



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 13, 2026 – 02:25 PM EDT

PDB ID : 9NX4 / pdb\_00009nx4  
Title : Crystal Structure of a P. Aeruginosa Gyrase Chimera In Complex with 20mer DNA and Ciprofloxacin  
Authors : Pedersen, L.C.; Doetsch, P.W.; Garcia-Villada, L.; Degtyareva, N.; Perera, U.L.  
Deposited on : 2025-03-25  
Resolution : 2.85 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

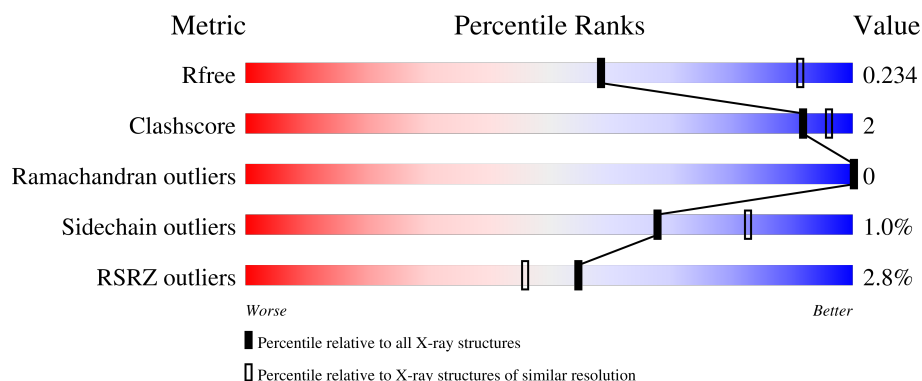
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


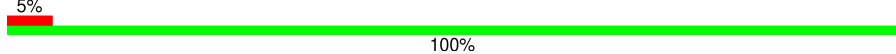
The reported resolution of this entry is 2.85 Å.

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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	942	
2	C	20	

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12116 atoms, of which 5912 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 DNA gyrase subunit B,DNA gyrase subunit A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	737	Total	C	H	N	O	S	0	5	1
			11344	3592	5648	997	1080	27			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	392	GLY	-	expression tag	UNP Q9S1C7
A	393	SER	-	expression tag	UNP Q9S1C7
A	394	ALA	-	expression tag	UNP Q9S1C7
A	395	ALA	-	expression tag	UNP Q9S1C7
A	396	ALA	-	expression tag	UNP Q9S1C7
A	999	GLY	-	linker	UNP Q9S1C7
A	1000	GLY	-	linker	UNP Q9S1C7
A	1001	SER	-	linker	UNP Q9S1C7

- Molecule 2 is a DNA chain called DNA (5'-D(\*AP\*GP\*CP\*CP\*GP\*TP\*AP\*GP\*GP\*GP\*CP\*CP\*CP\*TP\*AP\*CP\*GP\*GP\*CP\*T)-3').

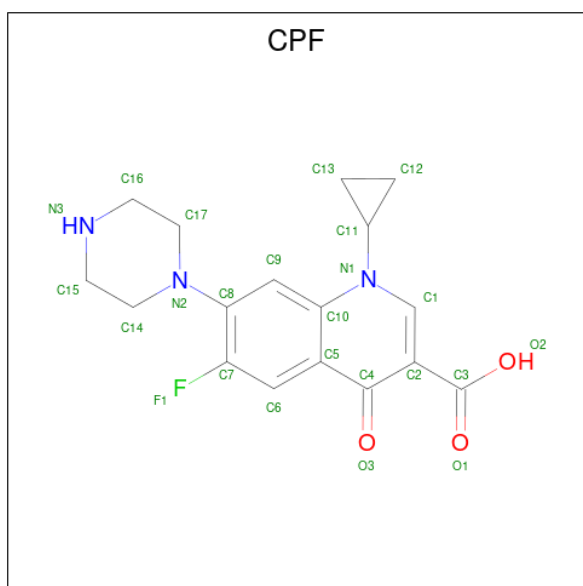
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	20	Total	C	H	N	O	P	0	0	0
			632	193	225	77	118	19			

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			18	6	5	7		

- Molecule 4 is 1-CYCLOPROPYL-6-FLUORO-4-OXO-7-PIPERAZIN-1-YL-1,4-DIHYDR OQUINOLINE-3-CARBOXYLIC ACID (CCD ID: CPF) (formula:  $C_{17}H_{18}FN_3O_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	F	H	N	O	0	0
			41	17	1	17	3	3		
4	C	1	Total	C	F	H	N	O	0	0
			41	17	1	17	3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 6 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mn	0	0
			1	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

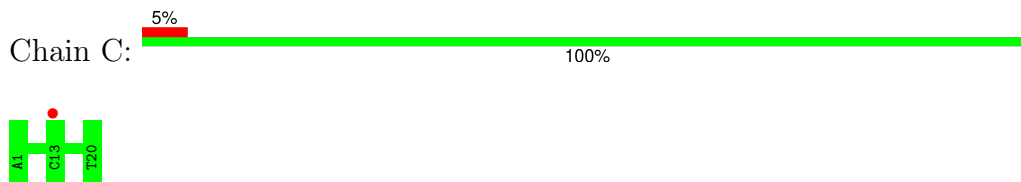
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	Cl	0	0
			2	2		
7	C	1	Total	Cl	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	15	Total 15	O 15	0	0
8	C	1	Total 1	O 1	0	0



- Molecule 1: DNA gyrase subunit B,DNA gyrase subunit A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	179.03Å 179.03Å 163.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.67 – 2.85 43.67 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.6 (43.67-2.85) 91.4 (43.67-2.85)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.205 , 0.234 0.205 , 0.234	Depositor DCC
$R_{free}$ test set	1818 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.2	Xtriage
Anisotropy	0.737	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 40.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12116	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 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, CPF, MN, CIT, CL

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	0.34	0/5809	0.51	1/7871 (0.0%)
2	C	0.44	0/456	0.65	0/702
All	All	0.34	0/6265	0.52	1/8573 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1328	GLN	N-CA-C	-5.38	100.13	108.90

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5696	5648	5619	19	0
2	C	407	225	225	0	0
3	A	13	5	5	0	0
4	A	24	17	17	0	0
4	C	24	17	17	0	0
5	A	20	0	0	2	0
6	A	1	0	0	0	0
7	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	1	0	0	0	0
8	A	15	0	0	0	0
8	C	1	0	0	0	0
All	All	6204	5912	5883	19	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 2.

All (19) 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:1215:PRO:O	1:A:1518:ARG:NH2	2.19	0.76
1:A:1382:GLU:OE1	1:A:1479:TYR:OH	2.11	0.68
1:A:1239:ARG:NH2	5:A:1603:SO4:O1	2.31	0.63
1:A:1088:THR:HG22	1:A:1092:MET:HE2	1.90	0.54
1:A:1294:ARG:NH2	1:A:1296:GLU:OE2	2.40	0.53
1:A:1384:GLN:HG3	1:A:1475:LEU:HD11	1.89	0.52
1:A:1024:TYR:O	1:A:1028:VAL:HG23	2.11	0.50
1:A:1386:VAL:HG12	1:A:1421:VAL:HG21	1.95	0.48
1:A:1092:MET:HA	1:A:1098:LEU:HD22	1.95	0.47
1:A:1167:LEU:HD21	1:A:1351:MET:HE3	1.97	0.46
1:A:1257:ARG:NH2	5:A:1606:SO4:O3	2.49	0.45
1:A:539:VAL:HG11	1:A:557:TYR:CZ	2.53	0.44
1:A:1350:ASP:O	1:A:1354:VAL:HG23	2.18	0.43
1:A:1063:TYR:HB3	1:A:1124:GLU:HB3	2.01	0.42
1:A:1316:VAL:O	1:A:1320:ASN:ND2	2.47	0.42
1:A:1390:ASN:O	1:A:1394:VAL:HG23	2.19	0.42
1:A:1327:LEU:HA	1:A:1327:LEU:HD12	1.76	0.41
1:A:1199:ASP:OD2	1:A:1504[A]:ARG:NH2	2.54	0.41
1:A:1189:GLU:OE1	1:A:1518:ARG:NH1	2.54	0.41

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	734/942 (78%)	713 (97%)	21 (3%)	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	589/786 (75%)	583 (99%)	6 (1%)	68	83

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	467	GLN
1	A	502	ASP
1	A	1072	ASP
1	A	1239	ARG
1	A	1252	GLU
1	A	1257	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	493	HIS
1	A	797	ASN
1	A	1154	GLN
1	A	1210	GLN
1	A	1334	ASN
1	A	1342	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 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$
5	SO4	A	1603	-	4,4,4	0.22	0	6,6,6	0.21	0
5	SO4	A	1606	-	4,4,4	0.31	0	6,6,6	0.19	0
4	CPF	A	1602	6	27,27,27	1.04	1 (3%)	40,40,40	1.30	5 (12%)
3	CIT	A	1601	6	12,12,12	1.30	1 (8%)	17,17,17	1.21	2 (11%)
5	SO4	A	1604	-	4,4,4	0.26	0	6,6,6	0.21	0
5	SO4	A	1605	-	4,4,4	0.28	0	6,6,6	0.36	0
4	CPF	C	101	-	27,27,27	1.09	1 (3%)	40,40,40	1.17	3 (7%)

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
4	CPF	A	1602	6	-	1/12/22/22	0/4/4/4
3	CIT	A	1601	6	-	7/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CPF	C	101	-	-	4/12/22/22	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	101	CPF	C8-N2	2.39	1.46	1.41
4	A	1602	CPF	O2-C3	-2.36	1.24	1.30
3	A	1601	CIT	C3-C6	-2.35	1.51	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	101	CPF	C12-C11-N1	3.87	124.99	118.87
4	A	1602	CPF	C10-N1-C11	3.67	123.71	119.88
3	A	1601	CIT	O7-C3-C6	-2.44	105.50	108.96
4	A	1602	CPF	C10-C5-C4	2.42	123.68	121.38
3	A	1601	CIT	O2-C1-O1	-2.38	117.20	123.33
4	A	1602	CPF	O1-C3-C2	-2.33	117.84	122.67
4	C	101	CPF	C10-C5-C4	2.33	123.59	121.38
4	A	1602	CPF	C9-C10-N1	2.20	122.40	120.49
4	C	101	CPF	C14-N2-C17	-2.09	106.86	111.57
4	A	1602	CPF	C13-C11-N1	2.05	122.11	118.87

There are no chirality outliers.

All (12) torsion outliers are listed below:

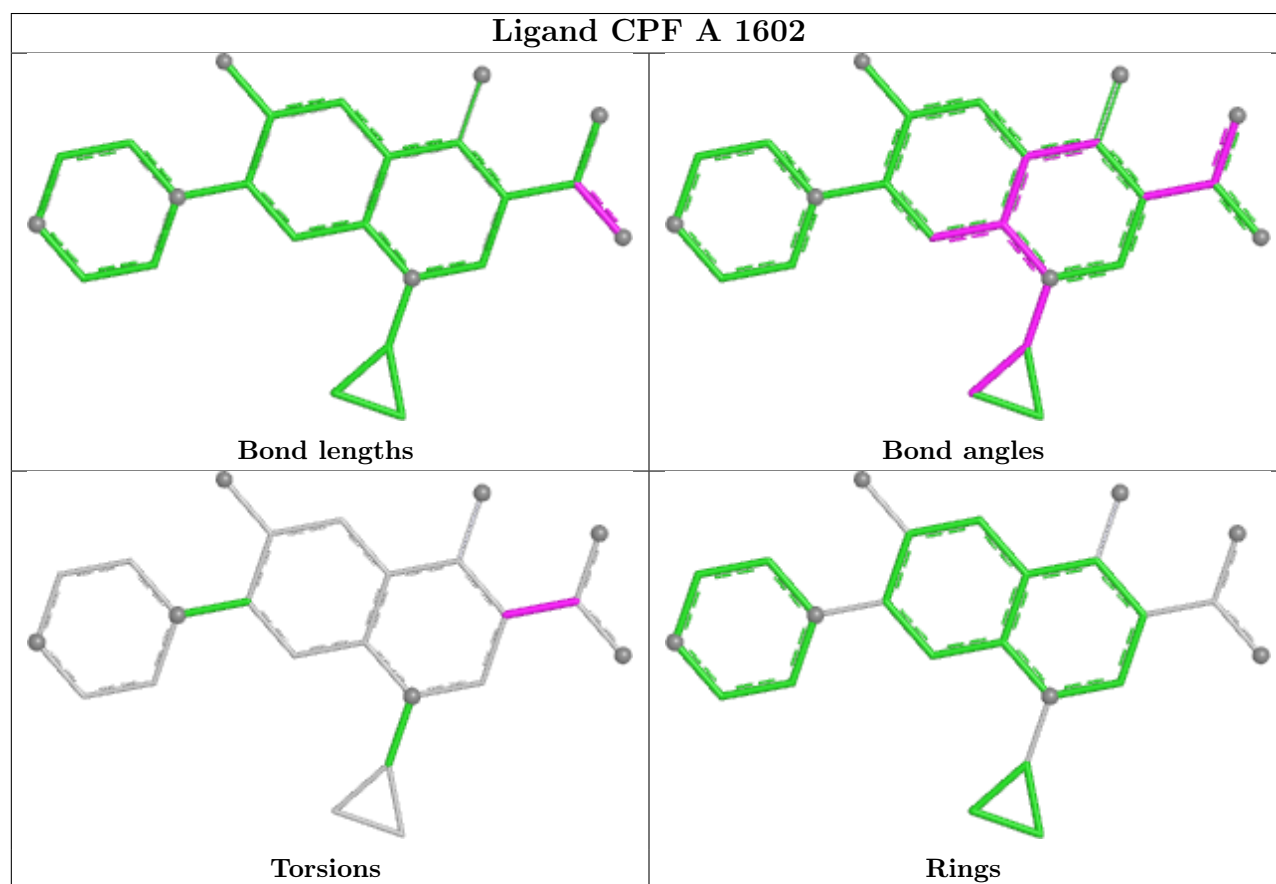
Mol	Chain	Res	Type	Atoms
3	A	1601	CIT	C1-C2-C3-O7
3	A	1601	CIT	C1-C2-C3-C4
3	A	1601	CIT	C1-C2-C3-C6
3	A	1601	CIT	O7-C3-C6-O5
3	A	1601	CIT	O7-C3-C6-O6
3	A	1601	CIT	C4-C3-C6-O5
3	A	1601	CIT	C4-C3-C6-O6
4	C	101	CPF	C13-C11-N1-C10
4	C	101	CPF	C13-C11-N1-C1
4	C	101	CPF	C12-C11-N1-C10
4	C	101	CPF	C12-C11-N1-C1
4	A	1602	CPF	C4-C2-C3-O1

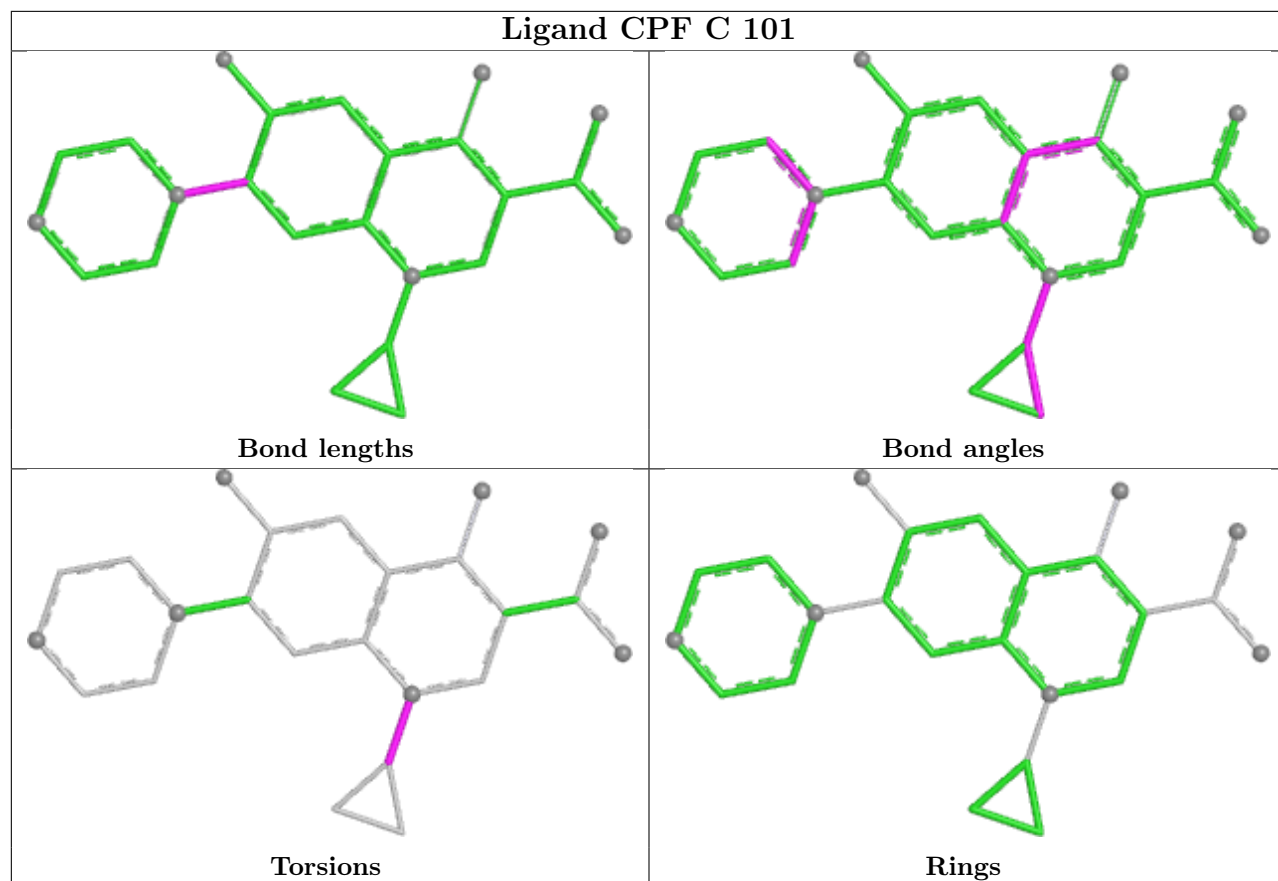
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1603	SO4	1	0
5	A	1606	SO4	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.





## 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	737/942 (78%)	0.30	20 (2%) 56 47	25, 60, 94, 117	2 (0%)
2	C	20/20 (100%)	0.24	1 (5%) 34 27	46, 60, 112, 114	0
All	All	757/962 (78%)	0.29	21 (2%) 55 46	25, 60, 96, 117	2 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1525	SER	7.8
1	A	459	ARG	5.1
1	A	1007	GLU	4.5
1	A	736	HIS	4.4
1	A	1299	LYS	4.4
1	A	544	GLN	4.2
1	A	480	ILE	3.9
1	A	798	ALA	3.6
1	A	1253	LYS	3.5
1	A	541	ARG	3.1
1	A	1446	ASP	3.0
1	A	750	GLU	2.9
1	A	561	SER	2.8
1	A	542	GLY	2.7
1	A	1311	GLY	2.5
1	A	559	THR	2.5
1	A	560	GLN	2.2
1	A	557	TYR	2.2
1	A	1313	VAL	2.1
1	A	1228	GLY	2.1
2	C	13	DC	2.1



## 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](#)

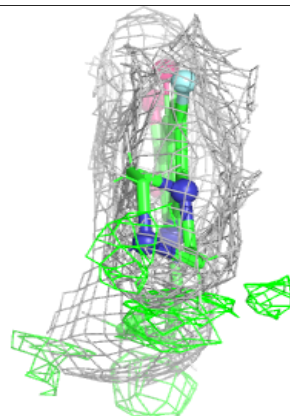
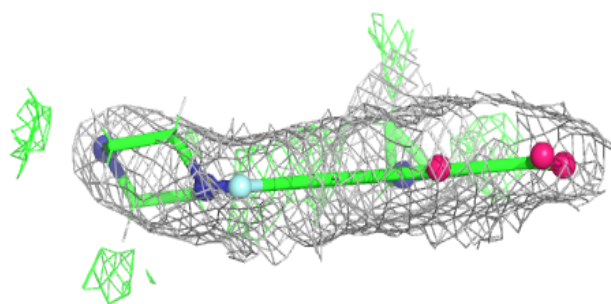
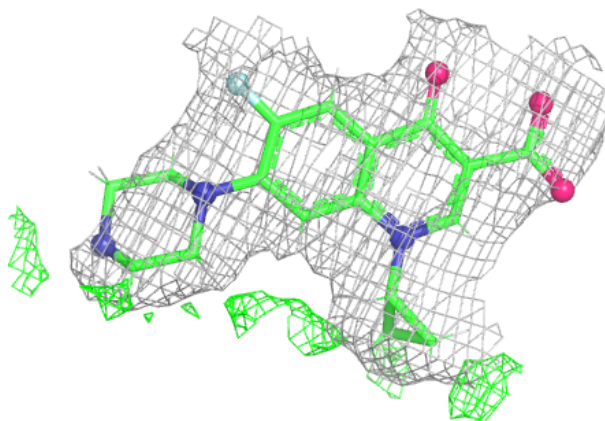
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
5	SO4	A	1606	5/5	0.63	0.10	109,113,124,147	0
5	SO4	A	1604	5/5	0.78	0.20	74,78,100,118	0
5	SO4	A	1603	5/5	0.78	0.23	67,78,106,107	0
7	CL	A	1608	1/1	0.80	0.13	68,68,68,68	0
4	CPF	C	101	24/24	0.83	0.18	58,80,109,116	0
7	CL	A	1609	1/1	0.85	0.29	72,72,72,72	0
5	SO4	A	1605	5/5	0.89	0.12	52,66,68,74	0
7	CL	C	102	1/1	0.91	0.10	70,70,70,70	0
3	CIT	A	1601	13/13	0.94	0.09	36,51,61,67	0
4	CPF	A	1602	24/24	0.96	0.09	39,47,73,82	0
6	MN	A	1607	1/1	0.98	0.04	55,55,55,55	0

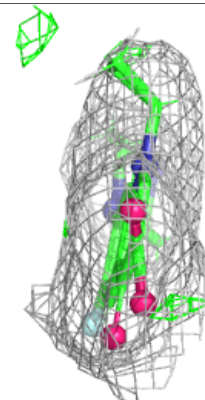
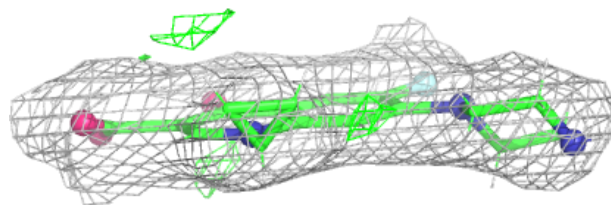
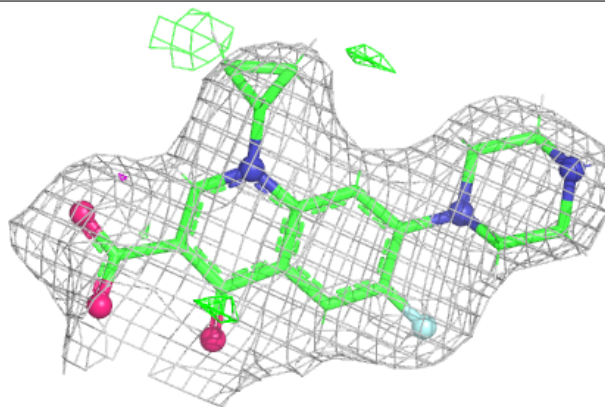
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around CPF C 101:**

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

**Electron density around CPF A 1602:**

$2mF_o-DF_c$  (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.