93%)	216 (98%)	5 (2%)	50	67
1	B	224/237 (94%)	220 (98%)	4 (2%)	59	75
1	C	210/237 (89%)	207 (99%)	3 (1%)	67	81
1	D	205/237 (86%)	202 (98%)	3 (2%)	65	79
All	All	860/948 (91%)	845 (98%)	15 (2%)	60	76

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	LEU
1	A	86	LEU
1	A	163	TYR
1	A	251	PHE
1	A	258	HIS
1	B	163	TYR
1	B	213	ASN
1	B	223	HIS
1	B	251	PHE
1	C	113	LYS
1	C	163	TYR
1	C	251	PHE
1	D	123	GLU
1	D	163	TYR
1	D	251	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

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
3	5AK	D	301	-	34,36,36	2.86	16 (47%)	35,51,51	2.64	8 (22%)
3	5AK	A	302	-	34,36,36	2.55	7 (20%)	35,51,51	2.18	4 (11%)
3	5AK	C	301	-	34,36,36	3.24	14 (41%)	35,51,51	2.80	6 (17%)
4	GOL	C	302	-	5,5,5	0.37	0	5,5,5	0.27	0
2	CIT	A	301	-	12,12,12	0.99	0	17,17,17	1.82	3 (17%)
2	CIT	B	301	-	12,12,12	1.04	0	17,17,17	1.60	2 (11%)
3	5AK	B	302	-	34,36,36	3.62	16 (47%)	35,51,51	2.66	9 (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
3	5AK	D	301	-	-	2/11/45/45	0/4/4/4
3	5AK	A	302	-	-	5/11/45/45	0/4/4/4
3	5AK	C	301	-	-	3/11/45/45	0/4/4/4
4	GOL	C	302	-	-	2/4/4/4	-
2	CIT	A	301	-	-	8/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CIT	B	301	-	-	8/16/16/16	-
3	5AK	B	302	-	-	3/11/45/45	0/4/4/4

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	302	5AK	BR-CAW	-10.15	1.69	1.90
3	A	302	5AK	C2-N3	10.11	1.48	1.32
3	B	302	5AK	C8-SAU	-9.31	1.50	1.75
3	C	301	5AK	C8-SAU	-8.29	1.53	1.75
3	D	301	5AK	C2-N3	8.13	1.45	1.32
3	B	302	5AK	C2-N3	7.95	1.44	1.32
3	A	302	5AK	C2-N1	7.75	1.48	1.33
3	C	301	5AK	BR-CAW	-7.52	1.75	1.90
3	C	301	5AK	C2-N3	7.28	1.43	1.32
3	D	301	5AK	C2-N1	6.51	1.46	1.33
3	B	302	5AK	C2-N1	6.16	1.45	1.33
3	C	301	5AK	C8-N9	-6.16	1.30	1.36
3	D	301	5AK	BR-CAW	-6.10	1.78	1.90
3	B	302	5AK	C8-N9	-5.89	1.30	1.36
3	C	301	5AK	CAN-CAY	-5.26	1.36	1.51
3	C	301	5AK	C2-N1	5.20	1.43	1.33
3	B	302	5AK	CAN-CAY	-4.96	1.37	1.51
3	B	302	5AK	C2'-C1'	-4.80	1.46	1.53
3	D	301	5AK	C8-N9	-4.64	1.31	1.36
3	D	301	5AK	CAN-CAY	-4.44	1.38	1.51
3	A	302	5AK	CAN-CAY	-4.25	1.39	1.51
3	C	301	5AK	C5-C4	-3.87	1.30	1.40
3	A	302	5AK	C8-N9	-3.65	1.32	1.36
3	B	302	5AK	C5-C4	-3.60	1.31	1.40
3	D	301	5AK	C5-C4	-3.39	1.32	1.40
3	B	302	5AK	C6-C5	-3.15	1.31	1.43
3	C	301	5AK	O4'-C4'	-3.10	1.38	1.45
3	D	301	5AK	C6-C5	-3.06	1.31	1.43
3	D	301	5AK	C2'-C1'	-3.03	1.49	1.53
3	C	301	5AK	C6-C5	-3.02	1.32	1.43
3	D	301	5AK	C2'-C3'	-2.95	1.45	1.53
3	D	301	5AK	C8-SAU	-2.93	1.67	1.75
3	D	301	5AK	C3'-C4'	-2.90	1.45	1.53
3	C	301	5AK	C4-N3	-2.79	1.31	1.35
3	B	302	5AK	C2'-C3'	-2.71	1.45	1.53
3	C	301	5AK	C2'-C1'	-2.67	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	5AK	C6-C5	-2.65	1.33	1.43
3	C	301	5AK	C2'-C3'	-2.65	1.46	1.53
3	A	302	5AK	C5-C4	-2.57	1.34	1.40
3	C	301	5AK	O2'-C2'	-2.53	1.37	1.43
3	D	301	5AK	O4'-C4'	-2.46	1.39	1.45
3	B	302	5AK	O3'-C3'	-2.36	1.37	1.43
3	D	301	5AK	C4-N3	-2.34	1.32	1.35
3	B	302	5AK	C4-N3	-2.33	1.32	1.35
3	B	302	5AK	O4'-C4'	-2.27	1.39	1.45
3	B	302	5AK	O2'-C2'	-2.24	1.37	1.43
3	D	301	5AK	O4'-C1'	-2.20	1.38	1.41
3	D	301	5AK	O3'-C3'	-2.19	1.37	1.43
3	C	301	5AK	O3'-C3'	-2.16	1.37	1.43
3	D	301	5AK	C1'-N9	-2.06	1.43	1.49
3	A	302	5AK	O4'-C1'	2.06	1.43	1.41
3	B	302	5AK	C1'-N9	-2.05	1.43	1.49
3	B	302	5AK	CAO-CAV	-2.03	1.49	1.51

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	301	5AK	N3-C2-N1	-13.28	107.92	128.68
3	B	302	5AK	N3-C2-N1	-12.83	108.63	128.68
3	D	301	5AK	N3-C2-N1	-12.83	108.63	128.68
3	A	302	5AK	N3-C2-N1	-11.15	111.25	128.68
2	A	301	CIT	O6-C6-C3	5.31	122.27	113.05
3	C	301	5AK	O4'-C4'-C5'	-5.07	98.26	109.21
2	B	301	CIT	O6-C6-C3	4.34	120.58	113.05
3	C	301	5AK	C1'-N9-C4	-3.93	119.82	126.71
3	D	301	5AK	O4'-C4'-C3'	-3.33	98.53	105.11
3	B	302	5AK	O4'-C1'-C2'	-3.32	102.07	106.93
3	B	302	5AK	C5'-C4'-C3'	-3.13	107.54	115.09
3	D	301	5AK	C1'-N9-C4	-3.03	121.40	126.71
3	C	301	5AK	C3'-C2'-C1'	3.02	105.52	100.98
3	B	302	5AK	O3'-C3'-C2'	-2.97	102.20	111.82
3	A	302	5AK	C5-C6-N6	-2.94	115.88	120.35
3	C	301	5AK	C2-N1-C6	2.90	123.72	118.75
3	D	301	5AK	C2-N1-C6	2.66	123.30	118.75
3	B	302	5AK	C5-C6-N6	-2.63	116.35	120.35
3	C	301	5AK	C5'-C4'-C3'	-2.61	108.78	115.09
3	D	301	5AK	O4'-C1'-C2'	-2.59	103.14	106.93
3	D	301	5AK	O2'-C2'-C3'	-2.58	103.47	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302	5AK	C1'-N9-C4	-2.47	122.38	126.71
3	B	302	5AK	C3'-C2'-C1'	2.47	104.69	100.98
3	B	302	5AK	O2'-C2'-C3'	-2.46	103.88	111.82
3	D	301	5AK	C2'-C3'-C4'	-2.38	98.02	102.64
3	B	302	5AK	C2-N1-C6	2.38	122.82	118.75
3	A	302	5AK	C5'-C4'-C3'	-2.32	109.50	115.09
3	D	301	5AK	C5-C6-N6	-2.29	116.87	120.35
3	A	302	5AK	C3'-C2'-C1'	2.07	104.10	100.98
2	A	301	CIT	O5-C6-C3	-2.07	119.32	122.25
2	A	301	CIT	O4-C5-C4	2.04	120.90	114.35
2	B	301	CIT	O4-C5-C4	2.01	120.82	114.35

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	CIT	C2-C3-C6-O6
2	A	301	CIT	O7-C3-C6-O5
2	A	301	CIT	O7-C3-C6-O6
2	B	301	CIT	C2-C3-C4-C5
2	B	301	CIT	C2-C3-C6-O6
3	C	301	5AK	O4'-C4'-C5'-O5'
3	C	301	5AK	C3'-C4'-C5'-O5'
2	B	301	CIT	C6-C3-C4-C5
3	A	302	5AK	O4'-C4'-C5'-O5'
3	A	302	5AK	C3'-C4'-C5'-O5'
3	D	301	5AK	NAS-CAM-CAN-CAY
4	C	302	GOL	O1-C1-C2-C3
2	A	301	CIT	C4-C3-C6-O5
2	A	301	CIT	C1-C2-C3-O7
4	C	302	GOL	O1-C1-C2-O2
2	B	301	CIT	O7-C3-C4-C5
3	A	302	5AK	NAS-CAM-CAN-CAY
3	C	301	5AK	NAS-CAM-CAN-CAY
2	B	301	CIT	O7-C3-C6-O6
2	A	301	CIT	C2-C3-C6-O5
2	A	301	CIT	C4-C3-C6-O6
2	B	301	CIT	C2-C3-C6-O5
2	B	301	CIT	C4-C3-C6-O6
2	B	301	CIT	C4-C3-C6-O5
2	A	301	CIT	C1-C2-C3-C4
3	D	301	5AK	C3'-C4'-C5'-O5'

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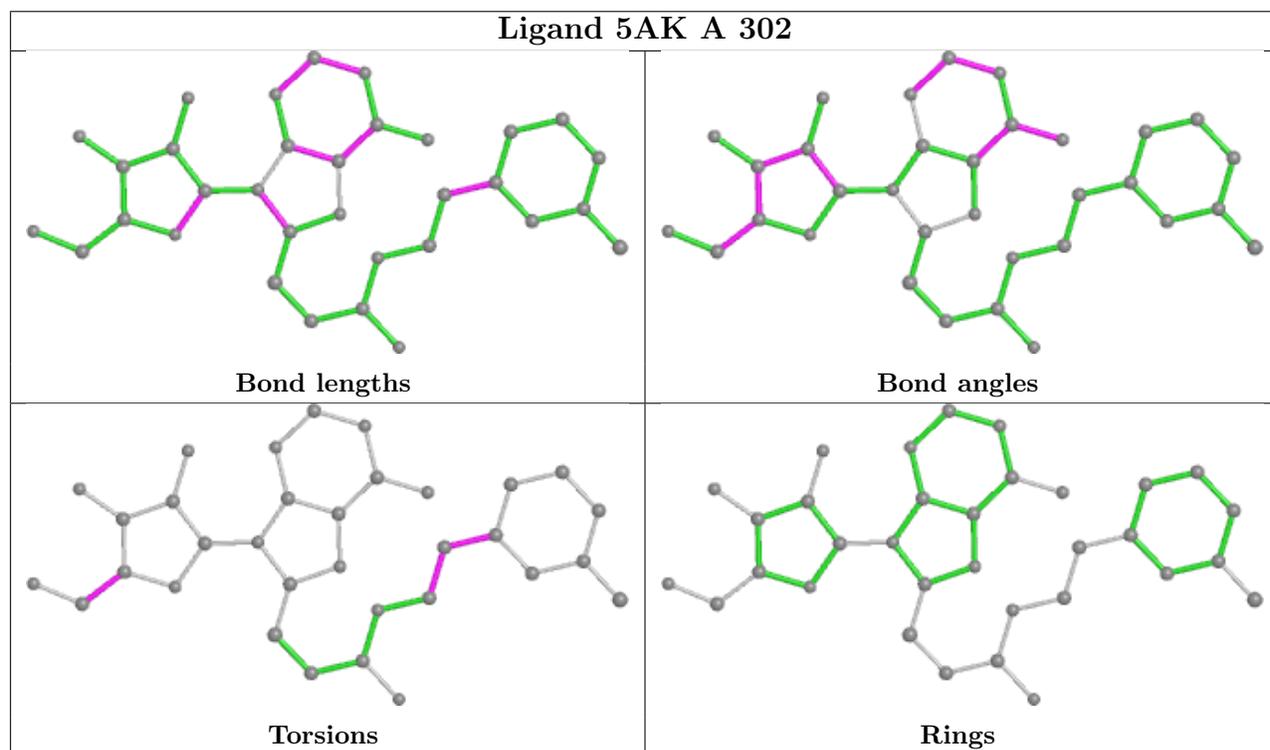
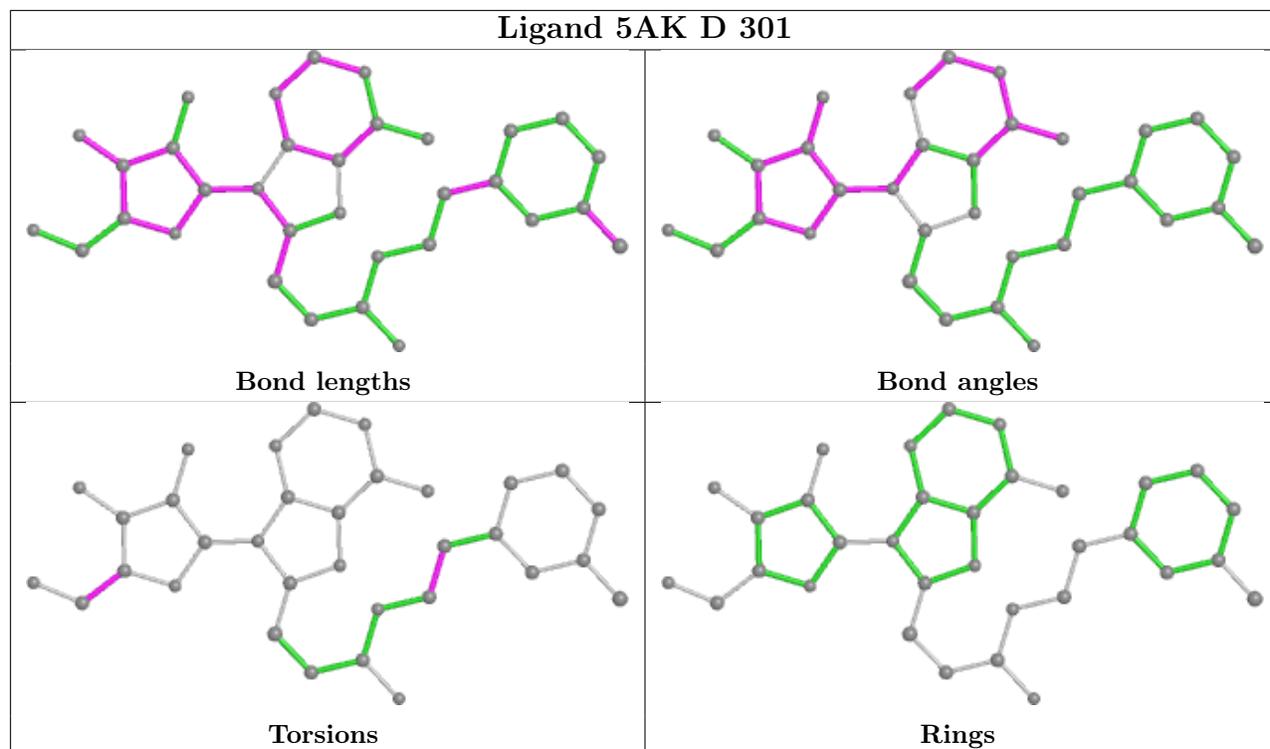
Mol	Chain	Res	Type	Atoms
3	B	302	5AK	NAS-CAM-CAN-CAY
3	A	302	5AK	CAM-CAN-CAY-CAJ
3	B	302	5AK	CAM-CAN-CAY-CAJ
3	B	302	5AK	CAM-CAN-CAY-CAK
3	A	302	5AK	CAM-CAN-CAY-CAK

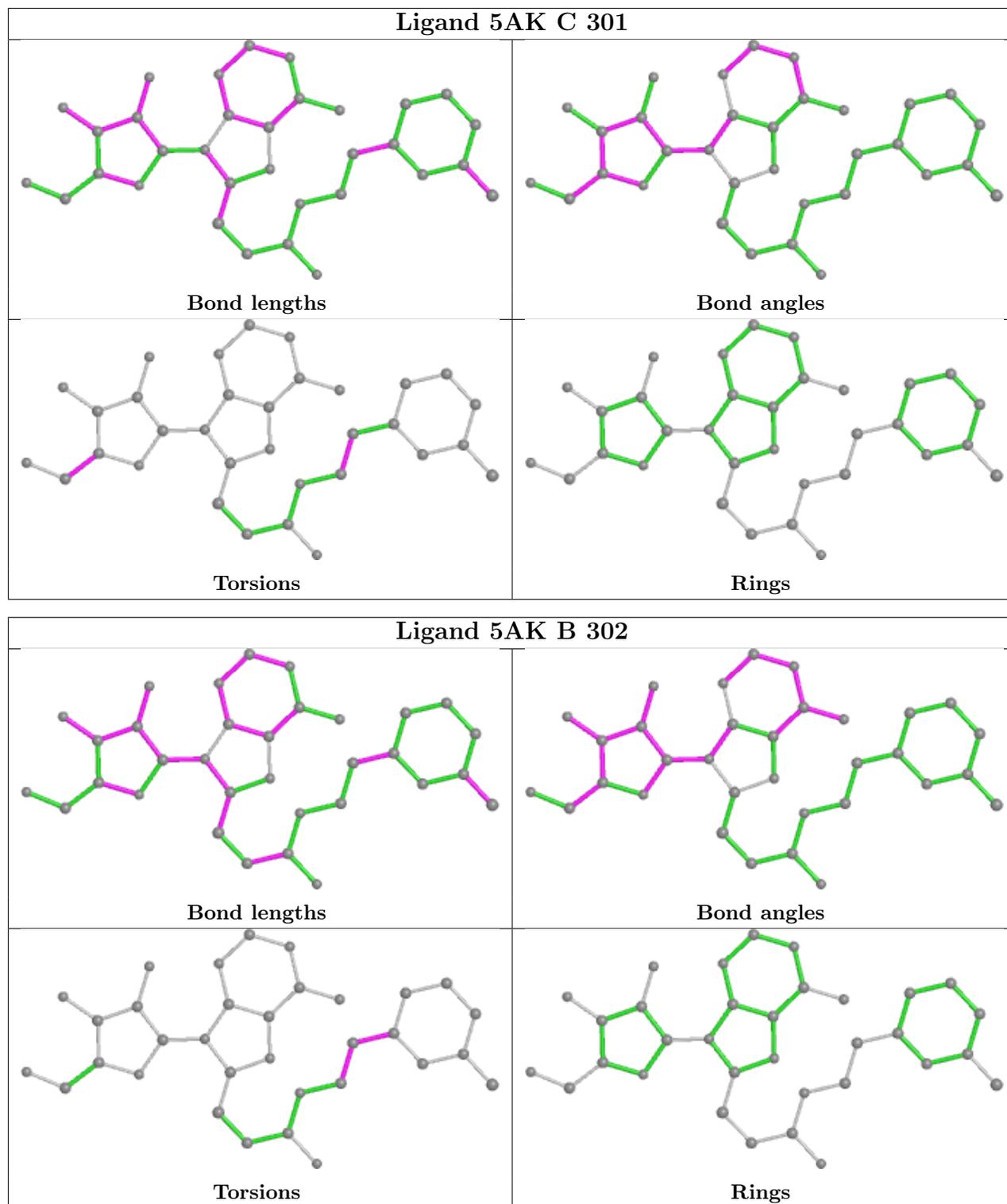
There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	301	5AK	4	0
3	A	302	5AK	2	0
3	C	301	5AK	1	0
3	B	302	5AK	2	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

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	263/272 (96%)	0.30	9 (3%) 45 52	25, 50, 90, 128	37 (14%)
1	B	260/272 (95%)	0.96	34 (13%) 3 4	29, 71, 114, 137	40 (15%)
1	C	260/272 (95%)	0.85	36 (13%) 2 4	27, 62, 114, 147	36 (13%)
1	D	253/272 (93%)	0.99	40 (15%) 2 2	35, 71, 128, 163	30 (11%)
All	All	1036/1088 (95%)	0.77	119 (11%) 4 7	25, 62, 117, 163	143 (13%)

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	90	LEU	6.6
1	B	20	MET	6.4
1	D	86	LEU	6.2
1	D	83	ALA	5.6
1	C	248	PHE	5.6
1	D	93	GLY	5.4
1	D	91	ALA	5.4
1	D	89	LEU	5.3
1	D	94	GLU	5.3
1	C	31	TYR	5.2
1	B	216	ASP	5.0
1	D	70	GLY	4.8
1	D	9	GLY	4.8
1	D	248	PHE	4.6
1	D	247	ARG	4.5
1	C	3	TYR	4.5
1	C	29	MET	4.4
1	A	248	PHE	4.3
1	B	70	GLY	4.1
1	B	230	ASP	4.0
1	D	217	PHE	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	95	TYR	4.0
1	C	92	LYS	3.7
1	D	18	LEU	3.7
1	C	24	PHE	3.6
1	C	65	ILE	3.6
1	A	110	GLY	3.5
1	C	95	TYR	3.5
1	D	78	TRP	3.5
1	B	217	PHE	3.4
1	B	89	LEU	3.4
1	C	88	LYS	3.4
1	D	109	TYR	3.3
1	B	91	ALA	3.3
1	D	13	SER	3.3
1	D	119	LEU	3.3
1	A	251	PHE	3.2
1	A	111	ILE	3.1
1	D	16	LEU	3.1
1	C	81	ALA	3.0
1	C	187	ILE	3.0
1	B	82	GLU	3.0
1	D	82	GLU	3.0
1	B	80	PRO	3.0
1	C	40	ILE	2.9
1	C	1	MET	2.9
1	A	250	SER	2.8
1	C	263	GLU	2.8
1	D	250	SER	2.8
1	B	3	TYR	2.8
1	B	55	TYR	2.8
1	B	109	TYR	2.8
1	D	80	PRO	2.8
1	B	213	ASN	2.8
1	C	212	VAL	2.7
1	D	81	ALA	2.7
1	C	19	ASN	2.7
1	C	93	GLY	2.7
1	C	18	LEU	2.7
1	C	78	TRP	2.7
1	B	83	ALA	2.6
1	B	84	ASP	2.6
1	D	20	MET	2.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	76	ALA	2.6
1	B	60	ASP	2.6
1	B	16	LEU	2.6
1	D	231	VAL	2.6
1	D	228	HIS	2.6
1	B	18	LEU	2.5
1	A	78	TRP	2.5
1	D	42	ILE	2.5
1	B	19	ASN	2.5
1	D	215	LYS	2.5
1	D	52	PHE	2.5
1	A	96	GLN	2.5
1	C	30	GLU	2.5
1	C	86	LEU	2.5
1	D	84	ASP	2.5
1	B	87	VAL	2.4
1	D	31	TYR	2.4
1	B	267	HIS	2.4
1	D	69	THR	2.4
1	A	217	PHE	2.4
1	C	188	ASN	2.4
1	D	87	VAL	2.4
1	D	234	ILE	2.3
1	C	94	GLU	2.3
1	C	82	GLU	2.3
1	C	246	ALA	2.3
1	B	198	PRO	2.3
1	A	90	LEU	2.3
1	B	229	ARG	2.3
1	B	30	GLU	2.3
1	D	85	LYS	2.3
1	C	87	VAL	2.3
1	C	230	ASP	2.3
1	C	116	ALA	2.3
1	B	215	LYS	2.2
1	D	230	ASP	2.2
1	B	66	GLY	2.2
1	C	76	ALA	2.2
1	C	91	ALA	2.2
1	D	203	LYS	2.2
1	C	67	ILE	2.2
1	C	224	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	226	ILE	2.1
1	B	227	LEU	2.1
1	B	24	PHE	2.1
1	C	247	ARG	2.1
1	D	229	ARG	2.1
1	C	198	PRO	2.1
1	B	114	LYS	2.1
1	B	167	LEU	2.1
1	C	236	TYR	2.1
1	D	71	HIS	2.0
1	B	49	LEU	2.0
1	B	57	GLU	2.0
1	B	96	GLN	2.0
1	B	172	MET	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.

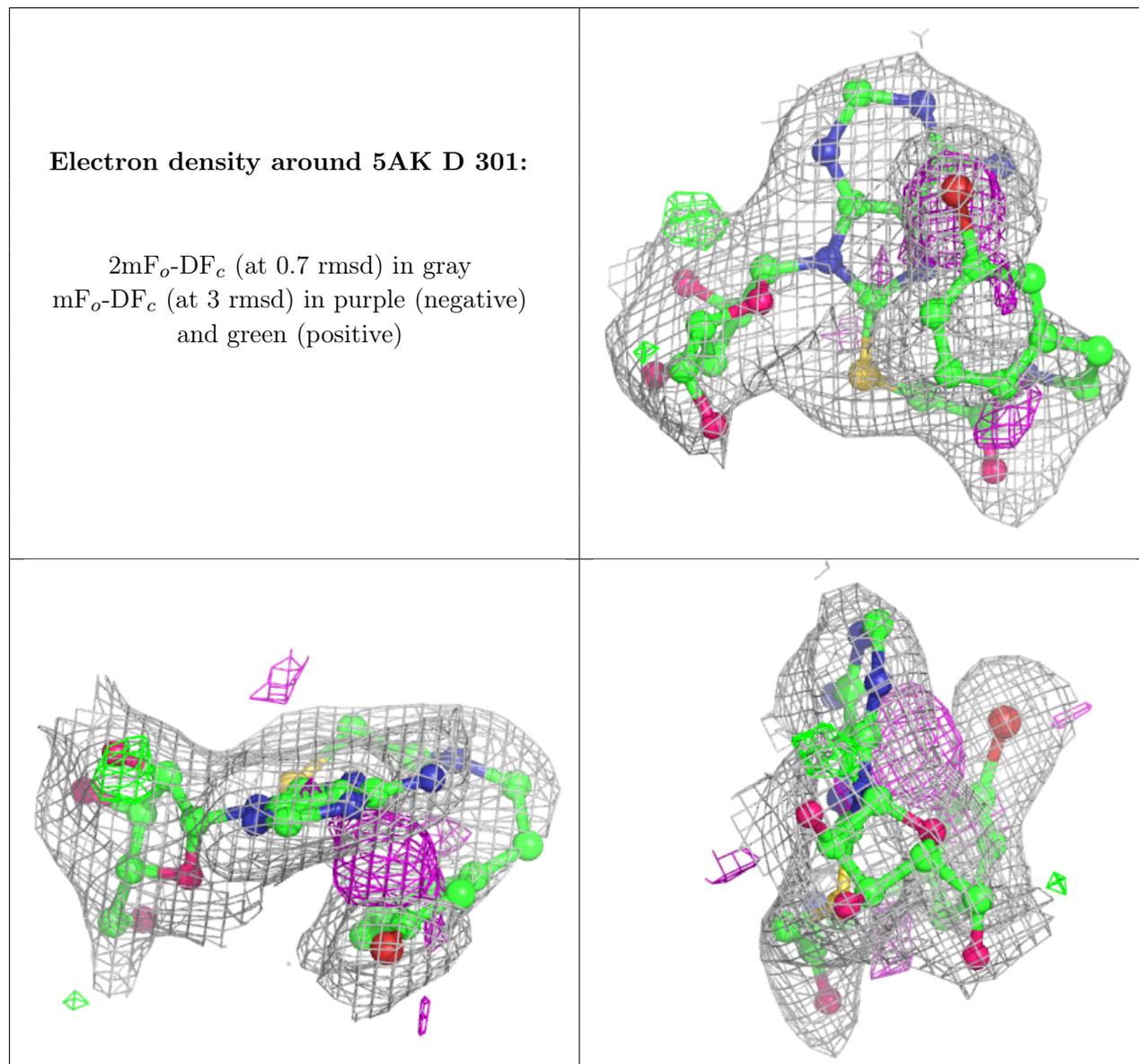
## 6.4 Ligands [i](#)

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
2	CIT	A	301	13/13	0.79	0.30	37,42,48,49	13
2	CIT	B	301	13/13	0.87	0.22	49,59,65,66	13
3	5AK	D	301	33/33	0.87	0.17	40,62,81,128	0
4	GOL	C	302	6/6	0.87	0.33	59,63,70,79	0
3	5AK	C	301	33/33	0.91	0.12	27,38,69,112	0
3	5AK	B	302	33/33	0.95	0.11	41,59,73,77	1
3	5AK	A	302	33/33	0.95	0.13	17,38,57,70	0

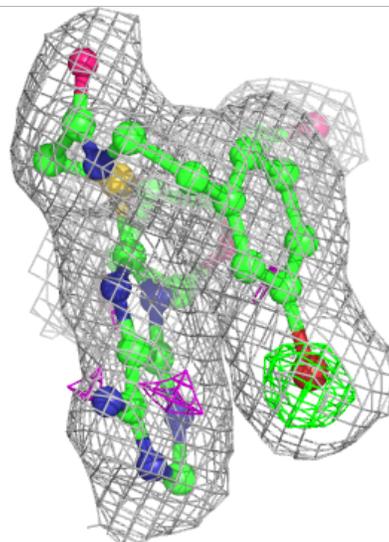
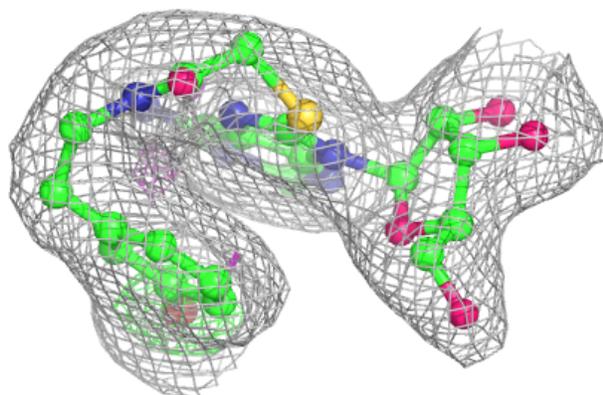
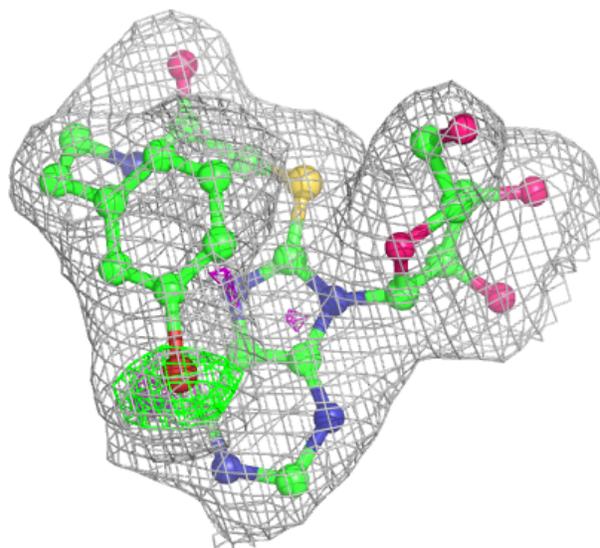
The following is a graphical depiction of the model fit to experimental electron density of all

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.



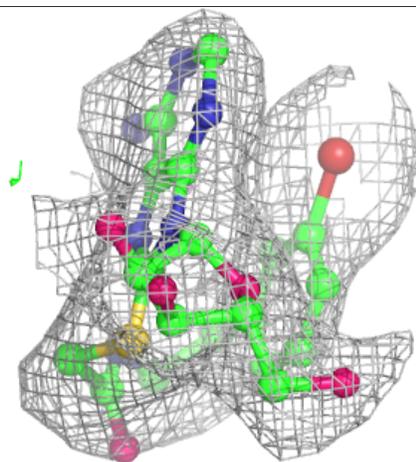
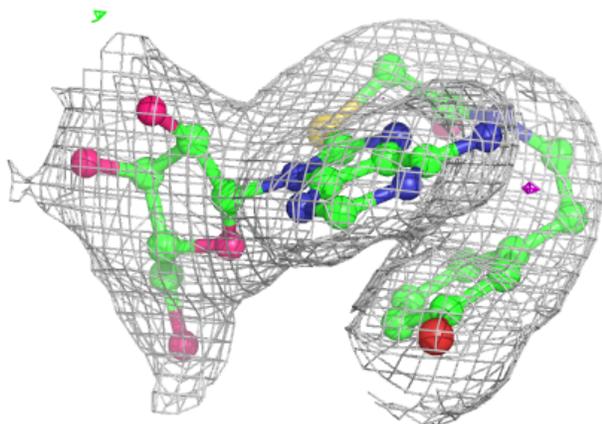
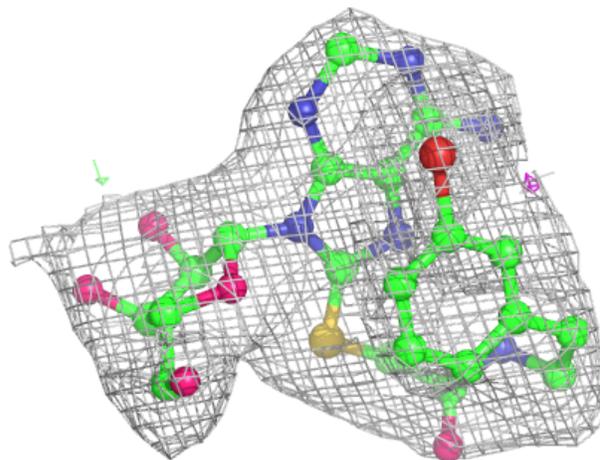
**Electron density around 5AK C 301:**

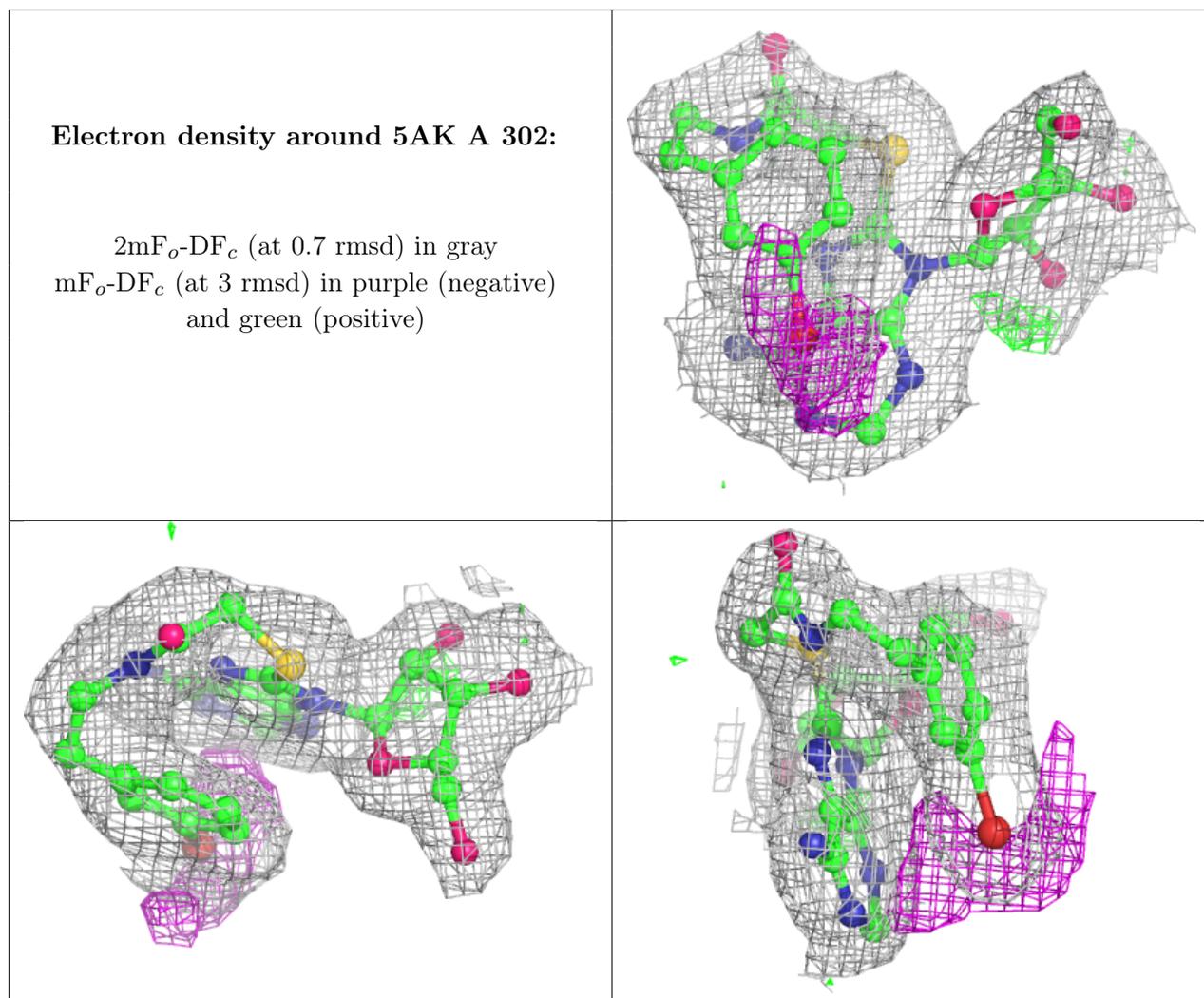
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 5AK B 302:**

$2mF_o-DF_c$  (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.