



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 02:36 AM UTC

PDB ID : 8USY / pdb_00008usy
Title : HIV-1 Integrase F185H N222K Complexed with Allosteric Inhibitor BI-D
Authors : Montermoso, S.; Gupta, K.; Eilers, G.; Bushman, F.D.; Van Duyne, G.D.
Deposited on : 2023-10-30
Resolution : 4.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

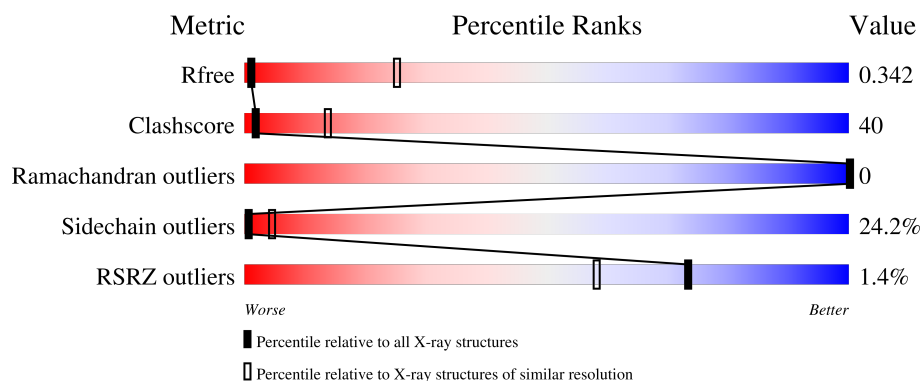
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.40 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}	180053	1088 (4.90-3.90)
Clashscore	190562	1135 (4.90-3.90)
Ramachandran outliers	187476	1026 (4.90-3.90)
Sidechain outliers	187428	1010 (4.90-3.90)
RSRZ outliers	180081	1084 (4.90-3.90)

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	293	% 22% 33% 15% • 27%
1	B	293	% 23% 37% 11% • 26%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4324 atoms, of which 869 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.

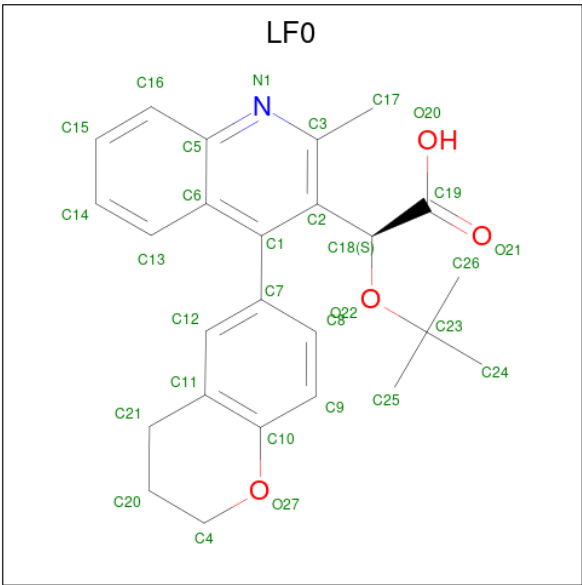
- Molecule 1 is a protein called Integrase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	214	Total	C	H	N	O	S	0	0	0
			2100	1080	407	303	304	6			
1	B	216	Total	C	H	N	O	S	0	0	0
			2112	1083	410	306	307	6			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	cloning artifact	UNP P12497
A	15	ALA	TYR	engineered mutation	UNP P12497
A	185	HIS	PHE	engineered mutation	UNP P12497
A	222	LYS	ASN	engineered mutation	UNP P12497
A	289	CYS	-	expression tag	UNP P12497
A	290	THR	-	expression tag	UNP P12497
A	291	LEU	-	expression tag	UNP P12497
A	292	GLU	-	expression tag	UNP P12497
A	293	TYR	-	expression tag	UNP P12497
B	1	HIS	-	cloning artifact	UNP P12497
B	15	ALA	TYR	engineered mutation	UNP P12497
B	185	HIS	PHE	engineered mutation	UNP P12497
B	222	LYS	ASN	engineered mutation	UNP P12497
B	289	CYS	-	expression tag	UNP P12497
B	290	THR	-	expression tag	UNP P12497
B	291	LEU	-	expression tag	UNP P12497
B	292	GLU	-	expression tag	UNP P12497
B	293	TYR	-	expression tag	UNP P12497

- Molecule 2 is (2S)-tert-butoxy[4-(3,4-dihydro-2H-chromen-6-yl)-2-methylquinolin-3-yl]ethanoic acid (CCD ID: LF0) (formula: C₂₅H₂₇NO₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			56	25	26	1	4		
2	A	1	Total	C	H	N	O	0	0
			56	25	26	1	4		

4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	106.03Å 106.03Å 245.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 4.40 20.00 – 4.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-4.40) 86.1 (20.00-4.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.05 (at 4.15Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.299 , 0.339 0.323 , 0.342	Depositor DCC
R_{free} test set	556 reflections (8.45%)	wwPDB-VP
Wilson B-factor (Å ²)	221.9	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 210.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4324	wwPDB-VP
Average B, all atoms (Å ²)	263.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.88% 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: LF0

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	0.78	0/1726	1.44	37/2327 (1.6%)
1	B	0.78	1/1735 (0.1%)	1.44	41/2341 (1.8%)
All	All	0.78	1/3461 (0.0%)	1.44	78/4668 (1.7%)

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	7
1	B	0	5
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	VAL	CA-CB	5.36	1.62	1.54

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	ARG	N-CA-C	9.70	121.85	111.28
1	A	78	HIS	N-CA-C	-9.67	94.38	109.76
1	A	190	GLY	N-CA-C	-9.45	100.30	111.36
1	B	188	LYS	N-CA-C	-8.78	102.52	113.23
1	B	253	ASP	N-CA-C	-8.75	97.33	110.28

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	ARG	Sidechain
1	A	166	ARG	Sidechain
1	A	224	ARG	Sidechain
1	A	231	ARG	Sidechain
1	A	262	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	1693	407	1733	160	1
1	B	1702	410	1742	137	0
2	A	60	52	52	7	0
All	All	3455	869	3527	276	1

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 40.

The worst 5 of 276 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:73:ILE:HA	1:A:89:ILE:HG13	1.44	0.98
1:A:95:GLN:HA	1:A:125:THR:HG21	1.44	0.98
1:A:250:VAL:HG13	1:A:259:VAL:HG22	1.55	0.89
1:A:187:ARG:HD2	1:A:191:ILE:HB	1.57	0.86
1:A:77:VAL:HG22	1:A:84:ILE:HG23	1.62	0.81

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:GLN:OE1	1:A:274:GLN:OE1[12_565]	1.94	0.26

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	210/293 (72%)	205 (98%)	5 (2%)	0	100	100
1	B	212/293 (72%)	210 (99%)	2 (1%)	0	100	100
All	All	422/586 (72%)	415 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	179/244 (73%)	129 (72%)	50 (28%)	0	3
1	B	180/244 (74%)	143 (79%)	37 (21%)	1	7
All	All	359/488 (74%)	272 (76%)	87 (24%)	1	4

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	96	GLU
1	B	198	GLU
1	B	107	ARG
1	B	160	LYS
1	B	209	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	114	HIS
1	B	148	GLN
1	B	254	ASN
1	B	171	HIS
1	A	148	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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	LF0	A	301	-	31,33,33	2.79	6 (19%)	41,49,49	1.75	10 (24%)
2	LF0	A	302	-	31,33,33	2.81	6 (19%)	41,49,49	1.70	10 (24%)

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	LF0	A	301	-	-	4/17/24/24	0/4/4/4
2	LF0	A	302	-	-	2/17/24/24	0/4/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	LF0	C1-C7	-8.12	1.40	1.49
2	A	302	LF0	C1-C7	-8.12	1.40	1.49
2	A	302	LF0	C2-C18	-7.31	1.39	1.53
2	A	301	LF0	C2-C18	-7.18	1.39	1.53
2	A	302	LF0	C21-C11	-6.85	1.39	1.51

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	302	LF0	C3-N1-C5	5.52	123.49	118.42
2	A	301	LF0	C3-N1-C5	5.23	123.22	118.42
2	A	302	LF0	C6-C5-N1	-3.84	118.73	122.80
2	A	301	LF0	C6-C5-N1	-3.59	119.00	122.80
2	A	301	LF0	C12-C7-C1	3.16	125.78	119.91

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	LF0	C2-C18-C19-O20
2	A	301	LF0	C2-C18-C19-O21
2	A	301	LF0	O22-C18-C19-O20
2	A	302	LF0	C2-C18-C19-O20
2	A	302	LF0	C2-C18-C19-O21

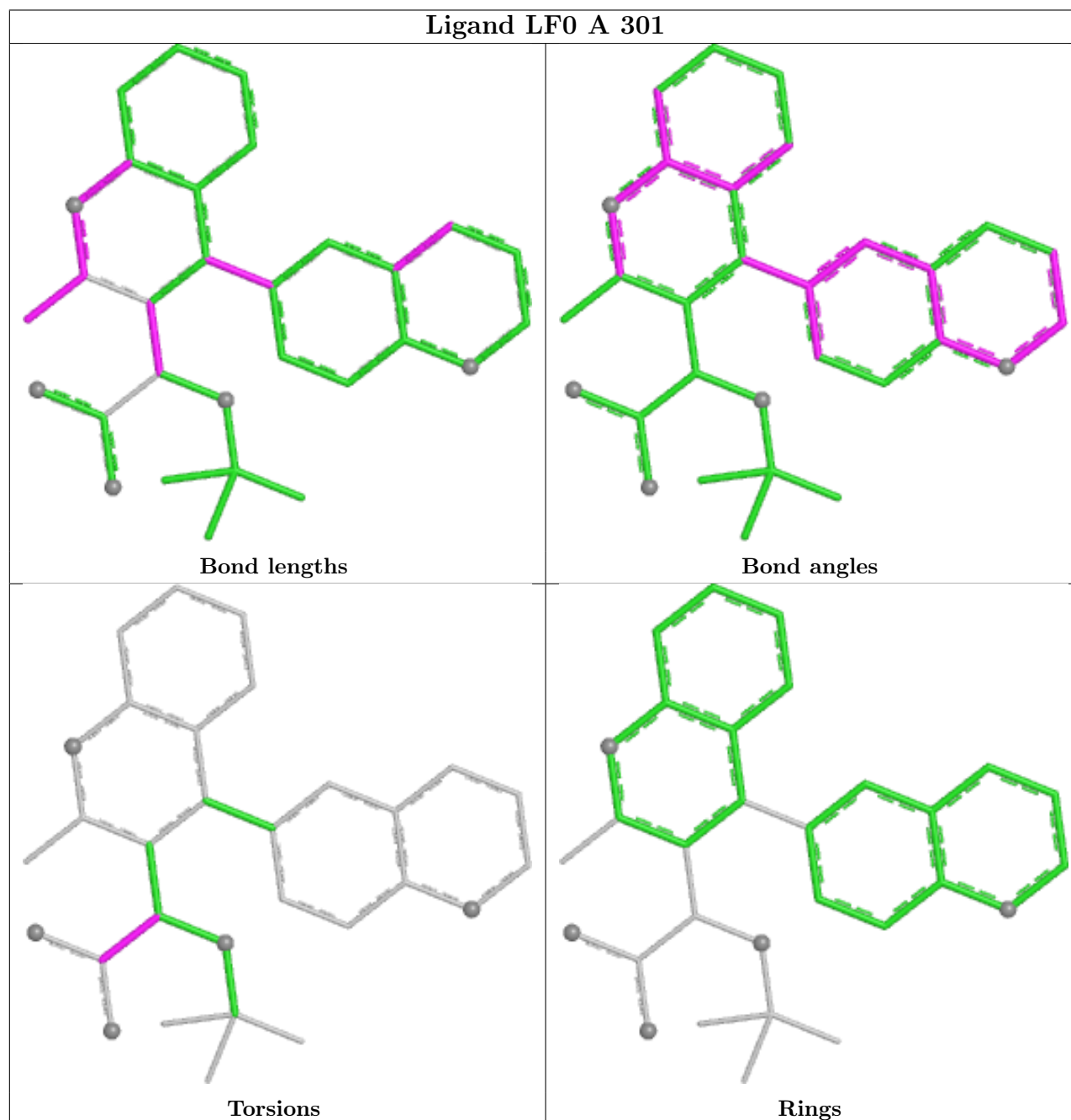
There are no ring outliers.

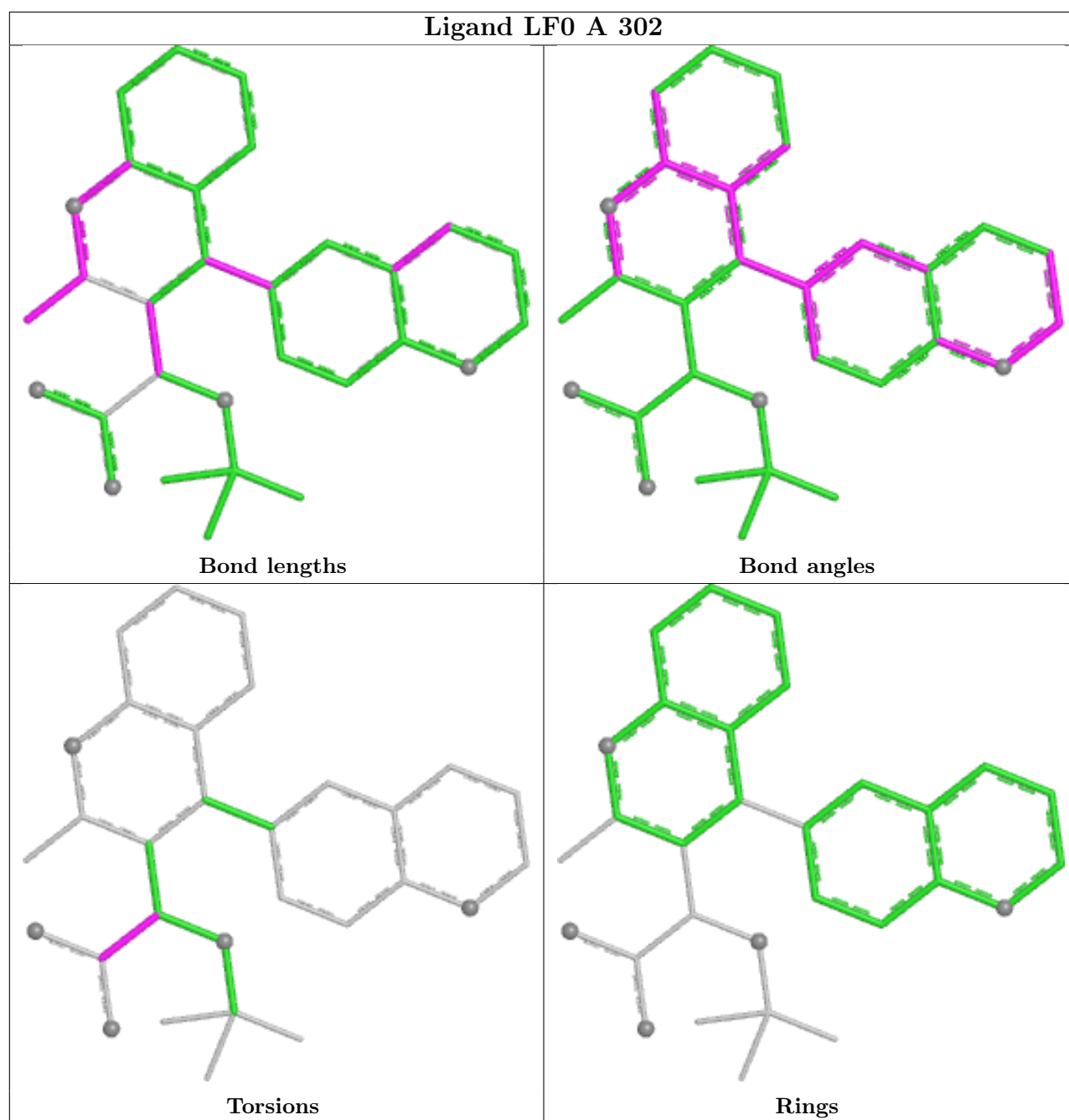
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	LF0	5	0
2	A	302	LF0	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	214/293 (73%)	0.17	4 (1%)	66 52	175, 273, 300, 300	0
1	B	216/293 (73%)	0.15	2 (0%)	81 67	179, 261, 300, 300	0
All	All	430/586 (73%)	0.16	6 (1%)	73 58	175, 268, 300, 300	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	ALA	4.6
1	B	192	GLY	4.1
1	A	147	SER	2.9
1	A	148	GLN	2.3
1	B	109	PRO	2.2

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](#)

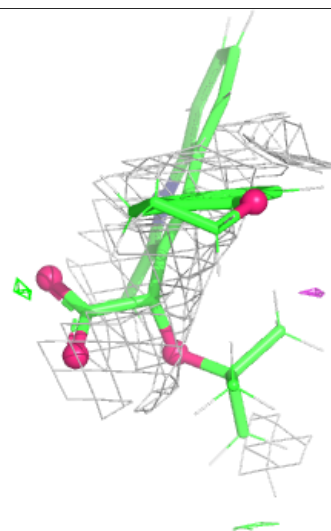
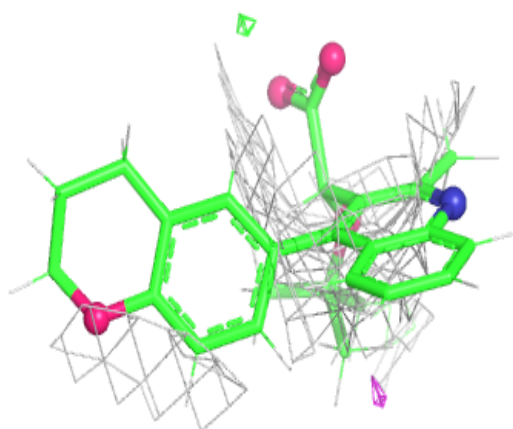
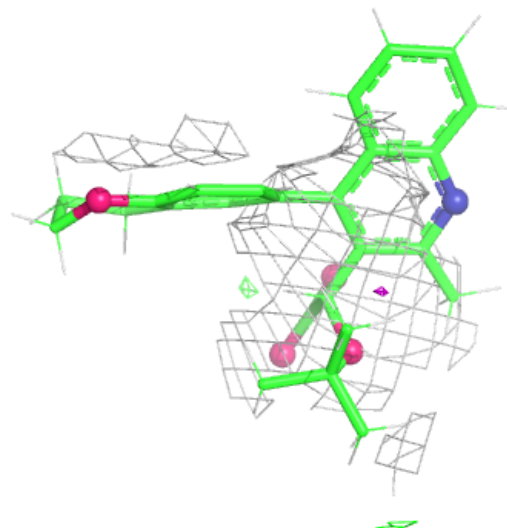
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists 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
2	LF0	A	301	30/30	0.82	0.17	300,300,300,300	0
2	LF0	A	302	30/30	0.88	0.23	283,283,283,283	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.

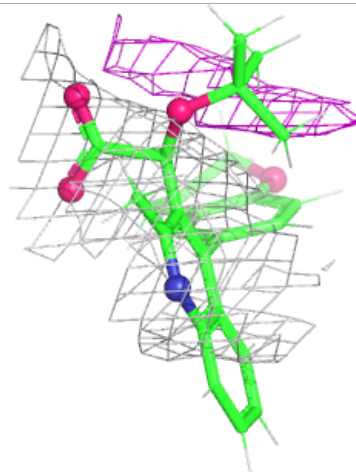
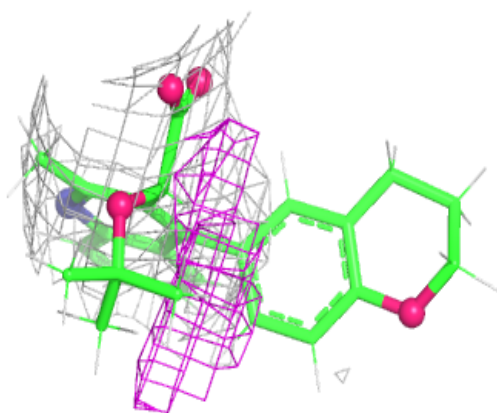
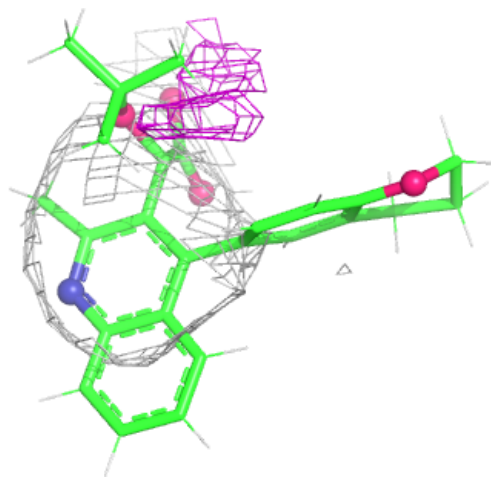
Electron density around LF0 A 301:

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 LF0 A 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.