



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:30 AM UTC

PDB ID : 6TKM / pdb\_00006tkm  
Title : Tankyrase 2 in complex with an inhibitor (OM-1800)  
Authors : Sowa, S.T.; Lehtio, L.  
Deposited on : 2019-11-28  
Resolution : 2.70 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](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)  
Xtrriage (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

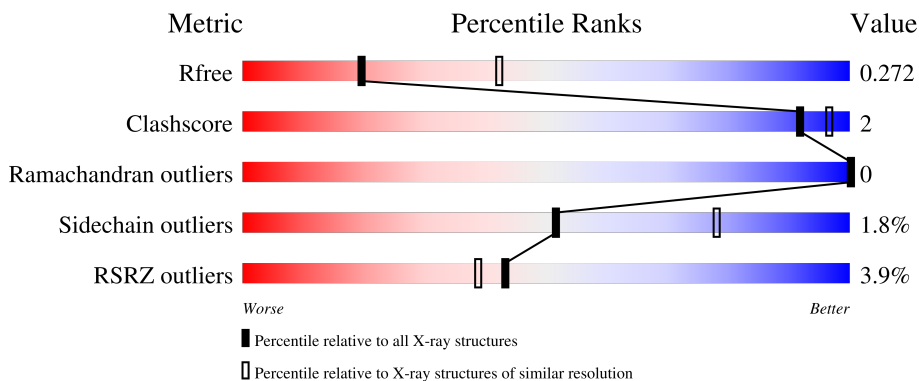
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	AAA	240	
1	BBB	240	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6564 atoms, of which 3186 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 Tankyrase-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	AAA	206	3219	1034	1577	300	298	10	103	0	0
1	BBB	203	3188	1025	1561	296	296	10	100	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	923	MET	-	initiating methionine	UNP Q9H2K2
AAA	924	HIS	-	expression tag	UNP Q9H2K2
AAA	925	HIS	-	expression tag	UNP Q9H2K2
AAA	926	HIS	-	expression tag	UNP Q9H2K2
AAA	927	HIS	-	expression tag	UNP Q9H2K2
AAA	928	HIS	-	expression tag	UNP Q9H2K2
AAA	929	HIS	-	expression tag	UNP Q9H2K2
AAA	930	SER	-	expression tag	UNP Q9H2K2
AAA	931	SER	-	expression tag	UNP Q9H2K2
AAA	932	GLY	-	expression tag	UNP Q9H2K2
AAA	933	VAL	-	expression tag	UNP Q9H2K2
AAA	934	ASP	-	expression tag	UNP Q9H2K2
AAA	935	LEU	-	expression tag	UNP Q9H2K2
AAA	936	GLY	-	expression tag	UNP Q9H2K2
AAA	937	THR	-	expression tag	UNP Q9H2K2
AAA	938	GLU	-	expression tag	UNP Q9H2K2
AAA	939	ASN	-	expression tag	UNP Q9H2K2
AAA	940	LEU	-	expression tag	UNP Q9H2K2
AAA	941	TYR	-	expression tag	UNP Q9H2K2
AAA	942	PHE	-	expression tag	UNP Q9H2K2
AAA	943	GLN	-	expression tag	UNP Q9H2K2
AAA	944	SER	-	expression tag	UNP Q9H2K2
AAA	945	MET	-	expression tag	UNP Q9H2K2
BBB	923	MET	-	initiating methionine	UNP Q9H2K2
BBB	924	HIS	-	expression tag	UNP Q9H2K2

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	AAA	1	Total	C	F	H	N	O	0	0
			62	28	1	24	7	2		
2	BBB	1	Total	C	F	H	N	O	0	0
			62	28	1	24	7	2		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total	Zn	0	0
			1	1		
3	BBB	1	Total	Zn	0	0
			1	1		


- Molecule 4 is water.

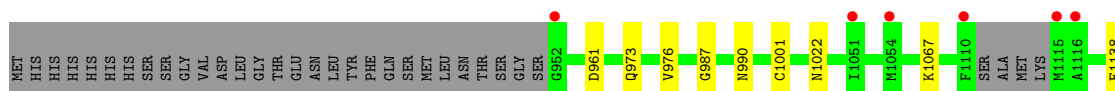
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	17	Total	O	0	0
			17	17		
4	BBB	14	Total	O	0	0
			14	14		

### 3 Residue-property plots [i](#)


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.

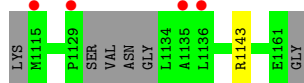
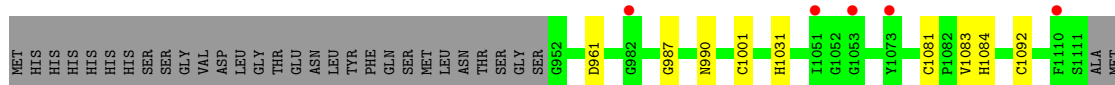
- Molecule 1: Tankyrase-2

Chain AAA:  3% 82% 14%



- Molecule 1: Tankyrase-2

Chain BBB:  4% 80% 15%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.32Å 77.41Å 148.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.73 – 2.70 29.73 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (29.73-2.70) 99.4 (29.73-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.34 (at 2.68Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.237 , 0.271 0.237 , 0.272	Depositor DCC
$R_{free}$ test set	700 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.9	Xtrriage
Anisotropy	0.866	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 23.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6564	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.02 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.6593e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: ZN, NG5

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	AAA	0.99	0/1685	1.36	1/2272 (0.0%)
1	BBB	0.99	0/1669	1.34	3/2248 (0.1%)
All	All	0.99	0/3354	1.35	4/4520 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	987	GLY	CA-C-O	-6.00	117.78	122.52
1	BBB	987	GLY	CA-C-O	-5.87	117.88	122.52
1	BBB	1031	HIS	CA-C-N	5.14	125.14	121.65
1	BBB	1031	HIS	C-N-CA	5.14	125.14	121.65

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	AAA	1642	1577	1551	5	0
1	BBB	1627	1561	1536	5	0
2	AAA	38	24	0	1	0
2	BBB	38	24	0	1	0
3	AAA	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BBB	1	0	0	0	0
4	AAA	17	0	0	0	0
4	BBB	14	0	0	0	0
All	All	3378	3186	3087	10	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.

The worst 5 of 10 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:BBB:1083:VAL:CG1	1:BBB:1092:CYS:SG	2.82	0.68
2:AAA:1201:NG5:NAW	2:AAA:1201:NG5:NAR	2.46	0.57
1:AAA:1145:GLU:OE2	1:BBB:1143:ARG:NH2	2.41	0.52
1:BBB:1083:VAL:HG13	1:BBB:1084:HIS:ND1	2.25	0.51
1:AAA:1022:ASN:O	1:AAA:1022:ASN:CG	2.57	0.48

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	AAA	202/240 (84%)	197 (98%)	5 (2%)	0	100	100
1	BBB	197/240 (82%)	191 (97%)	6 (3%)	0	100	100
All	All	399/480 (83%)	388 (97%)	11 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	AAA	171/204 (84%)	168 (98%)	3 (2%)	51	78
1	BBB	170/204 (83%)	167 (98%)	3 (2%)	51	78
All	All	341/408 (84%)	335 (98%)	6 (2%)	51	78

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	961	ASP
1	BBB	990	ASN
1	BBB	1001	CYS
1	AAA	990	ASN
1	AAA	961	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 4 ligands modelled in this entry, 2 are 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
2	NG5	AAA	1201	-	41,43,43	3.26	12 (29%)	50,61,61	1.54	9 (18%)
2	NG5	BBB	1201	-	41,43,43	3.18	12 (29%)	50,61,61	1.66	12 (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	NG5	AAA	1201	-	-	8/21/31/31	0/6/6/6
2	NG5	BBB	1201	-	-	11/21/31/31	0/6/6/6

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AAA	1201	NG5	CAG-CAJ	-11.09	1.32	1.47
2	BBB	1201	NG5	CAG-CAJ	-10.64	1.33	1.47
2	BBB	1201	NG5	NAL-NAK	-8.74	1.21	1.39
2	AAA	1201	NG5	NAL-NAK	-8.61	1.21	1.39
2	AAA	1201	NG5	CBF-NBE	-8.19	1.33	1.44

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	1201	NG5	CAO-CAN-CAQ	4.11	92.66	86.64
2	BBB	1201	NG5	CAX-NAW-CAV	3.94	121.95	117.31
2	BBB	1201	NG5	CAQ-CAP-NAR	-3.81	110.69	117.76
2	BBB	1201	NG5	CAU-CAV-NAW	3.74	121.31	118.74
2	AAA	1201	NG5	CAQ-CAP-NAR	-3.42	111.42	117.76

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

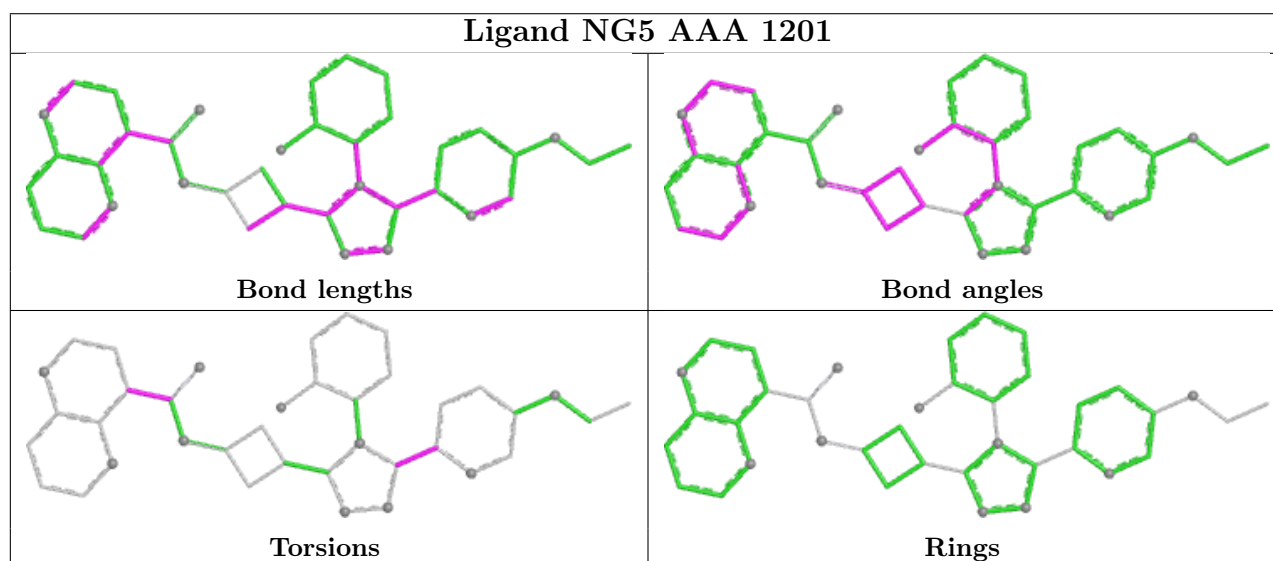
Mol	Chain	Res	Type	Atoms
2	AAA	1201	NG5	CAF-CAG-CAJ-NAK
2	AAA	1201	NG5	NAH-CAG-CAJ-NAK
2	AAA	1201	NG5	CAF-CAG-CAJ-NBE
2	AAA	1201	NG5	NAH-CAG-CAJ-NBE
2	BBB	1201	NG5	CAA-CAB-OAC-CAD

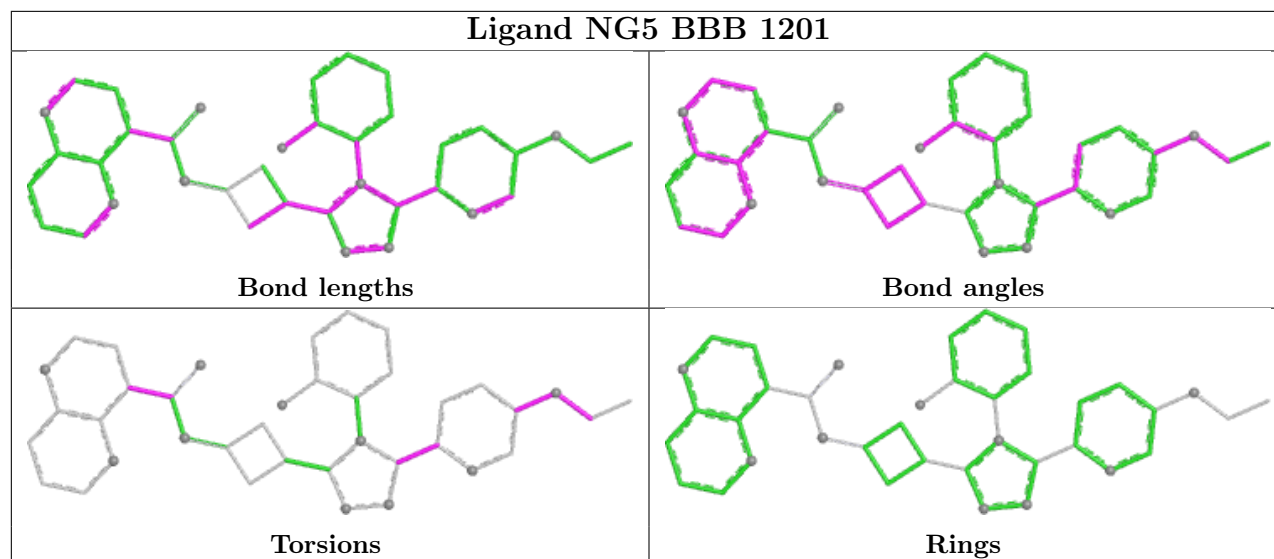
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	1201	NG5	1	0
2	BBB	1201	NG5	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 [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, 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	AAA	206/240 (85%)	0.38	7 (3%) 48 44	22, 36, 60, 84	0
1	BBB	203/240 (84%)	0.37	9 (4%) 39 35	25, 37, 73, 93	0
All	All	409/480 (85%)	0.38	16 (3%) 43 39	22, 37, 70, 93	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	1110	PHE	3.7
1	AAA	1051	ILE	3.5
1	AAA	1110	PHE	3.5
1	AAA	1116	ALA	2.9
1	BBB	1051	ILE	2.5

### 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](#)

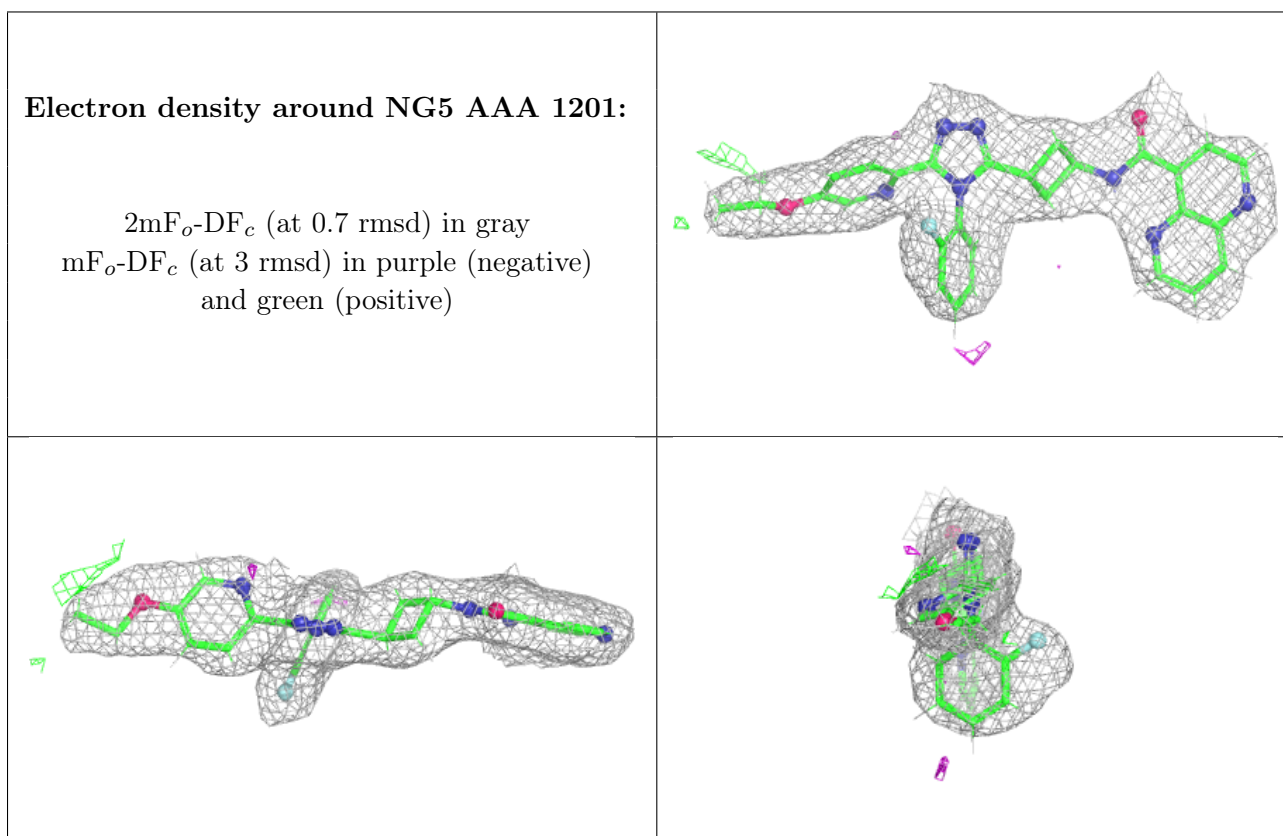
There are no oligosaccharides in this entry.

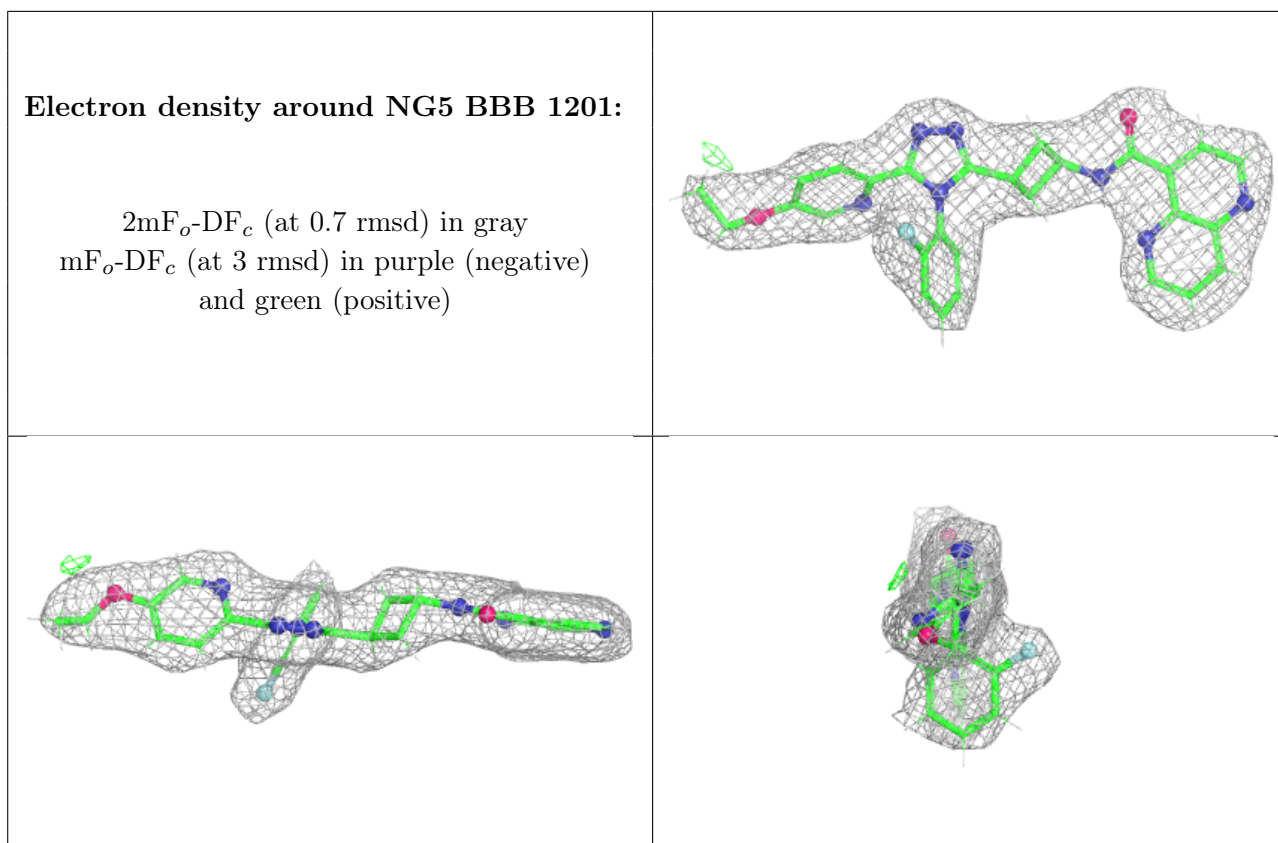
### 6.4 Ligands [i](#)

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
2	NG5	AAA	1201	38/38	0.93	0.08	29,30,33,33	0
2	NG5	BBB	1201	38/38	0.95	0.07	27,31,37,38	0
3	ZN	AAA	1202	1/1	0.99	0.02	37,37,37,37	0
3	ZN	BBB	1202	1/1	0.99	0.02	44,44,44,44	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.