



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 03:42 PM UTC

PDB ID : 9GIH / pdb\_00009gih  
Title : Structure of the mouse 8-oxoguanine DNA Glycosylase mOGG1 in complex with ligand TH14047  
Authors : Scaletti Hutchinson, E.; Stenmark, P.  
Deposited on : 2024-08-19  
Resolution : 2.27 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

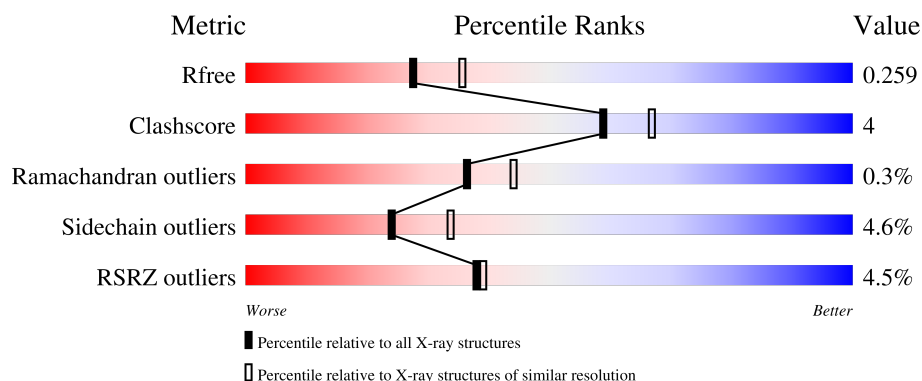
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.27 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))
$R_{free}$	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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>88%</div> <div>9%</div> <div>...</div> </div>
1	B	318	<div> <div>4%</div> <div>87%</div> <div>10%</div> <div>.</div> </div>
1	C	318	<div> <div>7%</div> <div>85%</div> <div>12%</div> <div>..</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14970 atoms, of which 7367 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.

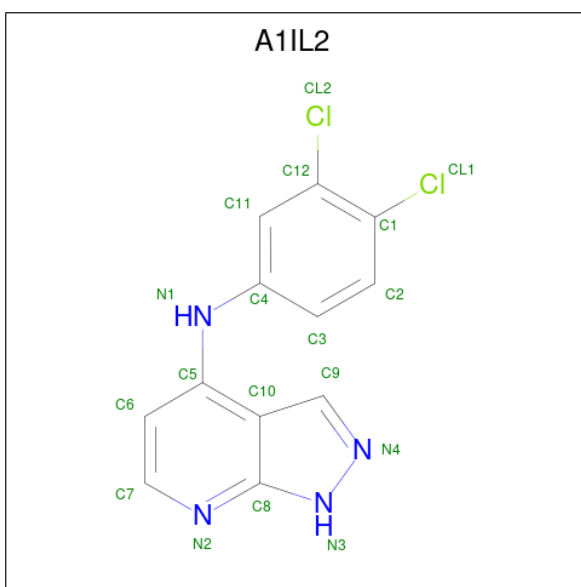
- Molecule 1 is a protein called N-glycosylase/DNA lyase.

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	310	Total	C	H	N	O	S	79	0	0
			4902	1573	2430	446	442	11			
1	C	314	Total	C	H	N	O	S	81	0	0
			4944	1585	2455	450	443	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 {N}-(3,4-dichlorophenyl)-1 {H}-pyrazolo[3,4-b]pyridin-4-amine (CCD ID: A1IL2) (formula: C<sub>12</sub>H<sub>8</sub>Cl<sub>2</sub>N<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).

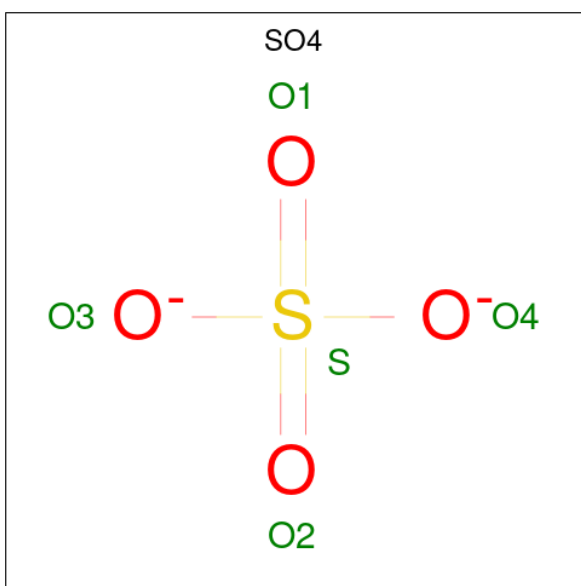


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	H	N	0	0
			26	12	2	8	4		

- 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 SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

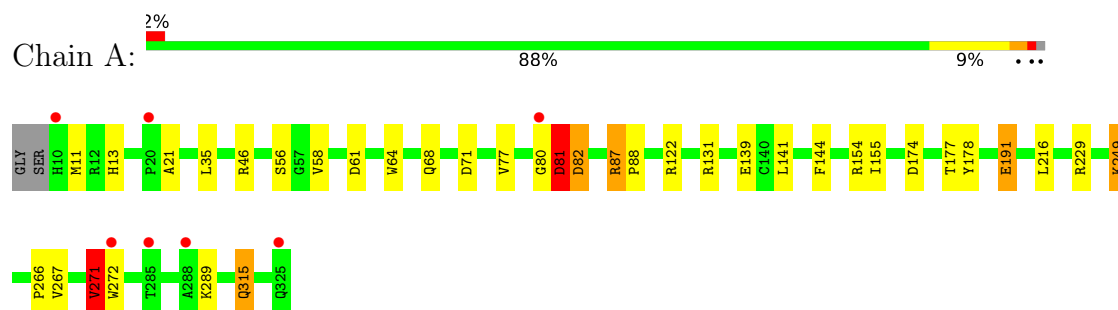
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	42	Total	O	0	0
			42	42		
5	B	28	Total	O	0	0
			28	28		
5	C	33	Total	O	0	0
			33	33		

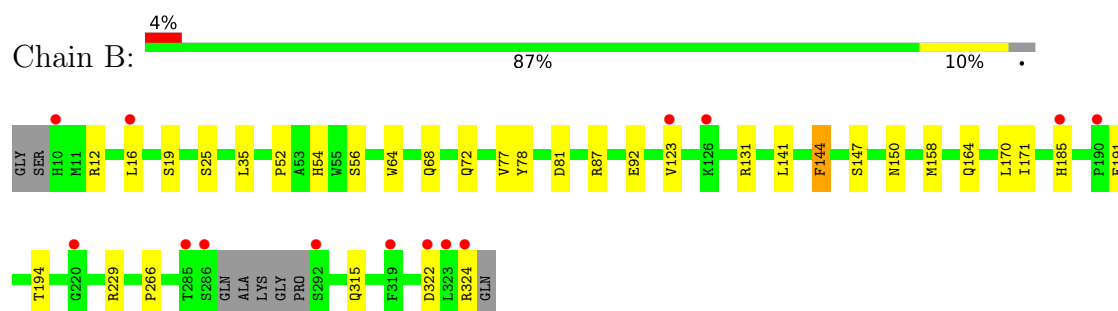
### 3 Residue-property plots

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.

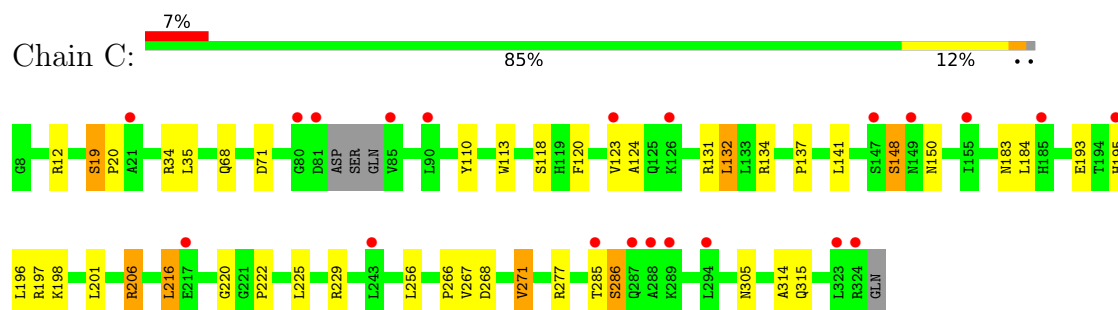
#### • Molecule 1: N-glycosylase/DNA lyase



#### • 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, $\alpha$ , $\beta$ , $\gamma$	79.98Å 80.76Å 166.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.41 – 2.27 83.41 – 2.27	Depositor EDS
% Data completeness (in resolution range)	98.0 (83.41-2.27) 98.0 (83.41-2.27)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.208 , 0.267 (Not available) , 0.259	Depositor DCC
$R_{free}$ test set	2417 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.2	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 33.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	14970	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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: SO4, NI, A1IL2

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	0.63	0/2586	1.14	8/3520 (0.2%)
1	B	0.62	0/2541	1.08	2/3458 (0.1%)
1	C	0.61	0/2559	1.09	3/3482 (0.1%)
All	All	0.62	0/7686	1.10	13/10460 (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	4
1	B	0	3
1	C	0	4
All	All	0	11

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	LYS	CB-CA-C	9.12	125.32	110.90
1	A	271	VAL	N-CA-CB	7.45	124.25	110.77
1	A	191	GLU	CB-CG-CD	6.98	124.46	112.60
1	B	81	ASP	CA-CB-CG	6.76	119.36	112.60
1	A	144	PHE	CA-CB-CG	-6.38	107.42	113.80
1	A	81	ASP	CA-CB-CG	6.08	118.68	112.60
1	B	144	PHE	CA-CB-CG	-6.02	107.78	113.80
1	C	71	ASP	CA-CB-CG	5.84	118.44	112.60
1	A	249	LYS	CA-CB-CG	5.73	125.56	114.10
1	C	110	TYR	N-CA-CB	5.39	118.04	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	183	ASN	CB-CA-C	5.37	119.22	109.83
1	A	71	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	229	ARG	CG-CD-NE	-5.07	100.85	112.00

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	ARG	Sidechain
1	A	154	ARG	Sidechain
1	A	81	ASP	Peptide
1	A	87	ARG	Sidechain
1	B	12	ARG	Sidechain
1	B	131	ARG	Sidechain
1	B	229	ARG	Sidechain
1	C	12	ARG	Sidechain
1	C	131	ARG	Sidechain
1	C	277	ARG	Sidechain
1	C	34	ARG	Sidechain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2515	2474	2460	24	0
1	B	2472	2430	2415	13	0
1	C	2489	2455	2436	28	0
2	A	18	8	0	3	0
3	A	1	0	0	0	0
4	A	5	0	0	0	0
5	A	42	0	0	1	0
5	B	28	0	0	0	0
5	C	33	0	0	0	0
All	All	7603	7367	7311	65	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 4.

All (65) 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:177:THR:HG21	5:A:534:HOH:O	1.58	1.01
1:C:132:LEU:CD2	1:C:256:LEU:HG	2.20	0.72
1:A:64:TRP:CE3	1:A:77:VAL:HG22	2.29	0.67
1:A:80:GLY:O	1:A:82:ASP:N	2.27	0.66
1:B:35:LEU:H	1:B:68:GLN:HE22	1.47	0.63
1:A:155:ILE:HD11	2:A:401:A1IL2:CL1	2.36	0.62
1:A:64:TRP:CZ3	1:A:77:VAL:HG22	2.35	0.62
1:C:193:GLU:OE2	1:C:206:ARG:NE	2.32	0.61
1:C:268:ASP:H	1:C:271:VAL:HG13	1.67	0.60
1:A:21:ALA:O	1:A:87:ARG:NH1	2.35	0.59
1:B:77:VAL:HG11	1:B:92:GLU:OE1	2.04	0.58
1:C:132:LEU:HD22	1:C:256:LEU:HG	1.84	0.58
1:C:134:ARG:CZ	1:C:229:ARG:HH11	2.17	0.57
1:A:80:GLY:O	1:A:82:ASP:HA	2.04	0.57
1:B:266:PRO:HD2	1:B:315:GLN:OE1	2.04	0.57
1:C:35:LEU:H	1:C:68:GLN:HE22	1.53	0.55
1:C:137:PRO:HD3	1:C:229:ARG:HH21	1.72	0.55
1:C:134:ARG:CZ	1:C:229:ARG:NH1	2.70	0.54
1:A:35:LEU:H	1:A:68:GLN:HE22	1.57	0.53
1:A:80:GLY:O	1:A:82:ASP:CA	2.57	0.53
1:C:137:PRO:HD3	1:C:229:ARG:NH2	2.23	0.52
1:A:13:HIS:HD2	1:A:174:ASP:OD2	1.91	0.52
1:B:25:SER:OG	1:B:72:GLN:NE2	2.43	0.52
1:B:170:LEU:O	1:B:171:ILE:HG12	2.10	0.52
1:A:267:VAL:HA	1:A:271:VAL:HG22	1.92	0.52
1:B:170:LEU:C	1:B:171:ILE:HG13	2.35	0.52
1:B:170:LEU:C	1:B:171:ILE:CG1	2.85	0.50
1:A:81:ASP:O	1:A:82:ASP:C	2.55	0.49
1:B:52:PRO:O	1:B:54:HIS:HD2	1.96	0.49
1:A:64:TRP:CZ3	1:A:77:VAL:CG2	2.94	0.49
1:A:80:GLY:O	1:A:81:ASP:C	2.56	0.49
1:C:266:PRO:HD2	1:C:315:GLN:OE1	2.13	0.48
1:A:46:ARG:HG3	1:A:139:GLU:OE2	2.14	0.48
1:C:193:GLU:CD	1:C:206:ARG:HG3	2.38	0.47
1:A:155:ILE:CD1	2:A:401:A1IL2:CL1	2.99	0.47
1:C:193:GLU:OE2	1:C:206:ARG:CD	2.62	0.47
1:C:196:LEU:HB3	1:C:201:LEU:HD12	1.97	0.47
1:B:170:LEU:O	1:B:171:ILE:CG1	2.64	0.45
1:B:150:ASN:HD21	1:B:158:MET:CE	2.30	0.45
1:C:267:VAL:HA	1:C:271:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:VAL:HG23	1:A:88:PRO:HG3	1.98	0.45
1:A:13:HIS:HE1	1:A:178:TYR:OH	2.01	0.44
1:A:315:GLN:NE2	2:A:401:A1IL2:N2	2.66	0.44
1:C:19:SER:N	1:C:20:PRO:HD3	2.34	0.43
1:A:141:LEU:C	1:A:141:LEU:HD23	2.43	0.43
1:C:184:LEU:HD12	1:C:222:PRO:HD3	1.99	0.43
1:A:266:PRO:HD2	1:A:315:GLN:OE1	2.19	0.43
1:B:141:LEU:HD23	1:B:141:LEU:C	2.44	0.43
1:C:137:PRO:CD	1:C:229:ARG:HH21	2.32	0.43
1:C:285:THR:O	1:C:285:THR:HG22	2.19	0.43
1:C:148:SER:C	1:C:150:ASN:N	2.74	0.43
1:C:137:PRO:CG	1:C:229:ARG:HH21	2.32	0.42
1:B:56:SER:HA	1:B:64:TRP:O	2.19	0.42
1:C:113:TRP:CE2	1:C:314:ALA:HB2	2.55	0.42
1:B:144:PHE:O	1:B:147:SER:OG	2.34	0.42
1:A:56:SER:HA	1:A:64:TRP:O	2.20	0.42
1:C:197:ARG:NE	1:C:206:ARG:HH22	2.17	0.42
1:C:268:ASP:H	1:C:271:VAL:CG1	2.31	0.42
1:C:285:THR:O	1:C:286:SER:C	2.63	0.42
1:A:267:VAL:HA	1:A:271:VAL:CG2	2.50	0.41
1:C:197:ARG:CD	1:C:206:ARG:HH22	2.34	0.41
1:C:216:LEU:HD23	1:C:216:LEU:HA	1.83	0.41
1:A:13:HIS:CD2	1:A:174:ASP:OD2	2.74	0.40
1:C:35:LEU:H	1:C:68:GLN:NE2	2.18	0.40
1:C:120:PHE:CE1	1:C:124:ALA:CB	3.05	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	314/318 (99%)	299 (95%)	13 (4%)	2 (1%)	21	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	306/318 (96%)	292 (95%)	14 (5%)	0	100	100
1	C	310/318 (98%)	289 (93%)	20 (6%)	1 (0%)	36	44
All	All	930/954 (98%)	880 (95%)	47 (5%)	3 (0%)	36	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	ASP
1	A	82	ASP
1	C	220	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	265/266 (100%)	254 (96%)	11 (4%)	26	37
1	B	261/266 (98%)	250 (96%)	11 (4%)	26	37
1	C	261/266 (98%)	247 (95%)	14 (5%)	20	27
All	All	787/798 (99%)	751 (95%)	36 (5%)	24	34

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	MET
1	A	58	VAL
1	A	61	ASP
1	A	122	ARG
1	A	191	GLU
1	A	216	LEU
1	A	249	LYS
1	A	271	VAL
1	A	272	TRP
1	A	289	LYS
1	A	315	GLN

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Mol	Chain	Res	Type
1	B	16	LEU
1	B	19	SER
1	B	78	TYR
1	B	87	ARG
1	B	123	VAL
1	B	164	GLN
1	B	185	HIS
1	B	191	GLU
1	B	194	THR
1	B	322	ASP
1	B	324	ARG
1	C	19	SER
1	C	118	SER
1	C	123	VAL
1	C	132	LEU
1	C	141	LEU
1	C	148	SER
1	C	195	HIS
1	C	198	LYS
1	C	206	ARG
1	C	216	LEU
1	C	225	LEU
1	C	271	VAL
1	C	286	SER
1	C	305	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	50	GLN
1	A	68	GLN
1	A	72	GLN
1	A	164	GLN
1	B	54	HIS
1	B	62	GLN
1	B	68	GLN
1	B	72	GLN
1	B	135	GLN
1	B	270	HIS
1	C	62	GLN
1	C	68	GLN

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Mol	Chain	Res	Type
1	C	72	GLN
1	C	97	HIS
1	C	112	HIS
1	C	119	HIS
1	C	135	GLN
1	C	150	ASN
1	C	164	GLN
1	C	183	ASN

### 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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z  > 2$
4	SO4	A	403	-	4,4,4	0.38	0	6,6,6	0.15	0
2	A1IL2	A	401	-	20,20,20	0.57	0	26,28,28	1.27	4 (15%)

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	A1IL2	A	401	-	-	0/4/4/4	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	A1IL2	N3-C8-N2	3.50	128.91	125.83
2	A	401	A1IL2	C10-C5-N1	-3.07	115.60	119.41
2	A	401	A1IL2	C10-C8-N2	-2.62	124.36	126.40
2	A	401	A1IL2	C4-N1-C5	2.18	132.30	126.73

There are no chirality outliers.

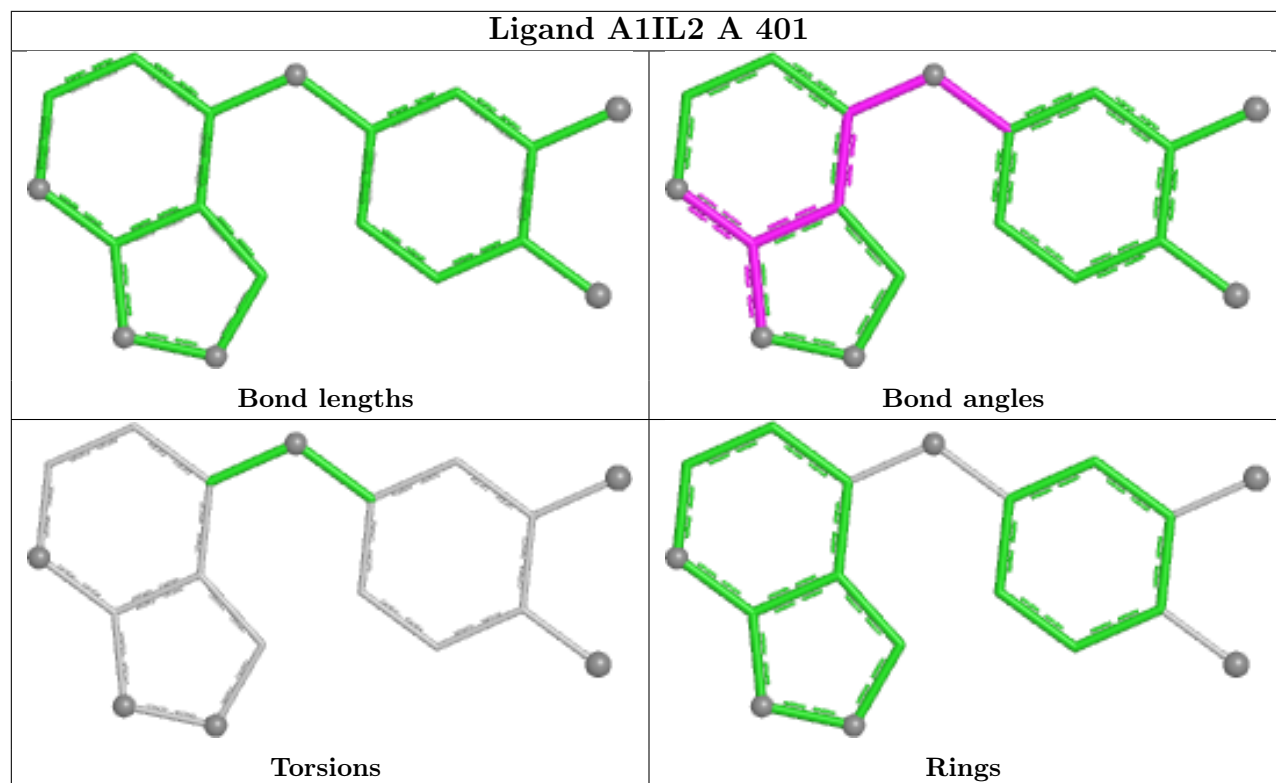
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	A1IL2	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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%)	0.04	7 (2%) 62 64	33, 50, 96, 137	0
1	B	310/318 (97%)	0.43	14 (4%) 38 39	38, 60, 102, 143	0
1	C	314/318 (98%)	0.38	21 (6%) 24 25	40, 60, 108, 136	0
All	All	940/954 (98%)	0.28	42 (4%) 38 39	33, 57, 102, 143	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	323	LEU	4.5
1	B	10	HIS	4.4
1	C	85	VAL	4.1
1	A	288	ALA	3.9
1	C	287	GLN	3.3
1	B	324	ARG	3.2
1	C	81	ASP	3.2
1	A	285	THR	3.1
1	C	288	ALA	3.0
1	B	16	LEU	3.0
1	C	80	GLY	3.0
1	B	126	LYS	2.7
1	C	324	ARG	2.7
1	B	285	THR	2.6
1	C	147	SER	2.6
1	B	323	LEU	2.6
1	A	80	GLY	2.6
1	B	220	GLY	2.6
1	A	20	PRO	2.5
1	C	185	HIS	2.5
1	B	190	PRO	2.5
1	C	155	ILE	2.5
1	C	149	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	90	LEU	2.4
1	A	10	HIS	2.4
1	C	126	LYS	2.4
1	B	185	HIS	2.4
1	C	123	VAL	2.3
1	C	195	HIS	2.3
1	C	21	ALA	2.3
1	C	289	LYS	2.3
1	B	286	SER	2.3
1	B	123	VAL	2.3
1	C	294	LEU	2.2
1	C	243	LEU	2.2
1	B	292	SER	2.2
1	A	325	GLN	2.2
1	A	272	TRP	2.1
1	C	285	THR	2.1
1	B	319	PHE	2.1
1	C	217	GLU	2.0
1	B	322	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](#)

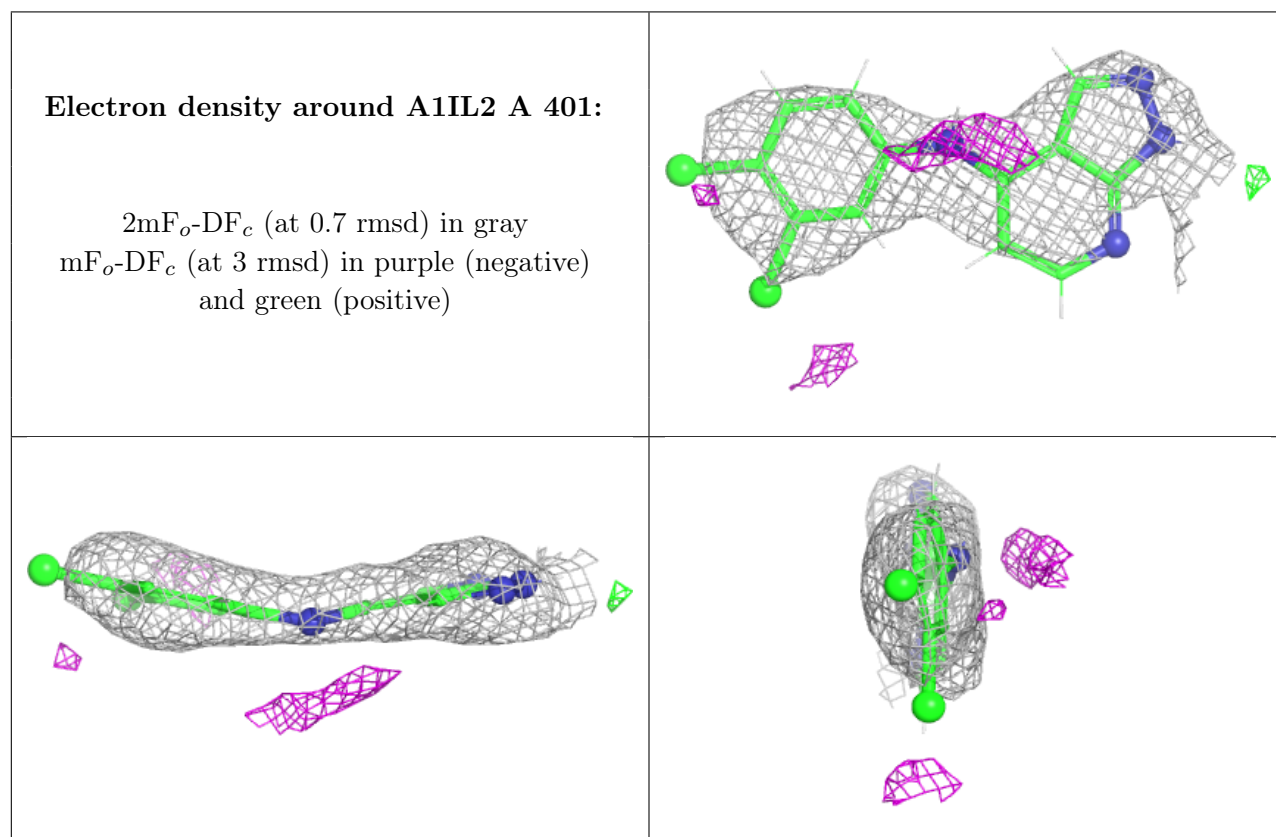
There are no oligosaccharides in this entry.

## 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
4	SO4	A	403	5/5	0.80	0.19	68,71,112,120	0
2	A1IL2	A	401	18/18	0.88	0.13	68,78,85,141	0
3	NI	A	402	1/1	1.00	0.01	46,46,46,46	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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.