



# Full wwPDB X-ray Structure Validation Report ⓘ

May 10, 2025 – 07:12 pm BST

PDB ID : 9F8V / pdb\_00009f8v  
Title : Structure of the mouse 8-oxoguanine DNA Glycosylase mOGG1 in complex with ligand TH7420  
Authors : Scaletti, E.; Kosenina, S.; Stenmark, P.  
Deposited on : 2024-05-07  
Resolution : 2.40 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	:	1.8.4, CSD as541be (2020)
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	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

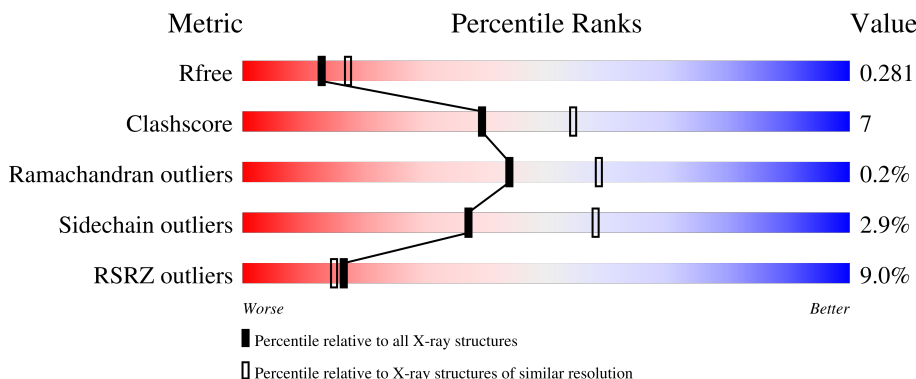
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	4642 (2.40-2.40)
Clashscore	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)

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	318	<div> <div>2%</div> <div>87%</div> <div>12%</div> <div>..</div> </div>
1	B	318	<div> <div>8%</div> <div>80%</div> <div>18%</div> <div>..</div> </div>
1	C	318	<div> <div>17%</div> <div>82%</div> <div>16%</div> <div>..</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15127 atoms, of which 7444 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.

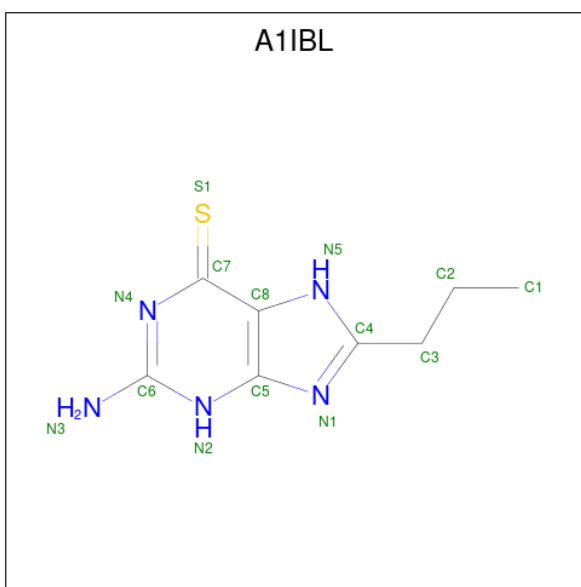
- Molecule 1 is a protein called N-glycosylase/DNA lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	316	Total	C	H	N	O	S	79	0	0
			4989	1599	2474	455	450	11			
1	B	316	Total	C	H	N	O	S	79	0	0
			4989	1599	2474	455	450	11			
1	C	315	Total	C	H	N	O	S	79	0	0
			4964	1591	2463	452	447	11			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	GLY	-	expression tag	UNP O08760
A	9	SER	-	expression tag	UNP O08760
A	10	HIS	-	expression tag	UNP O08760
B	8	GLY	-	expression tag	UNP O08760
B	9	SER	-	expression tag	UNP O08760
B	10	HIS	-	expression tag	UNP O08760
C	8	GLY	-	expression tag	UNP O08760
C	9	SER	-	expression tag	UNP O08760
C	10	HIS	-	expression tag	UNP O08760

- Molecule 2 is 2-azanyl-8-propyl-3,7-dihydropurine-6-thione (CCD ID: A1IBL) (formula: C<sub>8</sub>H<sub>11</sub>N<sub>5</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	S	0	0
			25	8	11	5	1		
2	B	1	Total	C	H	N	S	0	0
			25	8	11	5	1		
2	C	1	Total	C	H	N	S	0	0
			25	8	11	5	1		

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ni	0	0
			1	1		

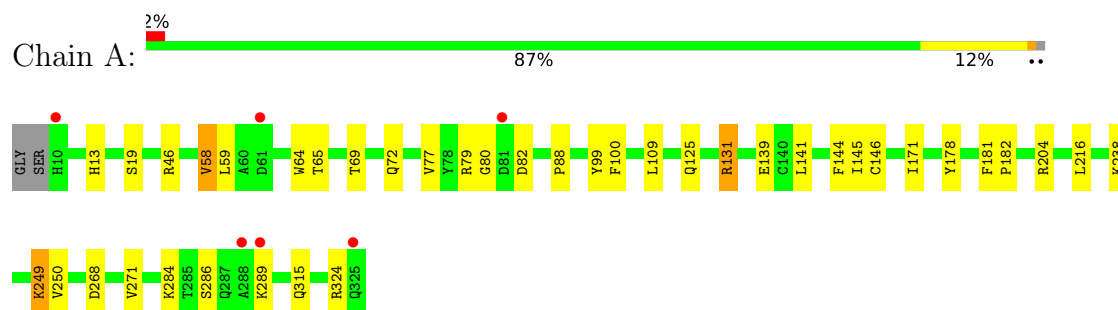
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	84	Total	O	0	0
			84	84		
4	B	18	Total	O	0	0
			18	18		
4	C	7	Total	O	0	0
			7	7		

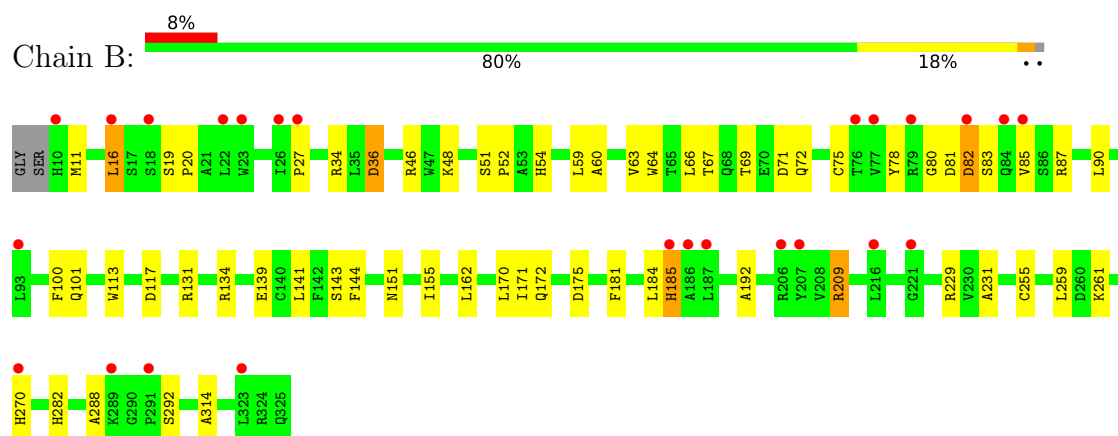
### 3 Residue-property plots [i](#)

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.

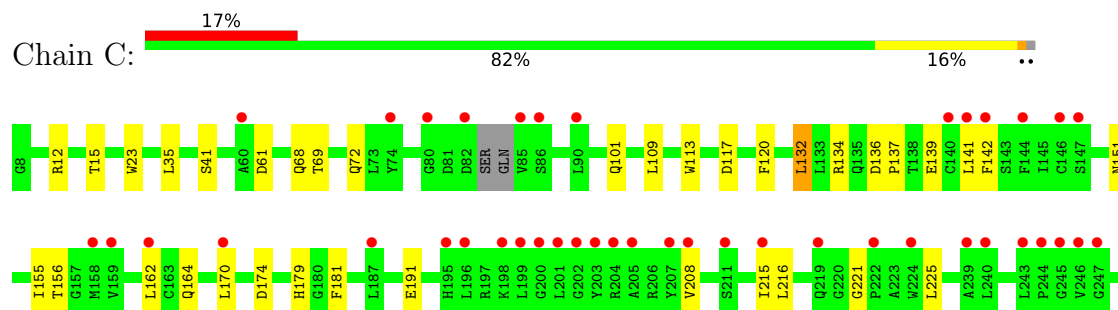
- Molecule 1: N-glycosylase/DNA lyase

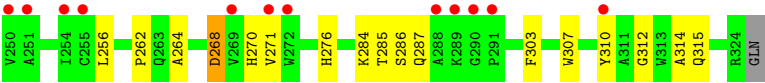


- Molecule 1: N-glycosylase/DNA lyase



- Molecule 1: N-glycosylase/DNA lyase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.50Å 81.60Å 170.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.96 – 2.40 58.96 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (58.96-2.40) 100.0 (58.96-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.8.0411	Depositor
R, $R_{free}$	0.229 , 0.281 0.229 , 0.281	Depositor DCC
$R_{free}$ test set	2258 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.1	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 41.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.004 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	15127	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: A1IBL, NI

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	0.66	0/2586	1.11	1/3520 (0.0%)
1	B	0.60	0/2586	1.12	4/3520 (0.1%)
1	C	0.53	0/2571	1.01	3/3498 (0.1%)
All	All	0.60	0/7743	1.08	8/10538 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	268	ASP	CA-CB-CG	7.38	119.98	112.60
1	B	117	ASP	CA-CB-CG	5.34	117.94	112.60
1	B	270	HIS	CA-CB-CG	5.29	119.09	113.80
1	C	156	THR	CB-CA-C	5.20	119.12	110.90
1	B	36	ASP	CA-CB-CG	5.17	117.77	112.60
1	B	144	PHE	CA-CB-CG	-5.16	108.64	113.80
1	A	65	THR	CB-CA-C	5.09	119.10	109.37
1	C	284	LYS	N-CA-C	-5.01	107.34	113.50

There are no chirality outliers.

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	131	ARG	Sidechain
1	A	79	ARG	Sidechain
1	B	209	ARG	Sidechain
1	B	82	ASP	Peptide

## 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	2515	2474	2460	27	0
1	B	2515	2474	2460	36	0
1	C	2501	2463	2446	38	0
2	A	14	11	0	1	0
2	B	14	11	0	0	0
2	C	14	11	0	1	0
3	A	1	0	0	0	0
4	A	84	0	0	3	0
4	B	18	0	0	2	0
4	C	7	0	0	0	0
All	All	7683	7444	7366	99	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 7.

All (99) 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:324:ARG:HD3	4:A:573:HOH:O	1.72	0.90
1:B:139:GLU:O	1:B:143:SER:OG	2.02	0.73
1:C:12:ARG:HH11	1:C:12:ARG:HG2	1.56	0.70
1:A:125:GLN:HE21	1:A:125:GLN:HA	1.59	0.65
1:A:141:LEU:C	1:A:141:LEU:HD23	2.22	0.64
1:A:80:GLY:HA2	1:A:171:ILE:HD12	1.79	0.64
1:C:215:ILE:HD13	1:C:225:LEU:HD11	1.80	0.62
1:C:142:PHE:CD1	1:C:208:VAL:HG13	2.35	0.61
1:A:77:VAL:HG23	1:A:88:PRO:HG3	1.83	0.60
1:B:46:ARG:HG3	1:B:139:GLU:OE2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:ILE:HG22	1:B:172:GLN:N	2.19	0.58
1:C:113:TRP:CE2	1:C:314:ALA:HB2	2.40	0.57
1:A:59:LEU:HD11	1:A:99:TYR:CD1	2.39	0.57
1:B:69:THR:OG1	1:B:72:GLN:HB2	2.05	0.56
1:A:13:HIS:HE1	1:A:178:TYR:OH	1.87	0.56
1:C:69:THR:OG1	1:C:72:GLN:HB2	2.06	0.56
1:B:113:TRP:CE2	1:B:314:ALA:HB2	2.40	0.56
1:B:141:LEU:HD23	1:B:141:LEU:C	2.30	0.56
1:C:315:GLN:NE2	2:C:401:A1IBL:N4	2.52	0.55
1:C:109:LEU:HD21	1:C:310:TYR:CD2	2.44	0.54
1:C:262:PRO:CB	1:C:310:TYR:CD1	2.92	0.53
1:A:69:THR:OG1	1:A:72:GLN:HB2	2.09	0.52
1:A:64:TRP:CE3	1:A:77:VAL:HG22	2.45	0.52
1:B:80:GLY:HA2	1:B:171:ILE:HD11	1.91	0.51
1:B:27:PRO:HA	1:B:72:GLN:OE1	2.10	0.51
1:C:120:PHE:C	1:C:120:PHE:CD1	2.89	0.51
1:C:286:SER:O	1:C:286:SER:OG	2.29	0.51
1:A:58:VAL:HG12	4:A:562:HOH:O	2.10	0.51
1:C:35:LEU:H	1:C:68:GLN:HE22	1.59	0.50
1:B:288:ALA:CB	4:B:509:HOH:O	2.58	0.50
1:C:142:PHE:CE1	1:C:208:VAL:HG13	2.45	0.50
1:A:109:LEU:HD21	4:A:575:HOH:O	2.10	0.50
1:C:132:LEU:CD2	1:C:256:LEU:HG	2.42	0.50
1:C:268:ASP:OD2	1:C:270:HIS:HB2	2.12	0.50
1:B:134:ARG:NH2	1:B:229:ARG:HD3	2.27	0.50
1:C:162:LEU:C	1:C:162:LEU:HD23	2.37	0.50
1:B:231:ALA:O	1:B:261:LYS:NZ	2.40	0.49
1:C:139:GLU:HG3	1:C:181:PHE:CD1	2.47	0.49
1:A:144:PHE:HB3	1:A:250:VAL:HG13	1.95	0.49
1:C:151:ASN:O	1:C:155:ILE:HG13	2.12	0.49
1:C:132:LEU:HD22	1:C:256:LEU:HG	1.96	0.48
1:C:262:PRO:HB3	1:C:310:TYR:CD1	2.49	0.48
1:C:12:ARG:HG2	1:C:174:ASP:OD1	2.14	0.48
1:B:170:LEU:C	1:B:171:ILE:HG13	2.38	0.48
1:A:284:LYS:HE3	1:B:288:ALA:HA	1.96	0.47
1:B:59:LEU:O	1:B:60:ALA:C	2.55	0.47
1:A:139:GLU:HG3	1:A:181:PHE:CD1	2.49	0.47
1:A:181:PHE:CD2	1:A:182:PRO:HD2	2.48	0.47
1:B:171:ILE:CG2	1:B:172:GLN:N	2.78	0.46
1:C:303:PHE:CD1	1:C:307:TRP:CH2	3.03	0.46
1:C:285:THR:CG2	1:C:287:GLN:HE21	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:15:THR:O	1:C:23:TRP:NE1	2.49	0.46
1:A:13:HIS:CE1	1:A:178:TYR:OH	2.68	0.46
1:C:303:PHE:CD1	1:C:307:TRP:CZ3	3.04	0.46
1:C:136:ASP:O	1:C:137:PRO:C	2.59	0.45
1:B:19:SER:N	1:B:20:PRO:CD	2.80	0.45
1:A:249:LYS:HD3	1:A:268:ASP:HB3	1.99	0.45
1:A:64:TRP:CZ3	1:A:77:VAL:HG22	2.51	0.45
1:B:141:LEU:C	1:B:141:LEU:CD2	2.90	0.45
1:B:139:GLU:HA	1:B:181:PHE:CE2	2.52	0.45
1:C:61:ASP:HA	1:C:170:LEU:HD11	1.98	0.45
1:C:164:GLN:HG2	1:C:179:HIS:CD2	2.51	0.45
1:B:54:HIS:CE1	1:B:67:THR:HG21	2.52	0.44
1:C:141:LEU:C	1:C:141:LEU:HD23	2.41	0.44
1:A:141:LEU:C	1:A:141:LEU:CD2	2.90	0.44
1:B:34:ARG:NH2	1:B:36:ASP:OD2	2.49	0.44
1:C:12:ARG:NH1	1:C:174:ASP:OD1	2.49	0.44
1:A:141:LEU:HD23	1:A:141:LEU:O	2.18	0.44
1:B:16:LEU:O	1:B:16:LEU:HD22	2.19	0.43
1:A:80:GLY:O	1:A:82:ASP:N	2.47	0.43
1:B:288:ALA:HB3	4:B:509:HOH:O	2.17	0.43
1:A:315:GLN:OE1	2:A:401:A1IBL:N4	2.51	0.43
1:B:162:LEU:C	1:B:162:LEU:HD23	2.44	0.43
1:A:141:LEU:CD2	1:A:145:ILE:HD12	2.50	0.42
1:B:151:ASN:O	1:B:155:ILE:HG13	2.20	0.42
1:B:100:PHE:O	1:B:131:ARG:HD3	2.20	0.42
1:C:264:ALA:O	1:C:312:GLY:HA3	2.20	0.42
1:B:51:SER:O	1:B:52:PRO:C	2.63	0.42
1:B:282:HIS:CE1	1:C:276:HIS:NE2	2.87	0.42
1:C:285:THR:HG21	1:C:287:GLN:HE21	1.85	0.42
1:C:101:GLN:CG	1:C:134:ARG:HB2	2.49	0.41
1:C:262:PRO:HB3	1:C:310:TYR:HD1	1.85	0.41
1:C:113:TRP:HE3	1:C:120:PHE:CZ	2.38	0.41
1:C:262:PRO:HB2	1:C:310:TYR:CD1	2.56	0.41
1:B:63:VAL:HG12	1:B:64:TRP:N	2.35	0.41
1:C:120:PHE:CD1	1:C:120:PHE:O	2.74	0.41
1:A:146:CYS:HA	1:A:204:ARG:HD3	2.01	0.41
1:B:139:GLU:HG3	1:B:181:PHE:CD1	2.56	0.41
1:B:184:LEU:O	1:B:185:HIS:C	2.63	0.41
1:B:192:ALA:HB3	1:B:209:ARG:HD2	2.02	0.41
1:B:66:LEU:HD22	1:B:75:CYS:HB3	2.03	0.41
1:A:46:ARG:CZ	1:A:58:VAL:CG1	2.99	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:PHE:O	1:A:131:ARG:HD3	2.20	0.40
1:C:216:LEU:HD23	1:C:221:GLY:HA2	2.03	0.40
1:B:101:GLN:O	1:B:131:ARG:NH1	2.55	0.40
1:B:81:ASP:O	1:B:83:SER:HB2	2.21	0.40
1:B:255:CYS:HA	1:B:259:LEU:HB2	2.04	0.40
1:A:181:PHE:CG	1:A:182:PRO:HD2	2.56	0.40
1:B:16:LEU:O	1:B:16:LEU:CD2	2.69	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	314/318 (99%)	298 (95%)	16 (5%)	0	100	100
1	B	314/318 (99%)	288 (92%)	25 (8%)	1 (0%)	37	51
1	C	311/318 (98%)	293 (94%)	17 (6%)	1 (0%)	37	51
All	All	939/954 (98%)	879 (94%)	58 (6%)	2 (0%)	44	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	85	VAL
1	C	117	ASP

### 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	265/266 (100%)	257 (97%)	8 (3%)	36	57
1	B	265/266 (100%)	254 (96%)	11 (4%)	25	43
1	C	263/266 (99%)	259 (98%)	4 (2%)	60	77
All	All	793/798 (99%)	770 (97%)	23 (3%)	37	58

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	58	VAL
1	A	216	LEU
1	A	238	LYS
1	A	249	LYS
1	A	271	VAL
1	A	286	SER
1	A	289	LYS
1	B	11	MET
1	B	16	LEU
1	B	48	LYS
1	B	71	ASP
1	B	78	TYR
1	B	82	ASP
1	B	87	ARG
1	B	90	LEU
1	B	175	ASP
1	B	185	HIS
1	B	292	SER
1	C	41	SER
1	C	132	LEU
1	C	191	GLU
1	C	271	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	68	GLN
1	A	97	HIS
1	A	112	HIS

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Mol	Chain	Res	Type
1	A	125	GLN
1	A	237	HIS
1	B	54	HIS
1	B	62	GLN
1	B	68	GLN
1	B	72	GLN
1	B	97	HIS
1	B	135	GLN
1	B	164	GLN
1	B	195	HIS
1	B	219	GLN
1	B	237	HIS
1	B	273	GLN
1	B	296	ASN
1	B	315	GLN
1	C	68	GLN
1	C	135	GLN
1	C	164	GLN
1	C	179	HIS
1	C	227	GLN
1	C	287	GLN
1	C	315	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	A1IBL	C	401	-	10,15,15	1.02	0	9,21,21	1.70	2 (22%)
2	A1IBL	B	401	-	10,15,15	0.93	0	9,21,21	1.80	2 (22%)
2	A1IBL	A	401	-	10,15,15	1.21	1 (10%)	9,21,21	1.44	1 (11%)

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	A1IBL	C	401	-	-	1/3/3/3	0/2/2/2
2	A1IBL	B	401	-	-	1/3/3/3	0/2/2/2
2	A1IBL	A	401	-	-	1/3/3/3	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	A1IBL	C3-C4	-2.18	1.47	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	A1IBL	N2-C5-N1	4.02	129.72	122.78
2	C	401	A1IBL	N2-C5-N1	3.84	129.41	122.78
2	A	401	A1IBL	N2-C5-N1	3.23	128.36	122.78
2	B	401	A1IBL	C5-N2-C6	-2.88	117.19	122.92
2	C	401	A1IBL	C5-N2-C6	-2.27	118.41	122.92

There are no chirality outliers.

All (3) torsion outliers are listed below:

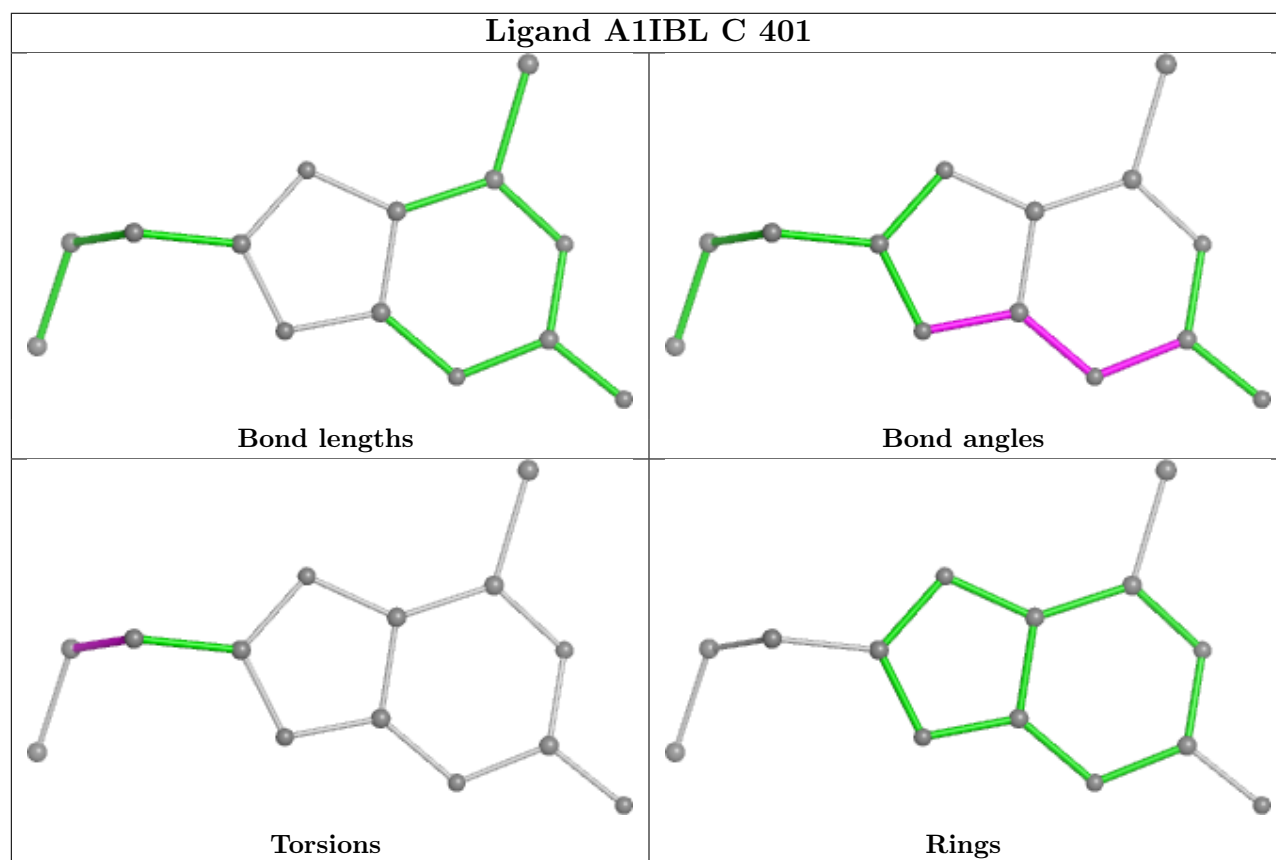
Mol	Chain	Res	Type	Atoms
2	B	401	A1IBL	C2-C3-C4-N5
2	A	401	A1IBL	C1-C2-C3-C4
2	C	401	A1IBL	C1-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

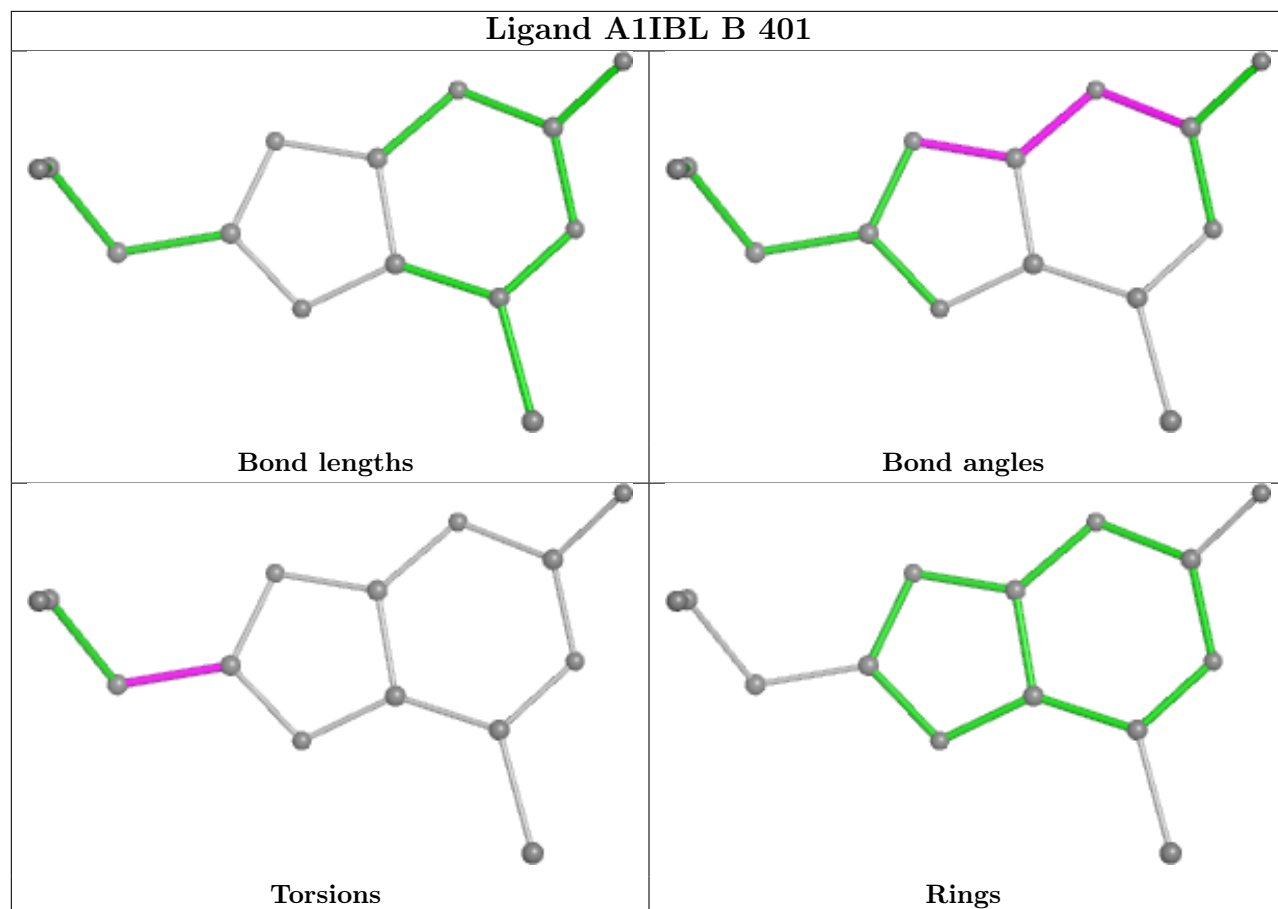
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	A1IBL	1	0
2	A	401	A1IBL	1	0

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.

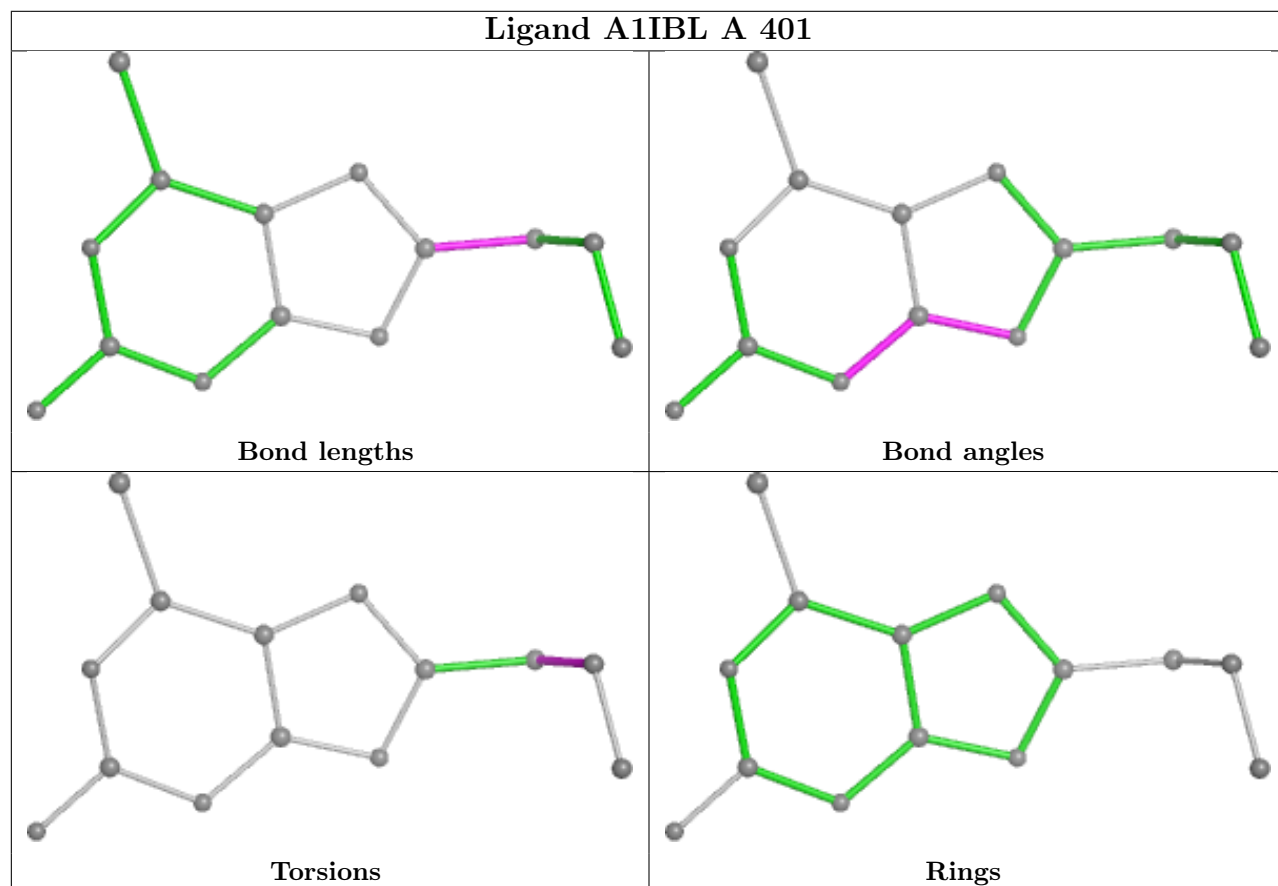




## Ligand A1IBL B 401



## Ligand A1IBL A 401



## 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	316/318 (99%)	-0.39	6 (1%) 66 62	27, 45, 98, 159	0
1	B	316/318 (99%)	0.65	25 (7%) 20 18	38, 74, 123, 181	0
1	C	315/318 (99%)	1.06	54 (17%) 5 5	42, 96, 144, 193	0
All	All	947/954 (99%)	0.44	85 (8%) 17 15	27, 71, 134, 193	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	203	TYR	5.2
1	C	201	LEU	4.7
1	C	247	GLY	4.3
1	C	245	GLY	4.2
1	C	200	GLY	3.9
1	C	142	PHE	3.9
1	B	93	LEU	3.8
1	C	196	LEU	3.7
1	C	205	ALA	3.7
1	C	85	VAL	3.6
1	C	202	GLY	3.5
1	B	216	LEU	3.5
1	C	251	ALA	3.4
1	C	240	LEU	3.4
1	A	10	HIS	3.4
1	C	207	TYR	3.3
1	C	208	VAL	3.3
1	C	162	LEU	3.3
1	B	291	PRO	3.2
1	C	199	LEU	3.1
1	C	158	MET	3.1
1	C	246	VAL	3.1
1	C	90	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	186	ALA	3.1
1	C	211	SER	3.1
1	C	195	HIS	3.0
1	A	61	ASP	3.0
1	C	291	PRO	3.0
1	C	255	CYS	3.0
1	B	185	HIS	3.0
1	C	269	VAL	2.9
1	C	272	TRP	2.9
1	C	140	CYS	2.9
1	B	289	LYS	2.9
1	C	187	LEU	2.8
1	C	290	GLY	2.8
1	A	325	GLN	2.8
1	A	288	ALA	2.8
1	C	146	CYS	2.7
1	B	22	LEU	2.6
1	B	77	VAL	2.6
1	B	270	HIS	2.6
1	C	82	ASP	2.6
1	B	84	GLN	2.6
1	C	170	LEU	2.5
1	C	224	TRP	2.5
1	C	141	LEU	2.5
1	C	215	ILE	2.5
1	C	80	GLY	2.5
1	B	206	ARG	2.5
1	B	207	TYR	2.4
1	B	10	HIS	2.4
1	B	26	ILE	2.4
1	C	147	SER	2.4
1	B	85	VAL	2.3
1	B	187	LEU	2.3
1	B	16	LEU	2.3
1	C	243	LEU	2.3
1	C	159	VAL	2.3
1	C	271	VAL	2.3
1	C	60	ALA	2.3
1	C	254	ILE	2.2
1	C	239	ALA	2.2
1	B	221	GLY	2.2
1	B	23	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	74	TYR	2.2
1	B	323	LEU	2.2
1	C	86	SER	2.2
1	B	79	ARG	2.2
1	C	244	PRO	2.2
1	A	289	LYS	2.2
1	B	76	THR	2.1
1	C	144	PHE	2.1
1	C	219	GLN	2.1
1	B	18	SER	2.1
1	B	82	ASP	2.1
1	C	222	PRO	2.1
1	C	198	LYS	2.1
1	C	250	VAL	2.1
1	C	310	TYR	2.1
1	C	289	LYS	2.1
1	A	81	ASP	2.1
1	C	288	ALA	2.0
1	B	27	PRO	2.0
1	C	204	ARG	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.

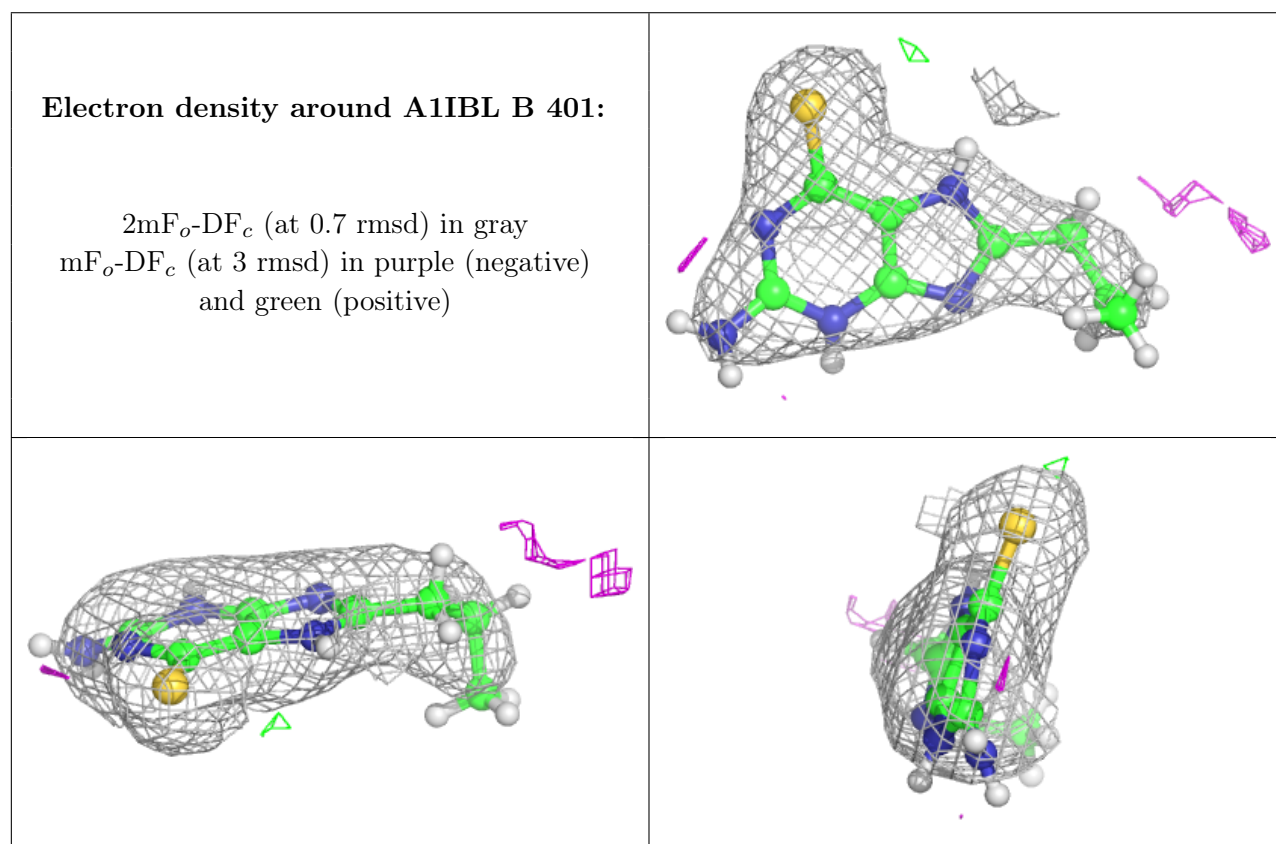
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	A1IBL	B	401	14/14	0.94	0.09	56,64,71,74	0
2	A1IBL	C	401	14/14	0.96	0.09	71,87,103,108	0
2	A1IBL	A	401	14/14	0.97	0.06	31,39,51,53	0

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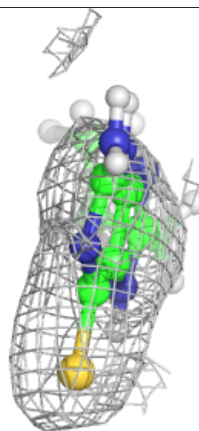
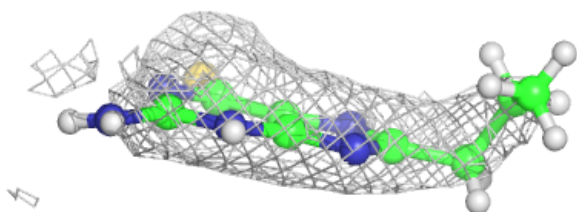
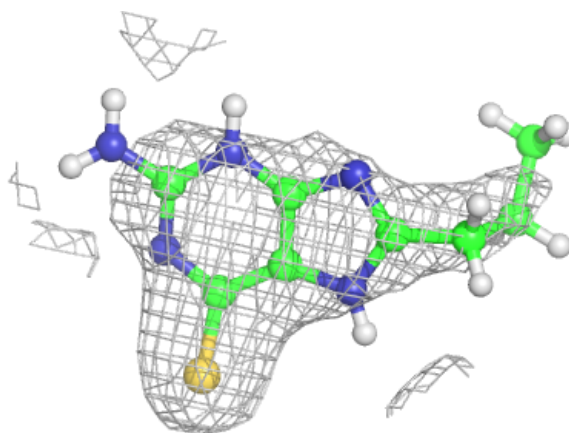
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NI	A	402	1/1	1.00	0.03	47,47,47,47	0

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.



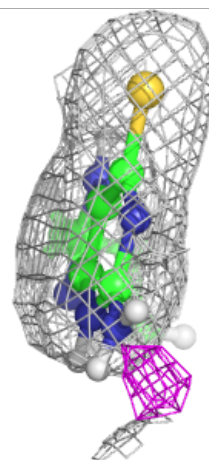
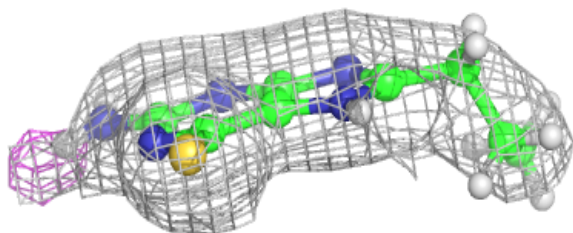
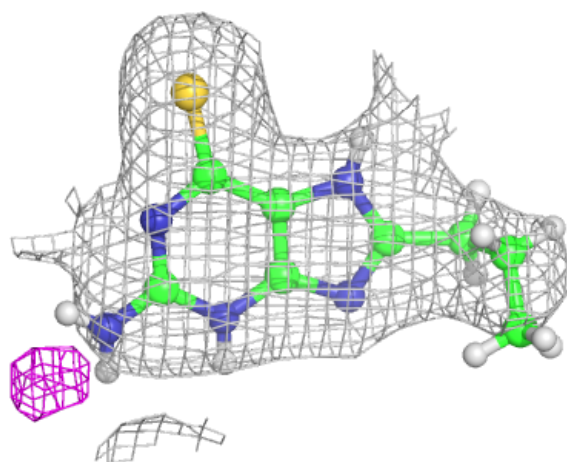
**Electron density around A1IBL C 401:**

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



**Electron density around A1IBL A 401:**

$2mF_o-DF_c$  (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.