



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:36 AM UTC

PDB ID : 5O83 / pdb_00005o83
Title : Discovery of CDZ173 (leniolisib), Representing a Structurally Novel Class of PI3K Delta-Selective Inhibitors
Authors : Gutmann, S.; Rummel, G.; Shrestha, B.
Deposited on : 2017-06-12
Resolution : 2.90 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

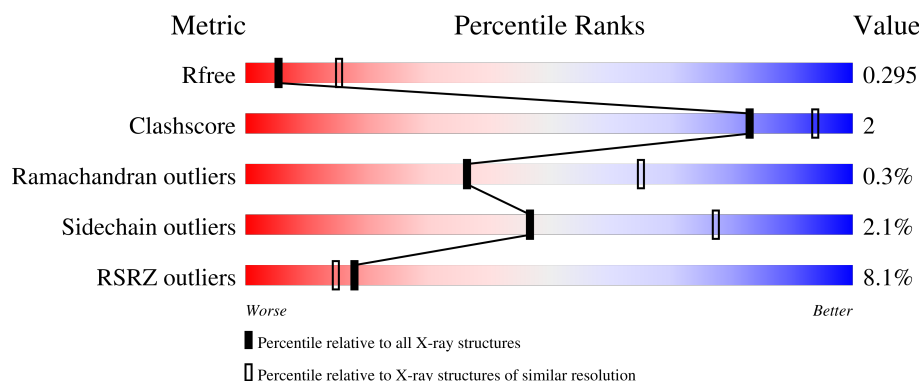
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	941	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5759 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.

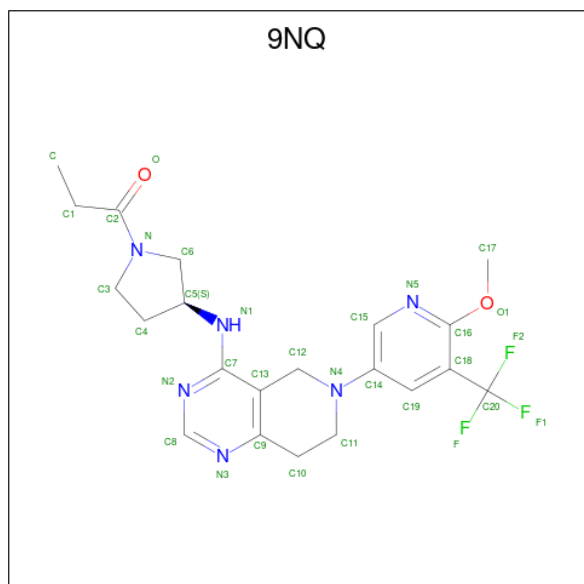
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic sub-unit delta isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	794	Total	C	N	O	S	0	0	1
			5672	3625	993	1006	48			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	GLN	-	expression tag	UNP O35904
A	105	GLY	-	expression tag	UNP O35904
A	508	GLN	-	insertion	UNP O35904

- Molecule 2 is Leniolisib (CCD ID: 9NQ) (formula: $C_{21}H_{25}F_3N_6O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			32	21	3	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	55	Total	O	0	0
			55	55		

- Molecule 1: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	142.12Å 63.99Å 116.54Å 90.00° 102.89° 90.00°	Depositor
Resolution (Å)	58.10 – 2.90 58.10 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (58.10-2.90) 99.5 (58.10-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.230 , 0.274 0.243 , 0.295	Depositor DCC
R_{free} test set	1141 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.522	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 87.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5759	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 9NQ

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	0/5793	1.36	14/7876 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	915	PHE	CA-CB-CG	8.22	122.02	113.80
1	A	887	TYR	CA-C-N	5.74	127.80	120.56
1	A	887	TYR	C-N-CA	5.74	127.80	120.56
1	A	706	THR	CA-C-N	5.30	128.23	120.71
1	A	706	THR	C-N-CA	5.30	128.23	120.71
1	A	955	ARG	CA-C-N	5.15	127.18	120.28
1	A	955	ARG	C-N-CA	5.15	127.18	120.28
1	A	745	CYS	CA-C-N	5.08	127.70	120.53
1	A	745	CYS	C-N-CA	5.08	127.70	120.53
1	A	954	GLU	CB-CG-CD	5.07	121.22	112.60
1	A	722	GLU	CA-C-N	5.07	127.33	120.38
1	A	722	GLU	C-N-CA	5.07	127.33	120.38
1	A	331	ARG	CA-C-N	5.03	129.33	122.34
1	A	331	ARG	C-N-CA	5.03	129.33	122.34

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	5672	0	4869	25	0
2	A	32	0	0	0	0
3	A	55	0	0	0	0
All	All	5759	0	4869	25	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 (25) 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:245:GLY:HA3	1:A:768:ALA:HB2	1.83	0.60
1:A:614:GLN:HG3	1:A:981:MET:HG2	1.88	0.55
1:A:462:ASN:HD21	1:A:464:ASN:HB2	1.75	0.52
1:A:330:GLY:O	1:A:369:PRO:HD2	2.11	0.51
1:A:801:TRP:HZ3	1:A:810:MET:HE2	1.76	0.50
1:A:609:PHE:HE1	1:A:646:PHE:CD2	2.31	0.48
1:A:779:LYS:HE3	1:A:782:ASP:HB2	1.95	0.48
1:A:834:ILE:HD12	1:A:855:LEU:HD11	1.96	0.47
1:A:462:ASN:HD22	1:A:468:ALA:HB2	1.80	0.46
1:A:808:LEU:HD11	1:A:963:ALA:HB2	1.98	0.45
1:A:759:LEU:O	1:A:777:ILE:HA	2.17	0.45
1:A:157:LEU:HD22	1:A:161:GLU:HB3	1.99	0.45
1:A:886:THR:HA	1:A:891:ILE:HD12	1.99	0.45
1:A:462:ASN:ND2	1:A:468:ALA:HB2	2.31	0.45
1:A:789:LEU:HD13	1:A:981:MET:HE2	1.99	0.44
1:A:700:LYS:HE3	1:A:780:ASN:HD22	1.83	0.43
1:A:278:HIS:CD2	1:A:280:SER:H	2.37	0.43
1:A:765:SER:HB3	1:A:772:GLY:HA3	2.00	0.43
1:A:630:THR:O	1:A:634:LEU:HB2	2.18	0.43
1:A:793:MET:O	1:A:797:MET:HG3	2.18	0.43
1:A:196:PHE:HA	1:A:276:MET:HB2	2.02	0.42
1:A:930:VAL:HB	1:A:931:PRO:HD3	2.00	0.42
1:A:421:ALA:HB2	1:A:441:MET:HG2	2.01	0.42
1:A:872:ILE:HD12	1:A:944:GLN:HG2	2.02	0.41
1:A:832:ASP:HB3	1:A:837:ILE:HD11	2.04	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	764/941 (81%)	737 (96%)	25 (3%)	2 (0%)	36	65

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	328	ILE
1	A	809	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	468/828 (56%)	458 (98%)	10 (2%)	47	77

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	418	ILE
1	A	473	ILE
1	A	604	THR
1	A	731	LEU
1	A	743	GLU
1	A	784	LEU
1	A	816	LEU
1	A	837	ILE
1	A	907	LEU

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Mol	Chain	Res	Type
1	A	915	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	155	GLN
1	A	278	HIS
1	A	291	ASN
1	A	349	HIS
1	A	462	ASN
1	A	526	HIS
1	A	696	ASN
1	A	721	GLN
1	A	773	ASN
1	A	780	ASN
1	A	943	GLN
1	A	976	HIS

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](#)

1 ligand is 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	9NQ	A	1101	-	35,35,35	0.30	0	41,51,51	0.85	1 (2%)

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	9NQ	A	1101	-	-	3/22/40/40	0/4/4/4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1101	9NQ	C12-N4-C11	2.96	120.37	113.05

There are no chirality outliers.

All (3) torsion outliers are listed below:

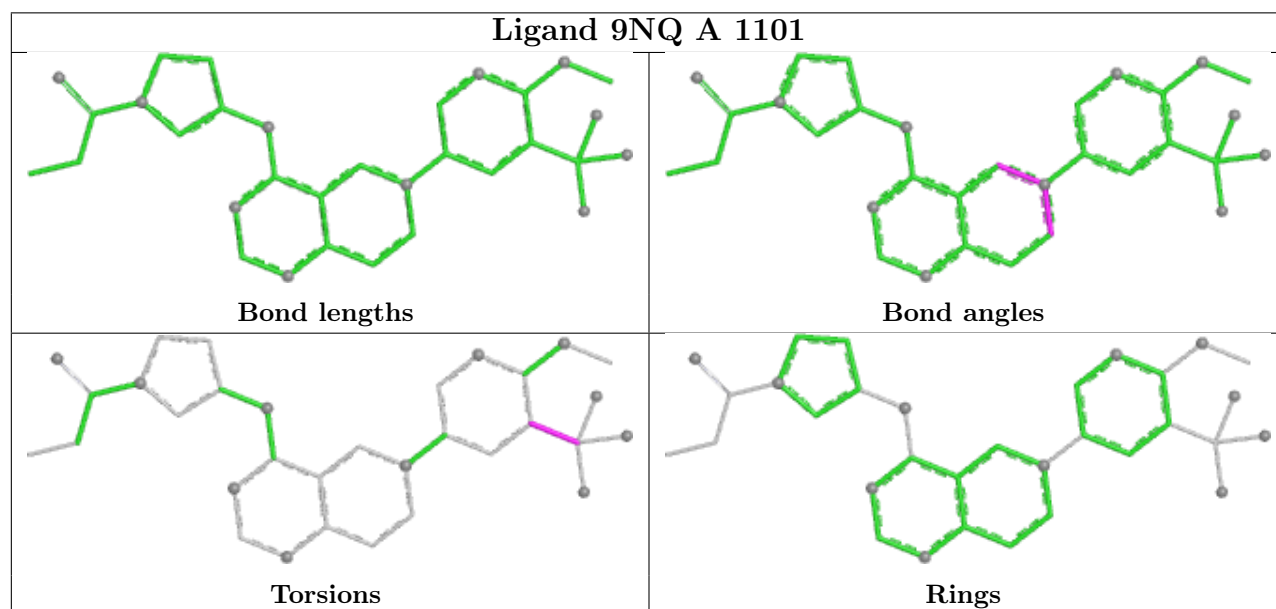
Mol	Chain	Res	Type	Atoms
2	A	1101	9NQ	C16-C18-C20-F2
2	A	1101	9NQ	C16-C18-C20-F
2	A	1101	9NQ	C16-C18-C20-F1

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.



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	794/941 (84%)	0.72	64 (8%) 18 15	26, 55, 86, 116	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	230	GLN	5.6
1	A	109	VAL	4.7
1	A	1027	TRP	4.3
1	A	318	SER	4.0
1	A	330	GLY	4.0
1	A	397	VAL	3.7
1	A	366	CYS	3.7
1	A	317	TRP	3.6
1	A	220	ALA	3.5
1	A	325	ILE	3.4
1	A	253	ASN	3.3
1	A	187	ASN	3.2
1	A	840	ASN	3.2
1	A	479	ALA	3.2
1	A	494	LEU	3.2
1	A	262	ILE	3.0
1	A	336	ASP	3.0
1	A	524	TYR	3.0
1	A	321	GLN	3.0
1	A	329	GLU	3.0
1	A	342	VAL	2.9
1	A	341	LEU	2.8
1	A	196	PHE	2.8
1	A	119	LEU	2.8
1	A	327	LEU	2.7
1	A	362	GLU	2.7
1	A	370	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	933	ILE	2.6
1	A	361	SER	2.5
1	A	491	ILE	2.5
1	A	930	VAL	2.5
1	A	423	LEU	2.5
1	A	229	ARG	2.5
1	A	199	SER	2.4
1	A	770	SER	2.4
1	A	324	SER	2.3
1	A	918	ASN	2.3
1	A	436	GLU	2.3
1	A	995	ILE	2.3
1	A	271	THR	2.3
1	A	216	LEU	2.2
1	A	934	LEU	2.2
1	A	319	LEU	2.2
1	A	453	LEU	2.2
1	A	592	VAL	2.2
1	A	467	SER	2.2
1	A	872	ILE	2.2
1	A	153	HIS	2.1
1	A	445	VAL	2.1
1	A	415	ASP	2.1
1	A	204	THR	2.1
1	A	528	LYS	2.1
1	A	458	THR	2.1
1	A	468	ALA	2.1
1	A	206	GLN	2.1
1	A	351	ASN	2.1
1	A	456	ALA	2.1
1	A	208	SER	2.0
1	A	523	LEU	2.0
1	A	1020	ASN	2.0
1	A	205	PHE	2.0
1	A	937	ASP	2.0
1	A	488	LEU	2.0
1	A	559	GLU	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 [i](#)

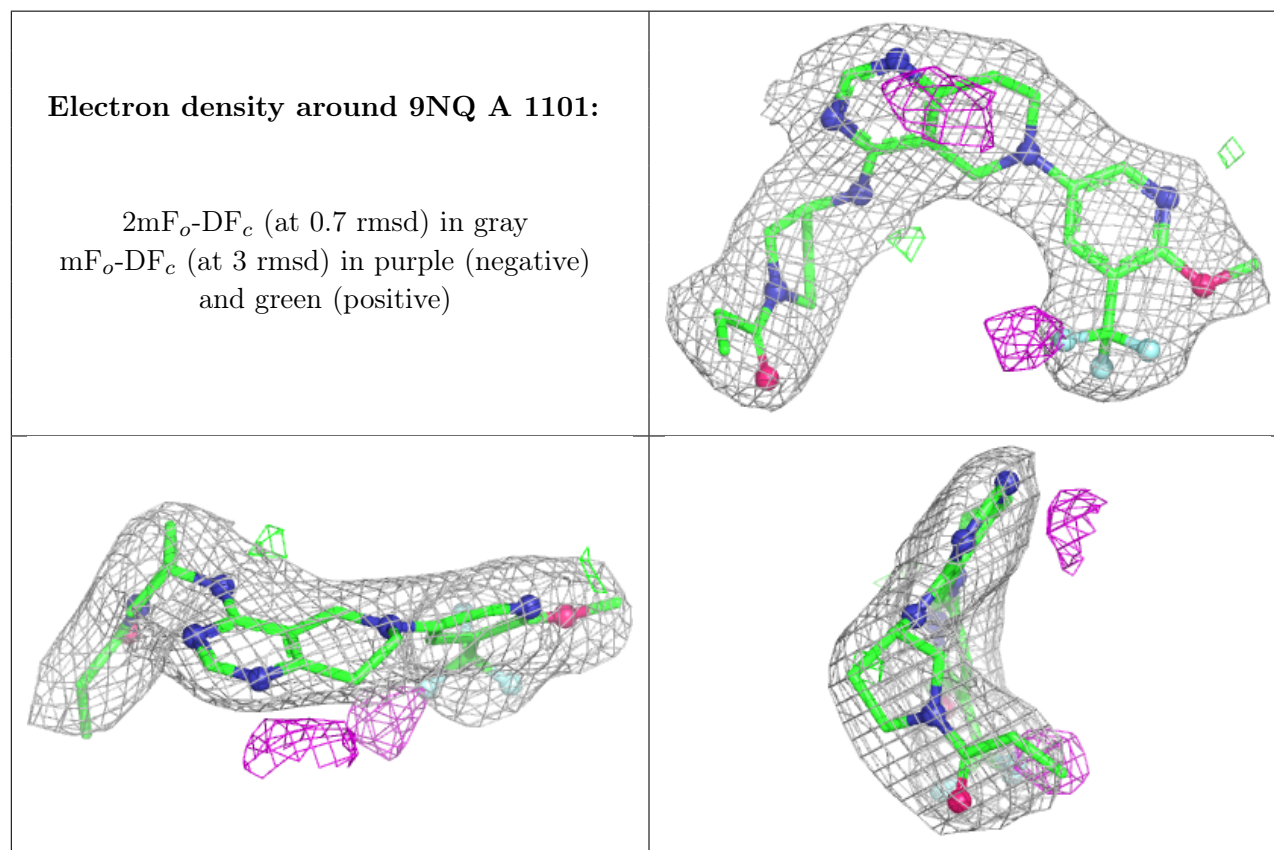
There are no oligosaccharides in this entry.

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	9NQ	A	1101	32/32	0.93	0.10	30,34,44,45	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.