



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 11:47 AM EDT

PDB ID : 6FH5  
Title : PI3Kg IN COMPLEX WITH Compound 7  
Authors : Petersen, J.; Barlaam, B.  
Deposited on : 2018-01-12  
Resolution : 2.84 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 : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

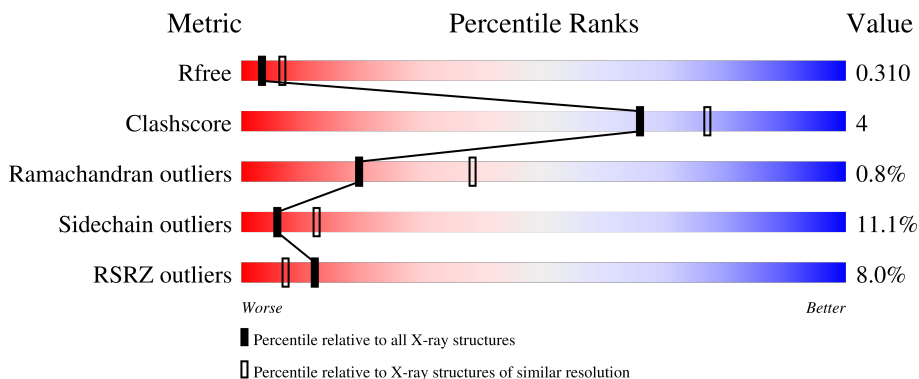
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.84 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))
$R_{free}$	130704	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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	966	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6562 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.

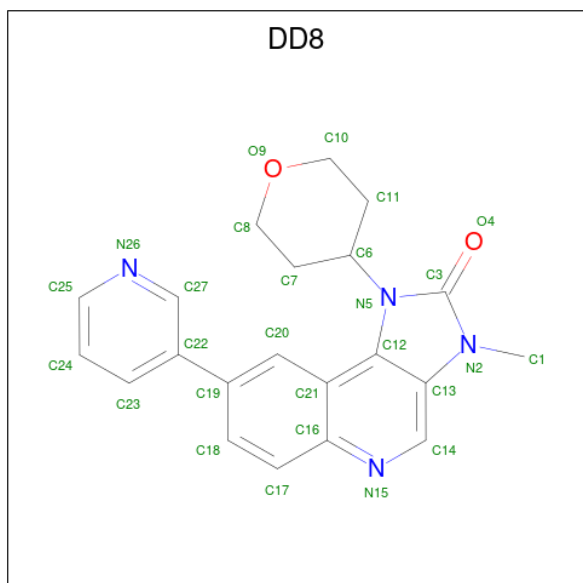
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic sub-unit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	802	6519	4193	1112	1179	35	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	MET	-	initiating methionine	UNP P48736
A	1103	HIS	-	expression tag	UNP P48736
A	1104	HIS	-	expression tag	UNP P48736
A	1105	HIS	-	expression tag	UNP P48736
A	1106	HIS	-	expression tag	UNP P48736
A	1107	HIS	-	expression tag	UNP P48736
A	1108	HIS	-	expression tag	UNP P48736

- Molecule 2 is 3-methyl-1-(oxan-4-yl)-8-pyridin-3-yl-imidazo[4,5-c]quinolin-2-one (three-letter code: DD8) (formula: C<sub>21</sub>H<sub>20</sub>N<sub>4</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	27	21	4	2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	16	16	16	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.59Å 67.07Å 104.90Å 90.00° 97.28° 90.00°	Depositor
Resolution (Å)	53.51 – 2.84 53.51 – 2.84	Depositor EDS
% Data completeness (in resolution range)	98.0 (53.51-2.84) 98.0 (53.51-2.84)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 2.86Å)	Xtrriage
Refinement program	BUSTER 2.11.6 PACIOREK	Depositor
R, $R_{free}$	0.235 , 0.296 0.246 , 0.310	Depositor DCC
$R_{free}$ test set	1156 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	78.8	Xtrriage
Anisotropy	0.436	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 70.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6562	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.11% 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: DD8

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	0.44	0/6655	0.66	0/8996

There are no bond length outliers.

There are no bond angle outliers.

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	6519	0	6556	52	0
2	A	27	0	0	0	0
3	A	16	0	0	0	0
All	All	6562	0	6556	52	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 4.

All (52) 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:629:GLN:HG2	1:A:1029:ILE:HG13	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:VAL:O	1:A:185:MET:HG2	1.93	0.67
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.84	0.60
1:A:471:HIS:H	1:A:471:HIS:CD2	2.20	0.60
1:A:225:HIS:CE1	1:A:304:HIS:HD2	2.20	0.58
1:A:983:VAL:HB	1:A:1082:VAL:HG21	1.85	0.57
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.86	0.57
1:A:464:VAL:HB	1:A:484:MET:HG2	1.87	0.55
1:A:579:ARG:HB2	1:A:610:LEU:HD11	1.89	0.55
1:A:498:ASN:HB3	1:A:501:LYS:HD3	1.88	0.55
1:A:216:ALA:O	1:A:217:ASN:HB2	2.07	0.54
1:A:779:LEU:HB3	1:A:780:PRO:HA	1.87	0.54
1:A:410:TRP:HB3	1:A:412:VAL:HG22	1.89	0.53
1:A:1028:ILE:HA	1:A:1051:ILE:HD13	1.90	0.53
1:A:584:LYS:HA	1:A:616:VAL:HG21	1.92	0.52
1:A:424:PRO:HD2	1:A:427:ALA:HB2	1.92	0.52
1:A:211:LEU:HD22	1:A:297:LEU:HB3	1.92	0.51
1:A:176:THR:HG21	1:A:673:HIS:HB2	1.92	0.51
1:A:215:ILE:HG12	1:A:220:ILE:HG12	1.93	0.49
1:A:983:VAL:HG22	1:A:984:PRO:HD2	1.94	0.49
1:A:217:ASN:N	1:A:218:ASN:HA	2.28	0.48
1:A:583:LEU:HG	1:A:610:LEU:HD22	1.96	0.48
1:A:271:VAL:HB	1:A:310:PRO:HG3	1.94	0.48
1:A:559:ILE:HG12	1:A:588:ALA:HB2	1.96	0.47
1:A:989:PRO:HA	1:A:992:LEU:HD12	1.97	0.47
1:A:804:MET:HB2	1:A:810:PRO:HD2	1.97	0.47
1:A:640:VAL:O	1:A:643:ILE:HG12	2.15	0.46
1:A:807:LYS:HD2	1:A:807:LYS:H	1.81	0.46
1:A:1051:ILE:H	1:A:1051:ILE:HG13	1.55	0.46
1:A:810:PRO:HB3	1:A:833:LYS:HG3	1.96	0.45
1:A:287:ILE:HA	1:A:290:PHE:HD2	1.80	0.45
1:A:366:ARG:HH21	1:A:519:LEU:HD22	1.81	0.45
1:A:990:ASP:O	1:A:994:VAL:HG23	2.16	0.45
1:A:843:LEU:HB3	1:A:1034:MET:HG3	1.99	0.45
1:A:739:ILE:HD13	1:A:872:THR:HB	1.99	0.44
1:A:834:HIS:HB2	1:A:876:ILE:HD12	1.99	0.44
1:A:648:LEU:HB3	1:A:680:PHE:CZ	2.53	0.44
1:A:224:ILE:HD13	1:A:233:ILE:HD12	1.99	0.43
1:A:500:ASP:O	1:A:503:THR:HG22	2.18	0.43
1:A:891:ILE:HG22	1:A:906:VAL:HG12	2.00	0.43
1:A:209:GLU:HB2	1:A:859:SER:HB3	2.01	0.43
1:A:364:LYS:HB3	1:A:519:LEU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1031:PHE:HE1	1:A:1048:ILE:HA	1.84	0.43
1:A:241:PRO:HA	1:A:244:ILE:HD12	2.01	0.43
1:A:354:LEU:HD13	1:A:529:LEU:HB2	2.01	0.42
1:A:508:PRO:HG2	1:A:707:ARG:HE	1.85	0.42
1:A:622:LEU:HD22	1:A:650:SER:HB2	2.01	0.42
1:A:176:THR:O	1:A:180:LEU:HB2	2.20	0.41
1:A:905:GLU:HB3	1:A:909:HIS:ND1	2.35	0.41
1:A:576:TRP:HZ3	1:A:607:THR:HG23	1.85	0.41
1:A:235:VAL:HG21	1:A:244:ILE:HG12	2.01	0.40
1:A:208:PRO:HD2	1:A:211:LEU:HD12	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	774/966 (80%)	732 (95%)	36 (5%)	6 (1%)	19 38

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	217	ASN
1	A	546	GLU
1	A	874	ASP
1	A	1086	TRP
1	A	406	GLU
1	A	916	PRO

### 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	721/864 (83%)	641 (89%)	80 (11%)	<b>6</b> <b>12</b>

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163	THR
1	A	180	LEU
1	A	194	LYS
1	A	207	LEU
1	A	213	LYS
1	A	217	ASN
1	A	220	ILE
1	A	226	ARG
1	A	238	ASP
1	A	245	LEU
1	A	269	ASP
1	A	282	VAL
1	A	285	THR
1	A	297	LEU
1	A	301	GLU
1	A	319	ARG
1	A	320	LYS
1	A	354	LEU
1	A	358	ASP
1	A	370	ILE
1	A	381	VAL
1	A	391	GLN
1	A	410	TRP
1	A	428	LEU
1	A	430	ASN
1	A	459	GLN
1	A	461	LEU
1	A	464	VAL
1	A	506	THR
1	A	511	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	520	LEU
1	A	531	LYS
1	A	555	LEU
1	A	574	LEU
1	A	575	LEU
1	A	583	LEU
1	A	596	VAL
1	A	601	GLN
1	A	607	THR
1	A	609	GLN
1	A	610	LEU
1	A	618	ASP
1	A	619	GLN
1	A	646	GLN
1	A	652	GLU
1	A	682	LEU
1	A	701	SER
1	A	707	ARG
1	A	717	LEU
1	A	721	LEU
1	A	744	LYS
1	A	760	SER
1	A	764	ILE
1	A	767	LEU
1	A	773	ASN
1	A	781	GLU
1	A	791	LEU
1	A	807	LYS
1	A	808	LYS
1	A	823	LEU
1	A	828	ILE
1	A	842	MET
1	A	845	LEU
1	A	865	LEU
1	A	876	ILE
1	A	904	ASP
1	A	912	LYS
1	A	964	ASP
1	A	982	ARG
1	A	997	THR
1	A	1013	CYS
1	A	1026	LEU

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Mol	Chain	Res	Type
1	A	1029	ILE
1	A	1035	LEU
1	A	1045	LYS
1	A	1051	ILE
1	A	1052	ARG
1	A	1059	LYS
1	A	1063	ASP
1	A	1078	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	225	HIS
1	A	299	ASN
1	A	304	HIS
1	A	471	HIS
1	A	711	GLN
1	A	951	ASN
1	A	1083	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 monosaccharides 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	DD8	A	1201	-	30,31,31	0.79	0	37,45,45	1.60	9 (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	DD8	A	1201	-	-	0/8/16/16	0/5/5/5

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	DD8	C14-N15-C16	4.48	122.14	116.96
2	A	1201	DD8	C13-N2-C3	-3.20	108.45	110.10
2	A	1201	DD8	N5-C3-N2	3.01	109.43	106.92
2	A	1201	DD8	C25-N26-C27	2.80	121.76	116.85
2	A	1201	DD8	C6-N5-C3	2.77	127.35	122.61
2	A	1201	DD8	C21-C16-N15	-2.39	120.29	122.82
2	A	1201	DD8	C1-N2-C3	2.32	125.63	123.59
2	A	1201	DD8	C10-O9-C8	2.23	117.10	109.88
2	A	1201	DD8	O4-C3-N2	-2.06	124.69	127.21

There are no chirality outliers.

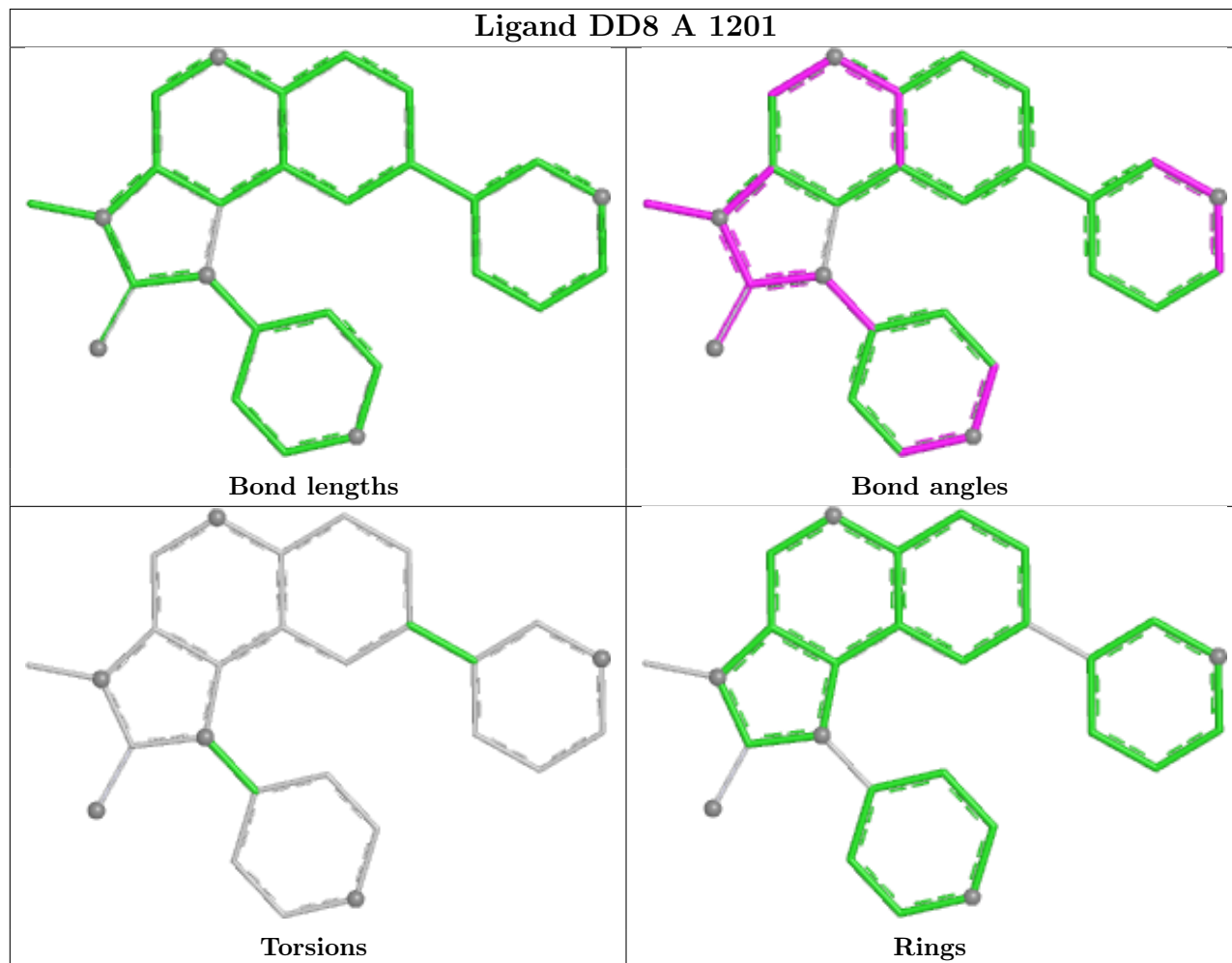
There are no torsion outliers.

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.



## 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	802/966 (83%)	0.46	64 (7%) <b>12</b> <b>7</b>	36, 77, 122, 204	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	524	CYS	13.9
1	A	352	VAL	7.5
1	A	531	LYS	7.2
1	A	235	VAL	6.6
1	A	212	TRP	5.7
1	A	523	TYR	5.4
1	A	217	ASN	5.4
1	A	529	LEU	5.0
1	A	404	PHE	4.7
1	A	211	LEU	4.5
1	A	220	ILE	4.4
1	A	525	HIS	4.4
1	A	747	LEU	4.3
1	A	749	ILE	4.3
1	A	354	LEU	4.1
1	A	1068	PHE	4.1
1	A	233	ILE	4.1
1	A	754	ALA	4.0
1	A	823	LEU	3.7
1	A	741	MET	3.6
1	A	281	LEU	3.6
1	A	564	LEU	3.6
1	A	215	ILE	3.5
1	A	522	ASN	3.5
1	A	355	TRP	3.4
1	A	245	LEU	3.3
1	A	219	CYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	521	ASP	3.0
1	A	293	VAL	3.0
1	A	216	ALA	3.0
1	A	236	SER	3.0
1	A	582	SER	2.9
1	A	1051	ILE	2.8
1	A	745	VAL	2.8
1	A	832	PHE	2.8
1	A	1072	ILE	2.7
1	A	907	LEU	2.7
1	A	356	ASP	2.6
1	A	530	PRO	2.6
1	A	287	ILE	2.5
1	A	813	LEU	2.5
1	A	834	HIS	2.5
1	A	1020	LEU	2.5
1	A	982	ARG	2.4
1	A	353	SER	2.4
1	A	995	MET	2.4
1	A	234	LYS	2.3
1	A	270	PHE	2.3
1	A	526	PRO	2.3
1	A	941	VAL	2.3
1	A	750	LYS	2.3
1	A	297	LEU	2.2
1	A	1064	ALA	2.2
1	A	752	LEU	2.2
1	A	244	ILE	2.2
1	A	222	ILE	2.2
1	A	681	LEU	2.1
1	A	180	LEU	2.1
1	A	272	LEU	2.1
1	A	382	PHE	2.1
1	A	760	SER	2.1
1	A	315	LEU	2.1
1	A	555	LEU	2.1
1	A	403	PRO	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](#)

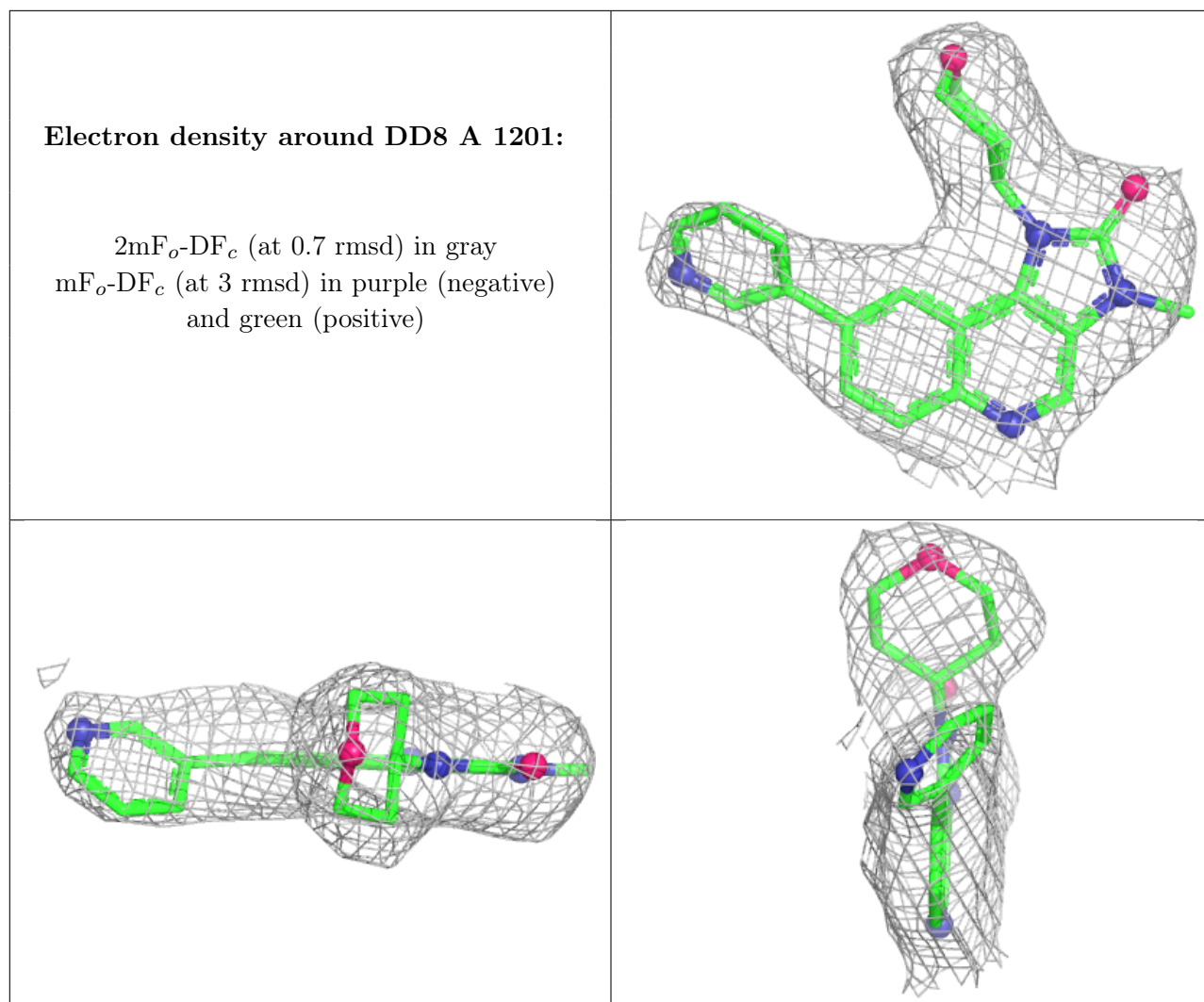
There are no monosaccharides in this entry.

### 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	DD8	A	1201	27/27	0.92	0.21	72,75,78,79	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.