



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:38 PM UTC

PDB ID : 9FNU / pdb_00009fnu
Title : Structure of the mouse 8-oxoguanine DNA Glycosylase mOGG1 in complex with ligand TH13579
Authors : Scaletti, E.; Stenmark, P.
Deposited on : 2024-06-11
Resolution : 2.00 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 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

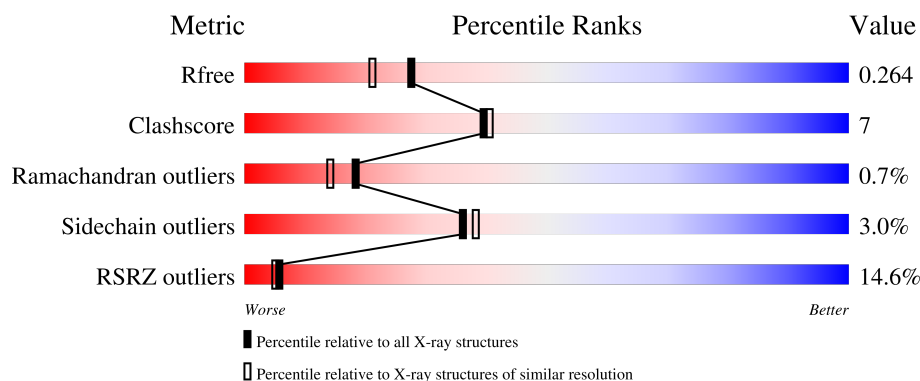
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 ≥ 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	5% 89% 8% ..
1	B	318	18% 75% 19% ..
1	C	318	19% 86% 12% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7622 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.

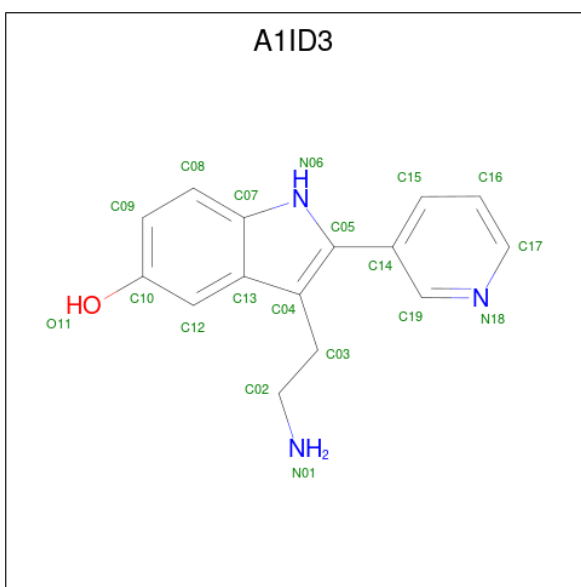
- Molecule 1 is a protein called N-glycosylase/DNA lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	2	0
			2514	1597	455	451	11			
1	B	305	Total	C	N	O	S	0	0	0
			2433	1554	438	430	11			
1	C	312	Total	C	N	O	S	0	0	0
			2464	1568	442	443	11			

There are 9 discrepancies between the modelled and reference sequences:

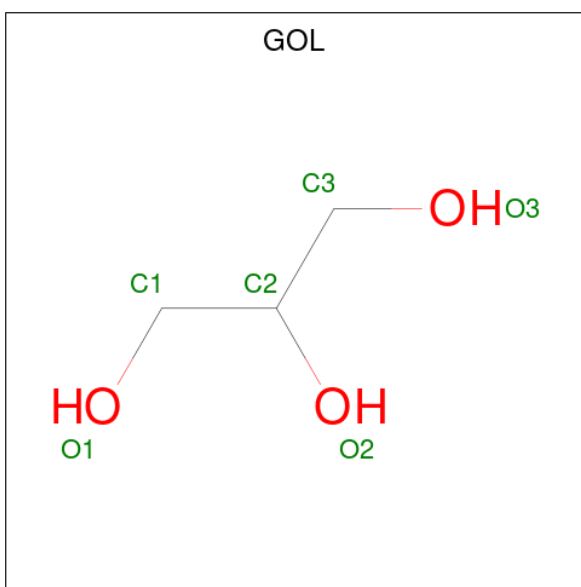
Chain	Residue	Modelled	Actual	Comment	Reference
A	8	GLY	-	expression tag	UNP O08760
A	9	SER	-	expression tag	UNP O08760
A	10	HIS	-	expression tag	UNP O08760
B	8	GLY	-	expression tag	UNP O08760
B	9	SER	-	expression tag	UNP O08760
B	10	HIS	-	expression tag	UNP O08760
C	8	GLY	-	expression tag	UNP O08760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

- Molecule 2 is 3-(2-azanylethyl)-2-pyridin-3-yl-1 {H}-indol-5-ol (CCD ID: A1ID3) (formula: C₁₅H₁₅N₃O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			19	15	3	1		
2	B	1	Total	C	N	O	0	0
			19	15	3	1		
2	C	1	Total	C	N	O	0	0
			19	15	3	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

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

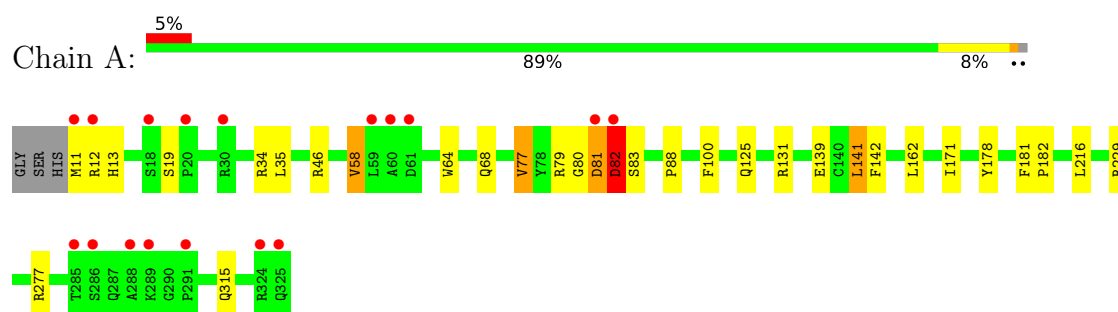
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	92	Total 92	O 92	0	0
5	B	31	Total 31	O 31	0	0
5	C	24	Total 24	O 24	0	0

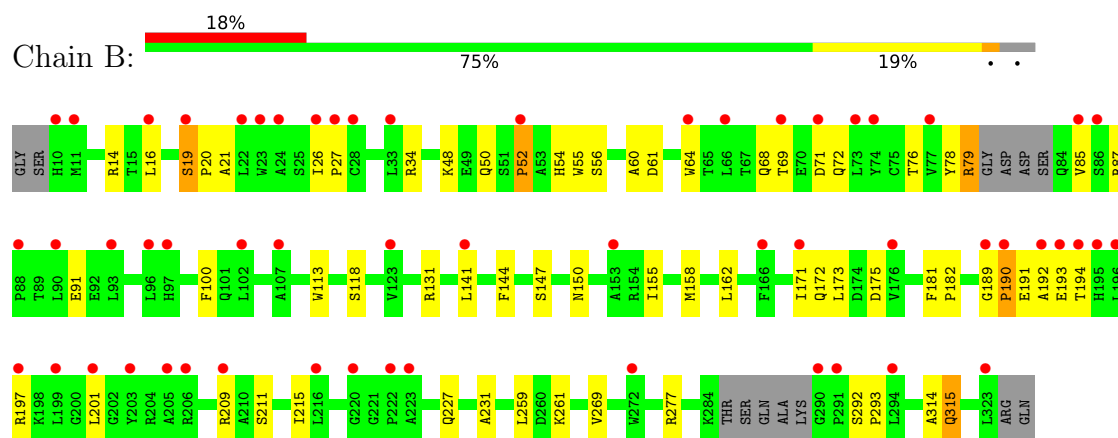
3 Residue-property plots

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.

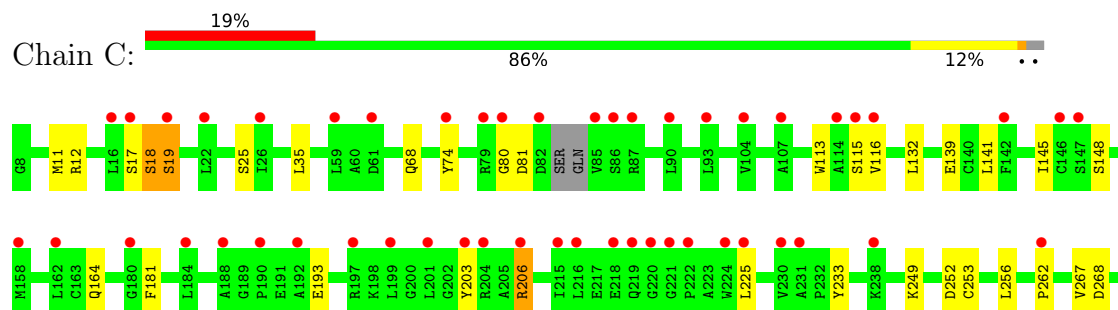
• Molecule 1: N-glycosylase/DNA lyase

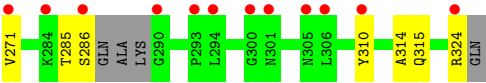


• Molecule 1: N-glycosylase/DNA lyase



• 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, α , β , γ	80.89Å 81.11Å 170.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.16 – 2.00 73.16 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (73.16-2.00) 99.9 (73.16-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0411	Depositor
R, R_{free}	0.217 , 0.256 0.224 , 0.264	Depositor DCC
R_{free} test set	3760 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7622	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: A1ID3, NI, GOL

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	0.65	0/2584	1.00	0/3518
1	B	0.56	0/2502	0.99	1/3405 (0.0%)
1	C	0.54	0/2533	1.00	0/3450
All	All	0.59	0/7619	0.99	1/10373 (0.0%)

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	2
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	315	GLN	N-CA-CB	-5.06	102.47	110.06

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	ARG	Sidechain
1	A	229	ARG	Sidechain
1	A	277	ARG	Sidechain
1	A	79	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	277	ARG	Sidechain
1	B	79	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	2514	0	2452	25	0
1	B	2433	0	2383	45	0
1	C	2464	0	2386	29	0
2	A	19	0	0	0	0
2	B	19	0	0	0	0
2	C	19	0	0	0	0
3	A	6	0	8	0	0
4	A	1	0	0	0	0
5	A	92	0	0	0	0
5	B	31	0	0	2	0
5	C	24	0	0	1	0
All	All	7622	0	7229	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:B:150:ASN:HD21	1:B:158:MET:HE1	1.32	0.94
1:C:203:TYR:HA	1:C:206:ARG:NH1	1.86	0.91
1:A:141:LEU:C	1:A:141:LEU:HD23	2.01	0.86
1:C:315:GLN:NE2	5:C:501:HOH:O	2.12	0.81
1:A:46:ARG:NH2	1:A:58:VAL:HG11	2.01	0.75
1:B:21:ALA:O	1:B:87:ARG:NH1	2.19	0.74
1:B:269:VAL:HG23	5:B:507:HOH:O	1.88	0.73
1:C:145:ILE:O	1:C:145:ILE:HG22	1.88	0.71
1:A:46:ARG:CZ	1:A:58:VAL:HG11	2.21	0.69
1:B:141:LEU:HD23	1:B:141:LEU:C	2.17	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:GLN:NE2	5:B:501:HOH:O	2.25	0.68
1:C:203:TYR:HA	1:C:206:ARG:CZ	2.22	0.68
1:C:203:TYR:O	1:C:206:ARG:HD2	1.94	0.68
1:C:132:LEU:CD2	1:C:256:LEU:HG	2.24	0.67
1:B:150:ASN:ND2	1:B:158:MET:HE1	2.10	0.65
1:A:13:HIS:HE1	1:A:178:TYR:OH	1.78	0.65
1:C:268:ASP:O	1:C:271:VAL:HG12	1.96	0.65
1:B:14:ARG:NH1	1:B:76:THR:OG1	2.26	0.65
1:B:193:GLU:OE2	1:B:197:ARG:NE	2.30	0.64
1:C:132:LEU:HD22	1:C:256:LEU:HG	1.78	0.64
1:B:79:ARG:C	1:B:171:ILE:HD11	2.24	0.63
1:B:91:GLU:H	1:B:91:GLU:CD	2.08	0.62
1:C:11:MET:HE1	1:C:80:GLY:O	2.01	0.60
1:C:206:ARG:HD2	1:C:206:ARG:H	1.67	0.60
1:A:81:ASP:O	1:A:83:SER:N	2.36	0.58
1:B:150:ASN:HD21	1:B:158:MET:CE	2.12	0.57
1:B:259:LEU:O	1:B:261:LYS:NZ	2.30	0.57
1:A:77:VAL:HG23	1:A:88:PRO:HG3	1.86	0.57
1:C:113:TRP:CE2	1:C:314:ALA:HB2	2.41	0.56
1:B:79:ARG:O	1:B:171:ILE:HD11	2.07	0.54
1:C:145:ILE:O	1:C:145:ILE:CG2	2.54	0.54
1:A:46:ARG:CZ	1:A:58:VAL:CG1	2.86	0.53
1:A:141:LEU:C	1:A:141:LEU:CD2	2.75	0.53
1:C:233:TYR:OH	1:C:252:ASP:OD1	2.23	0.52
1:B:100:PHE:O	1:B:131:ARG:HD3	2.10	0.52
1:C:203:TYR:O	1:C:206:ARG:CD	2.57	0.52
1:B:193:GLU:O	1:B:197:ARG:N	2.40	0.51
1:B:158:MET:HG2	1:B:201:LEU:HD12	1.91	0.51
1:A:80:GLY:HA2	1:A:171:ILE:HD12	1.93	0.50
1:A:181:PHE:CD2	1:A:182:PRO:HD2	2.47	0.50
1:A:82:ASP:N	1:A:82:ASP:OD1	2.43	0.49
1:B:50:GLN:HA	1:B:50:GLN:OE1	2.13	0.49
1:C:267:VAL:HA	1:C:271:VAL:HG11	1.93	0.49
1:C:17:SER:O	1:C:19:SER:N	2.43	0.49
1:B:34:ARG:HA	1:B:68:GLN:HE22	1.78	0.49
1:B:141:LEU:C	1:B:141:LEU:CD2	2.86	0.49
1:B:144:PHE:O	1:B:147:SER:HB3	2.13	0.49
1:B:113:TRP:CE2	1:B:314:ALA:HB2	2.49	0.48
1:A:13:HIS:CE1	1:A:178:TYR:OH	2.63	0.48
1:A:141:LEU:HD23	1:A:141:LEU:O	2.15	0.47
1:C:262:PRO:CB	1:C:310:TYR:CD1	2.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:PHE:HA	1:B:147:SER:HB2	1.97	0.47
1:B:172:GLN:O	1:B:173:LEU:HD23	2.15	0.47
1:C:18:SER:O	1:C:19:SER:CB	2.62	0.47
1:C:262:PRO:HB2	1:C:310:TYR:CD1	2.49	0.47
1:B:144:PHE:O	1:B:147:SER:CB	2.63	0.46
1:B:26:ILE:HG23	1:B:27:PRO:HD2	1.98	0.46
1:B:231:ALA:O	1:B:261:LYS:HE3	2.16	0.46
1:A:64:TRP:CZ3	1:A:77:VAL:HG22	2.50	0.46
1:B:16:LEU:C	1:B:16:LEU:HD23	2.41	0.45
1:B:52:PRO:O	1:B:54:HIS:CD2	2.69	0.45
1:B:56:SER:HA	1:B:64:TRP:O	2.15	0.45
1:B:292:SER:O	1:B:293:PRO:C	2.60	0.45
1:C:25:SER:HB3	1:C:74:TYR:CE1	2.52	0.45
1:C:193:GLU:OE2	1:C:206:ARG:HG3	2.16	0.45
1:A:46:ARG:HG3	1:A:139:GLU:OE2	2.17	0.45
1:B:211:SER:O	1:B:215:ILE:HG13	2.16	0.45
1:C:35:LEU:H	1:C:68:GLN:HE22	1.65	0.45
1:A:81:ASP:C	1:A:83:SER:N	2.75	0.45
1:B:141:LEU:HD23	1:B:141:LEU:O	2.16	0.44
1:C:285:THR:O	1:C:286:SER:C	2.61	0.44
1:A:35:LEU:H	1:A:68:GLN:HE22	1.65	0.44
1:B:181:PHE:CD1	1:B:182:PRO:HD2	2.53	0.44
1:B:190:PRO:O	1:B:192:ALA:N	2.52	0.43
1:B:48:LYS:O	1:B:55:TRP:HA	2.18	0.43
1:C:249:LYS:NZ	1:C:253:CYS:SG	2.92	0.43
1:A:35:LEU:H	1:A:68:GLN:NE2	2.17	0.43
1:C:148:SER:HB2	1:C:203:TYR:OH	2.19	0.42
1:B:190:PRO:C	1:B:192:ALA:H	2.26	0.42
1:B:69:THR:C	1:B:71:ASP:H	2.26	0.42
1:C:12:ARG:HH11	1:C:12:ARG:HG2	1.83	0.42
1:B:60:ALA:O	1:B:61:ASP:HB2	2.20	0.42
1:C:139:GLU:HG3	1:C:181:PHE:CD2	2.54	0.42
1:A:162:LEU:C	1:A:162:LEU:HD23	2.44	0.42
1:A:46:ARG:NH2	1:A:58:VAL:CG1	2.78	0.42
1:B:19:SER:N	1:B:20:PRO:CD	2.83	0.42
1:A:11:MET:HE3	1:A:11:MET:HB2	1.93	0.42
1:C:115:SER:OG	1:C:116:VAL:HG13	2.19	0.41
1:B:150:ASN:HB3	1:B:155:ILE:HG13	2.02	0.41
1:B:69:THR:C	1:B:71:ASP:N	2.75	0.41
1:A:100:PHE:O	1:A:131:ARG:HD3	2.22	0.40
1:B:189:GLY:O	1:B:192:ALA:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:GLU:O	1:B:192:ALA:C	2.65	0.40
1:A:34:ARG:HA	1:A:68:GLN:HE22	1.86	0.40
1:A:81:ASP:O	1:A:82:ASP:C	2.64	0.40
1:A:141:LEU:HD23	1:A:142:PHE:N	2.32	0.40
1:B:100:PHE:O	1:B:131:ARG:CD	2.69	0.40
1:B:162:LEU:HD23	1:B:162:LEU:C	2.46	0.40
1:C:132:LEU:HD21	1:C:256:LEU:HG	2.02	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	315/318 (99%)	299 (95%)	15 (5%)	1 (0%)	36	35
1	B	299/318 (94%)	283 (95%)	13 (4%)	3 (1%)	12	8
1	C	306/318 (96%)	281 (92%)	23 (8%)	2 (1%)	18	14
All	All	920/954 (96%)	863 (94%)	51 (6%)	6 (1%)	18	14

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	190	PRO
1	C	18	SER
1	C	19	SER
1	A	82	ASP
1	B	19	SER
1	B	85	VAL

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	264/266 (99%)	255 (97%)	9 (3%)	32	33
1	B	256/266 (96%)	248 (97%)	8 (3%)	35	37
1	C	258/266 (97%)	252 (98%)	6 (2%)	44	49
All	All	778/798 (98%)	755 (97%)	23 (3%)	36	38

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	77	VAL
1	A	81	ASP
1	A	82	ASP
1	A	125	GLN
1	A	141	LEU
1	A	216	LEU
1	A	315	GLN
1	B	52	PRO
1	B	72	GLN
1	B	78	TYR
1	B	118	SER
1	B	175	ASP
1	B	194	THR
1	B	209	ARG
1	B	227	GLN
1	C	81	ASP
1	C	141	LEU
1	C	164	GLN
1	C	206	ARG
1	C	225	LEU
1	C	324	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	50	GLN
1	A	68	GLN
1	A	97	HIS
1	A	112	HIS
1	A	119	HIS
1	A	125	GLN
1	B	54	HIS
1	B	68	GLN
1	B	72	GLN
1	B	84	GLN
1	B	97	HIS
1	B	112	HIS
1	B	135	GLN
1	B	149	ASN
1	B	150	ASN
1	B	164	GLN
1	B	185	HIS
1	B	195	HIS
1	B	219	GLN
1	C	62	GLN
1	C	68	GLN
1	C	135	GLN
1	C	149	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 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	A1ID3	B	401	-	21,21,21	1.82	4 (19%)	28,29,29	1.69	5 (17%)
2	A1ID3	C	401	-	21,21,21	2.02	4 (19%)	28,29,29	1.52	5 (17%)
3	GOL	A	402	-	5,5,5	0.13	0	5,5,5	0.31	0
2	A1ID3	A	401	-	21,21,21	1.88	5 (23%)	28,29,29	1.17	3 (10%)

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	A1ID3	B	401	-	-	0/7/7/7	0/3/3/3
2	A1ID3	C	401	-	-	0/7/7/7	0/3/3/3
3	GOL	A	402	-	-	0/4/4/4	-
2	A1ID3	A	401	-	-	0/7/7/7	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	A1ID3	C14-C05	-5.74	1.39	1.47
2	A	401	A1ID3	C14-C05	-5.11	1.40	1.47
2	C	401	A1ID3	C05-N06	-4.87	1.32	1.38
2	B	401	A1ID3	C14-C05	-4.10	1.41	1.47
2	B	401	A1ID3	C13-C07	-4.06	1.36	1.41
2	A	401	A1ID3	C13-C07	-4.04	1.36	1.41
2	B	401	A1ID3	C05-N06	-4.03	1.33	1.38
2	A	401	A1ID3	C05-N06	-2.75	1.34	1.38
2	A	401	A1ID3	C07-N06	-2.70	1.33	1.38
2	B	401	A1ID3	C07-N06	-2.37	1.34	1.38
2	C	401	A1ID3	C05-C04	2.25	1.40	1.38
2	C	401	A1ID3	C13-C07	-2.24	1.38	1.41
2	A	401	A1ID3	C12-C10	2.24	1.42	1.39

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	A1ID3	C04-C05-N06	-4.97	106.02	109.61
2	C	401	A1ID3	C17-N18-C19	3.65	123.24	116.85
2	B	401	A1ID3	C14-C05-N06	3.55	124.22	119.74
2	B	401	A1ID3	C15-C14-C05	3.29	124.68	120.76
2	B	401	A1ID3	C07-N06-C05	3.13	112.57	109.28
2	A	401	A1ID3	C17-N18-C19	2.93	121.98	116.85
2	C	401	A1ID3	C14-C05-N06	2.77	123.22	119.74
2	C	401	A1ID3	C14-C19-N18	-2.67	119.53	123.50
2	B	401	A1ID3	C17-N18-C19	2.61	121.43	116.85
2	C	401	A1ID3	C08-C07-C13	-2.52	119.75	122.19
2	A	401	A1ID3	C02-C03-C04	-2.48	106.10	113.19
2	A	401	A1ID3	C15-C14-C05	-2.46	117.84	120.76
2	C	401	A1ID3	C07-C13-C04	-2.30	104.74	106.84

There are no chirality outliers.

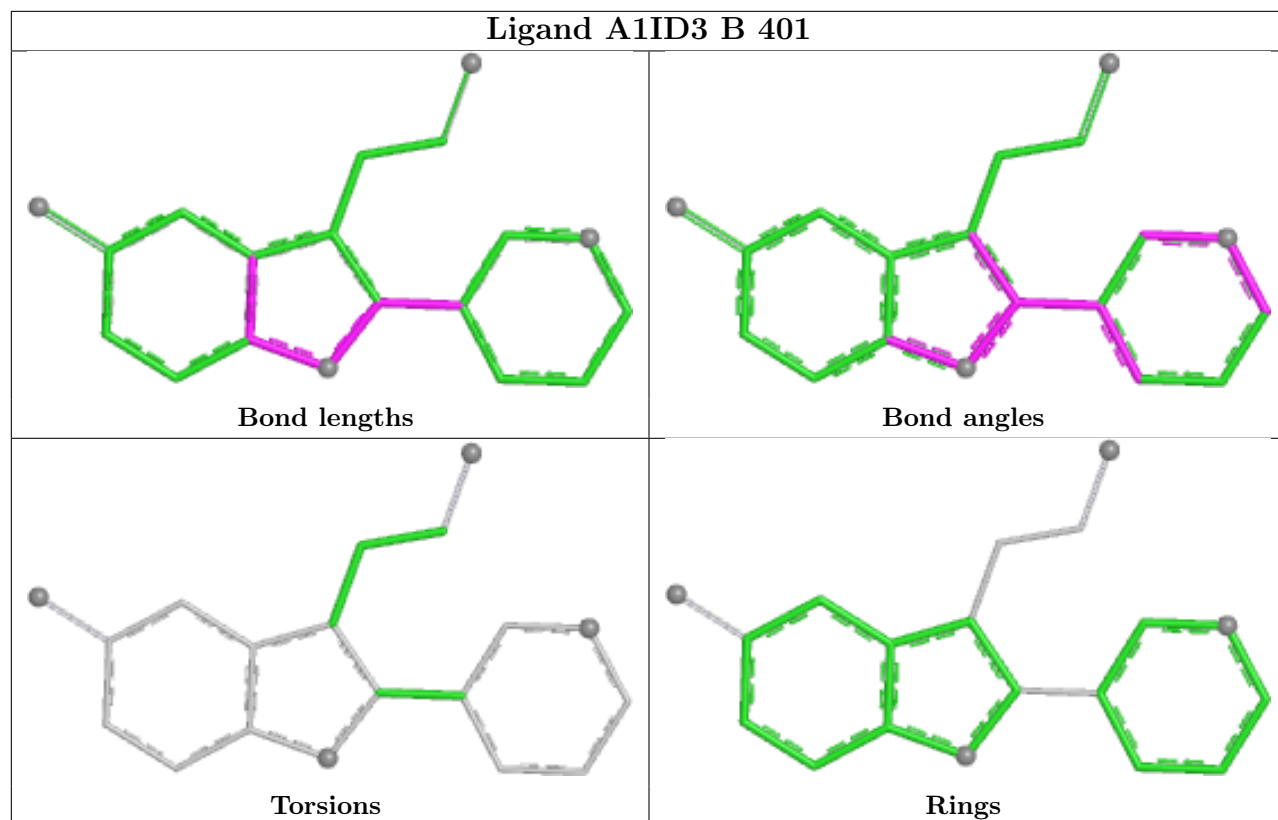
There are no torsion outliers.

There are no ring outliers.

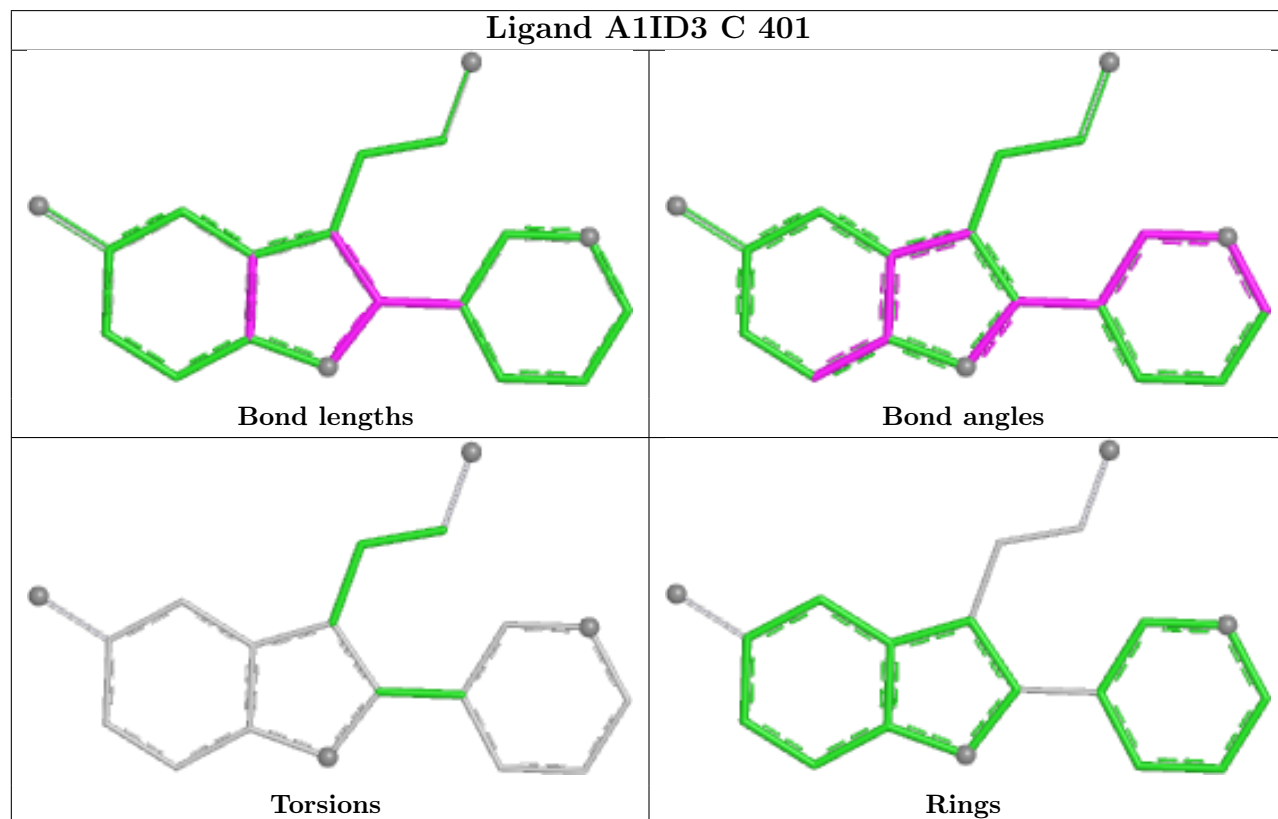
No monomer is involved in short contacts.

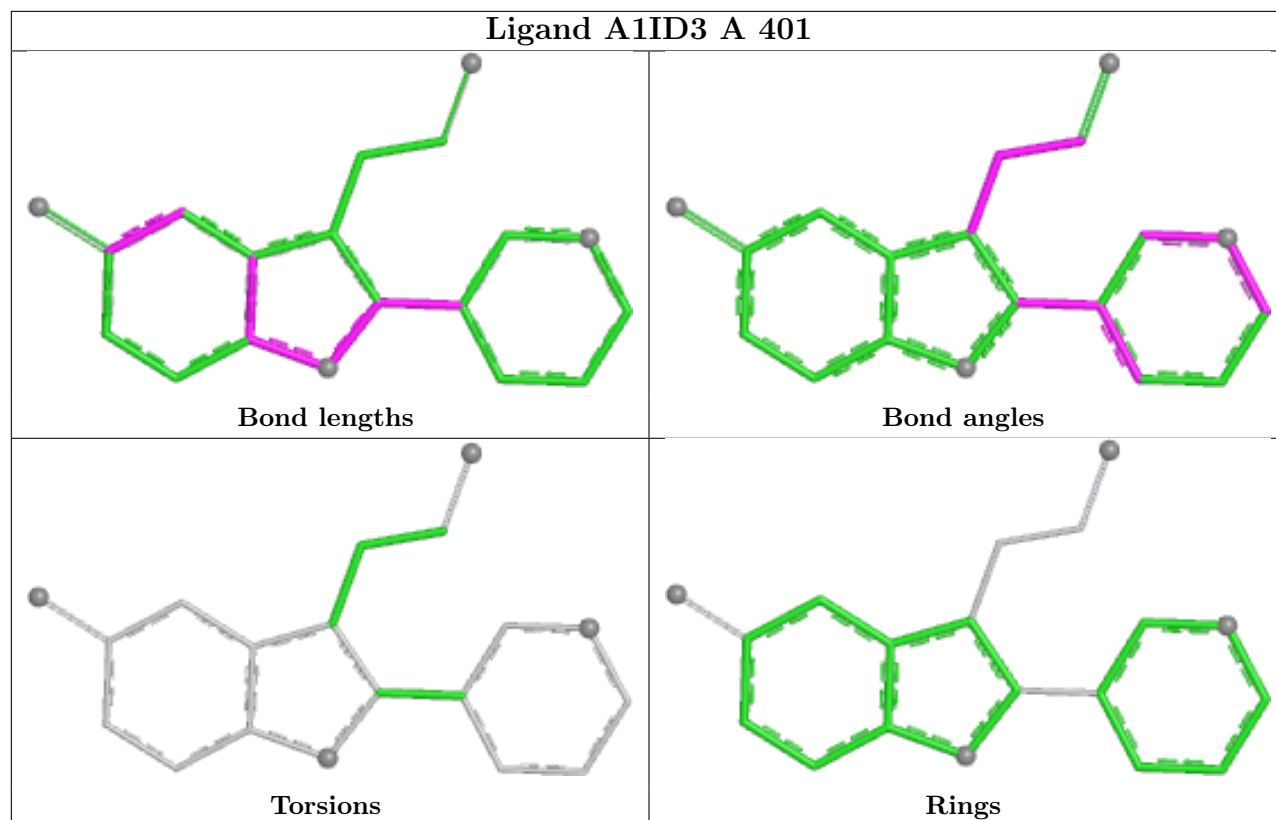
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 A1ID3 B 401



Ligand A1ID3 C 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, 95th 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 ²)	Q<0.9
1	A	315/318 (99%)	0.31	17 (5%) 31 30	20, 42, 79, 136	3 (0%)
1	B	305/318 (95%)	1.13	57 (18%) 3 3	34, 60, 98, 121	0
1	C	312/318 (98%)	1.26	62 (19%) 3 2	35, 64, 109, 129	0
All	All	932/954 (97%)	0.90	136 (14%) 6 5	20, 56, 99, 136	3 (0%)

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	203	TYR	6.5
1	C	16	LEU	4.9
1	B	74	TYR	4.6
1	C	146	CYS	4.5
1	C	85	VAL	4.4
1	B	16	LEU	4.2
1	B	93	LEU	4.2
1	C	324	ARG	4.0
1	B	26	ILE	3.9
1	A	325	GLN	3.9
1	C	221	GLY	3.8
1	A	288	ALA	3.7
1	C	90	LEU	3.7
1	C	294	LEU	3.7
1	B	85	VAL	3.7
1	A	289	LYS	3.7
1	C	201	LEU	3.6
1	B	77	VAL	3.6
1	B	290	GLY	3.6
1	B	96	LEU	3.6
1	A	291	PRO	3.4
1	B	190	PRO	3.4
1	B	24	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	23	TRP	3.3
1	C	147	SER	3.3
1	B	189	GLY	3.3
1	B	71	ASP	3.2
1	A	61	ASP	3.2
1	A	81	ASP	3.2
1	B	28	CYS	3.2
1	B	192	ALA	3.1
1	C	116	VAL	3.1
1	B	90	LEU	3.1
1	B	22	LEU	3.1
1	C	219	GLN	3.1
1	C	188	ALA	3.1
1	B	199	LEU	3.0
1	B	206	ARG	3.0
1	B	10	HIS	3.0
1	B	195	HIS	2.9
1	C	197	ARG	2.9
1	C	306	LEU	2.9
1	C	215	ILE	2.8
1	A	30	ARG	2.8
1	A	11	MET	2.8
1	A	286	SER	2.8
1	C	114	ALA	2.8
1	C	218	GLU	2.8
1	B	323	LEU	2.7
1	B	11	MET	2.7
1	B	196	LEU	2.7
1	C	310	TYR	2.7
1	B	64	TRP	2.7
1	C	290	GLY	2.7
1	A	285	THR	2.7
1	C	93	LEU	2.7
1	B	291	PRO	2.7
1	C	26	ILE	2.7
1	C	271	VAL	2.7
1	B	194	THR	2.6
1	B	52	PRO	2.6
1	B	222	PRO	2.6
1	B	19	SER	2.6
1	C	17	SER	2.6
1	C	115	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	284	LYS	2.6
1	B	294	LEU	2.6
1	C	286	SER	2.6
1	C	216	LEU	2.6
1	B	171	ILE	2.6
1	C	162	LEU	2.6
1	C	82	ASP	2.5
1	C	19	SER	2.5
1	B	102	LEU	2.5
1	C	22	LEU	2.5
1	B	272	TRP	2.5
1	C	305	ASN	2.5
1	C	225	LEU	2.5
1	B	197	ARG	2.5
1	C	204	ARG	2.5
1	C	86	SER	2.4
1	C	222	PRO	2.4
1	C	220	GLY	2.4
1	C	231	ALA	2.4
1	C	184	LEU	2.4
1	B	220	GLY	2.4
1	C	142	PHE	2.4
1	C	158	MET	2.4
1	B	69	THR	2.4
1	C	74	TYR	2.3
1	C	199	LEU	2.3
1	B	123	VAL	2.3
1	B	176	VAL	2.3
1	C	104	VAL	2.3
1	B	27	PRO	2.3
1	B	209	ARG	2.3
1	B	216	LEU	2.3
1	C	107	ALA	2.3
1	A	20	PRO	2.2
1	A	82	ASP	2.2
1	B	33	LEU	2.2
1	B	203	TYR	2.2
1	C	238	LYS	2.2
1	B	66	LEU	2.2
1	B	73	LEU	2.2
1	A	324	ARG	2.2
1	B	88	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	190	PRO	2.2
1	B	107	ALA	2.2
1	B	97	HIS	2.2
1	B	201	LEU	2.2
1	C	293	PRO	2.1
1	C	230	VAL	2.1
1	C	80	GLY	2.1
1	A	60	ALA	2.1
1	C	192	ALA	2.1
1	C	87	ARG	2.1
1	C	301	ASN	2.1
1	A	18	SER	2.1
1	B	86	SER	2.1
1	B	141	LEU	2.1
1	C	206	ARG	2.1
1	C	224	TRP	2.1
1	B	153	ALA	2.1
1	B	223	ALA	2.1
1	C	59	LEU	2.0
1	C	61	ASP	2.0
1	A	12	ARG	2.0
1	C	79	ARG	2.0
1	C	262	PRO	2.0
1	C	180	GLY	2.0
1	C	300	GLY	2.0
1	B	166	PHE	2.0
1	B	193	GLU	2.0
1	B	205	ALA	2.0
1	A	59	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

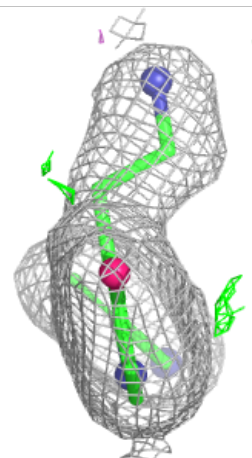
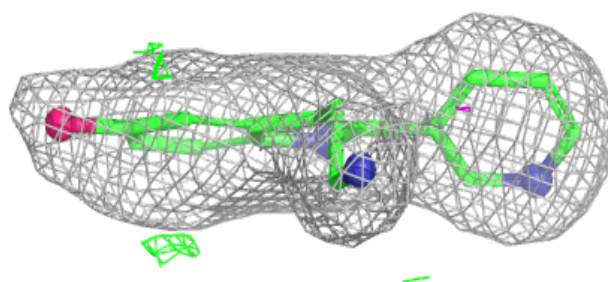
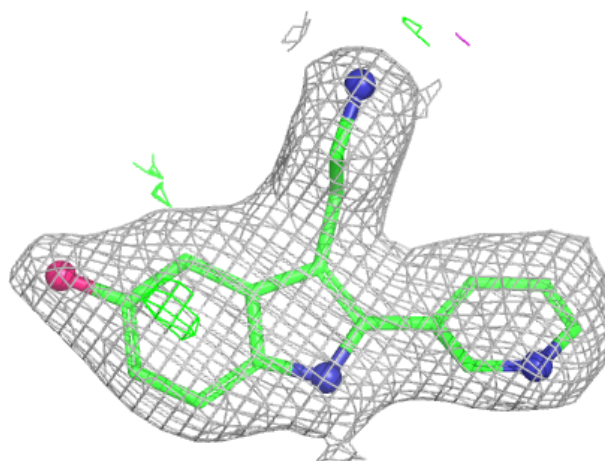
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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
3	GOL	A	402	6/6	0.91	0.10	42,45,52,55	0
2	A1ID3	C	401	19/19	0.92	0.10	43,51,69,72	0
2	A1ID3	B	401	19/19	0.92	0.10	41,48,63,67	0
2	A1ID3	A	401	19/19	0.96	0.07	30,36,45,49	0
4	NI	A	403	1/1	1.00	0.02	35,35,35,35	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.

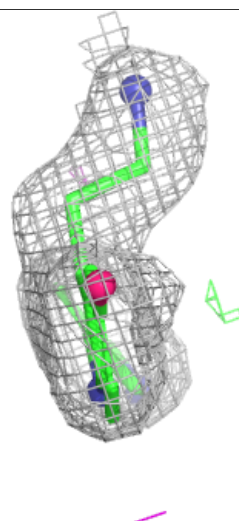
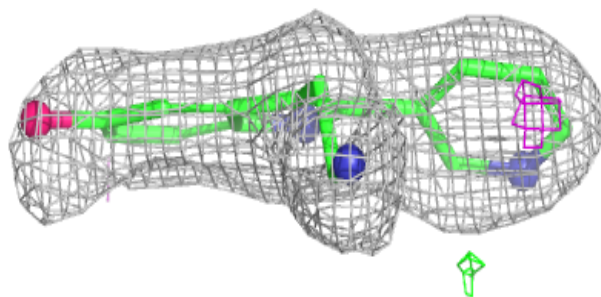
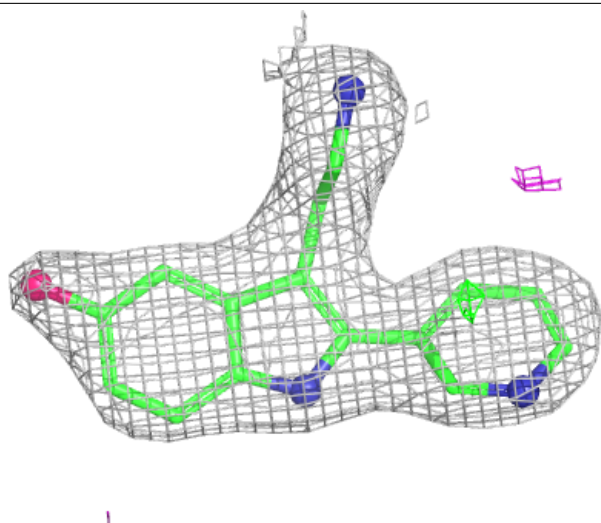
Electron density around A1ID3 C 401:

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



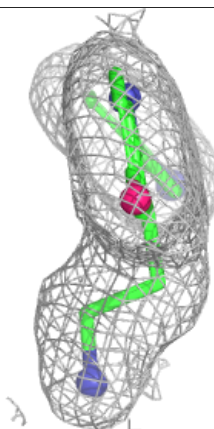
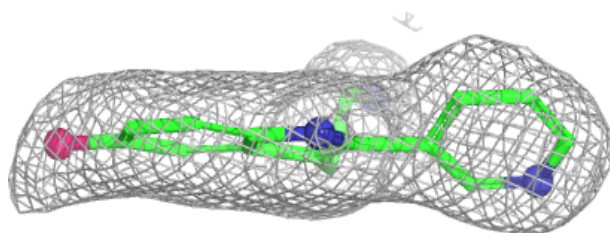
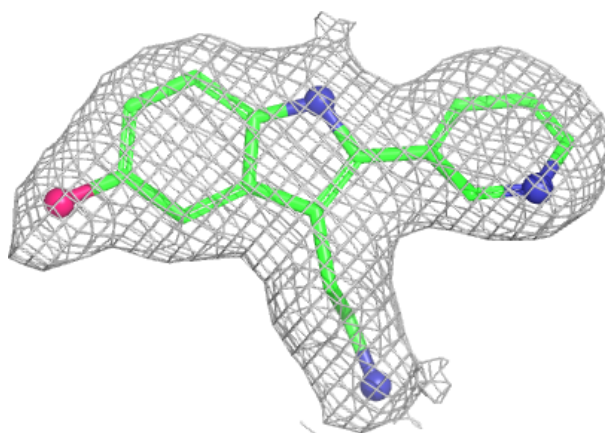
Electron density around A1ID3 B 401:

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



Electron density around A1ID3 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.