



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 07:43 PM EDT

PDB ID : 5IS5 / pdb_00005is5
Title : Discovery and Pharmacological Characterization of Novel Quinazoline-based PI3K delta-selective Inhibitors
Authors : Gutmann, S.; Rummel, G.; Shrestha, B.
Deposited on : 2016-03-15
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

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

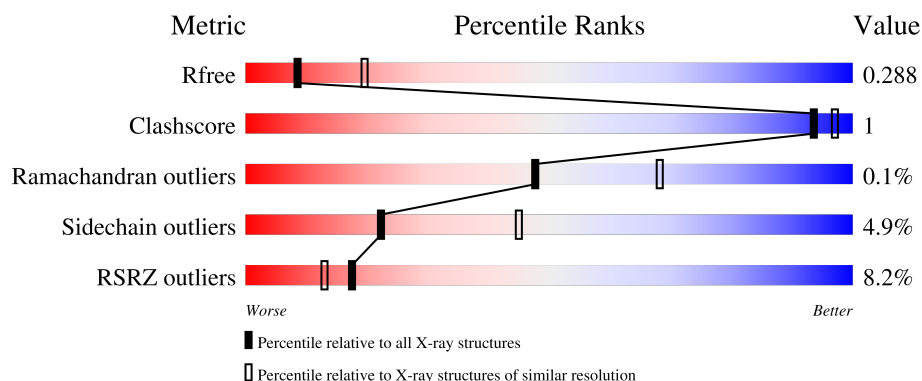
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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 ≥ 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	1044	

2 Entry composition [i](#)

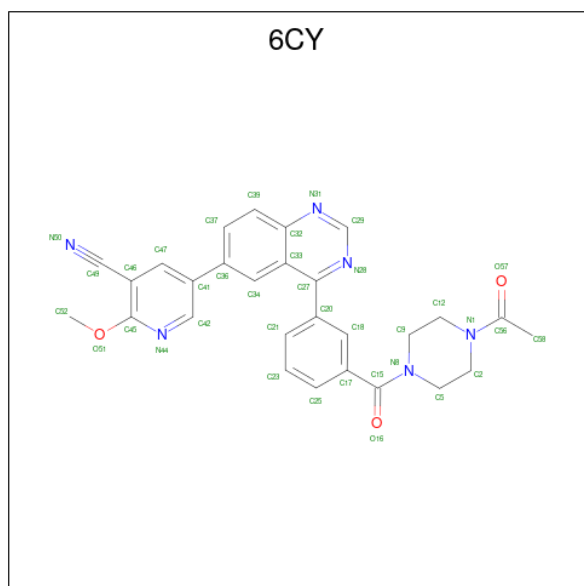
There are 3 unique types of molecules in this entry. The entry contains 5917 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	785	Total	C	N	O	S	0	0	0
			5648	3615	983	1000	50			

- Molecule 2 is 5-{4-[3-(4-acetylpiperazine-1-carbonyl)phenyl]quinazolin-6-yl}-2-methoxypyridine-3-carbonitrile (CCD ID: 6CY) (formula: C₂₈H₂₄N₆O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			37	28	6	3		

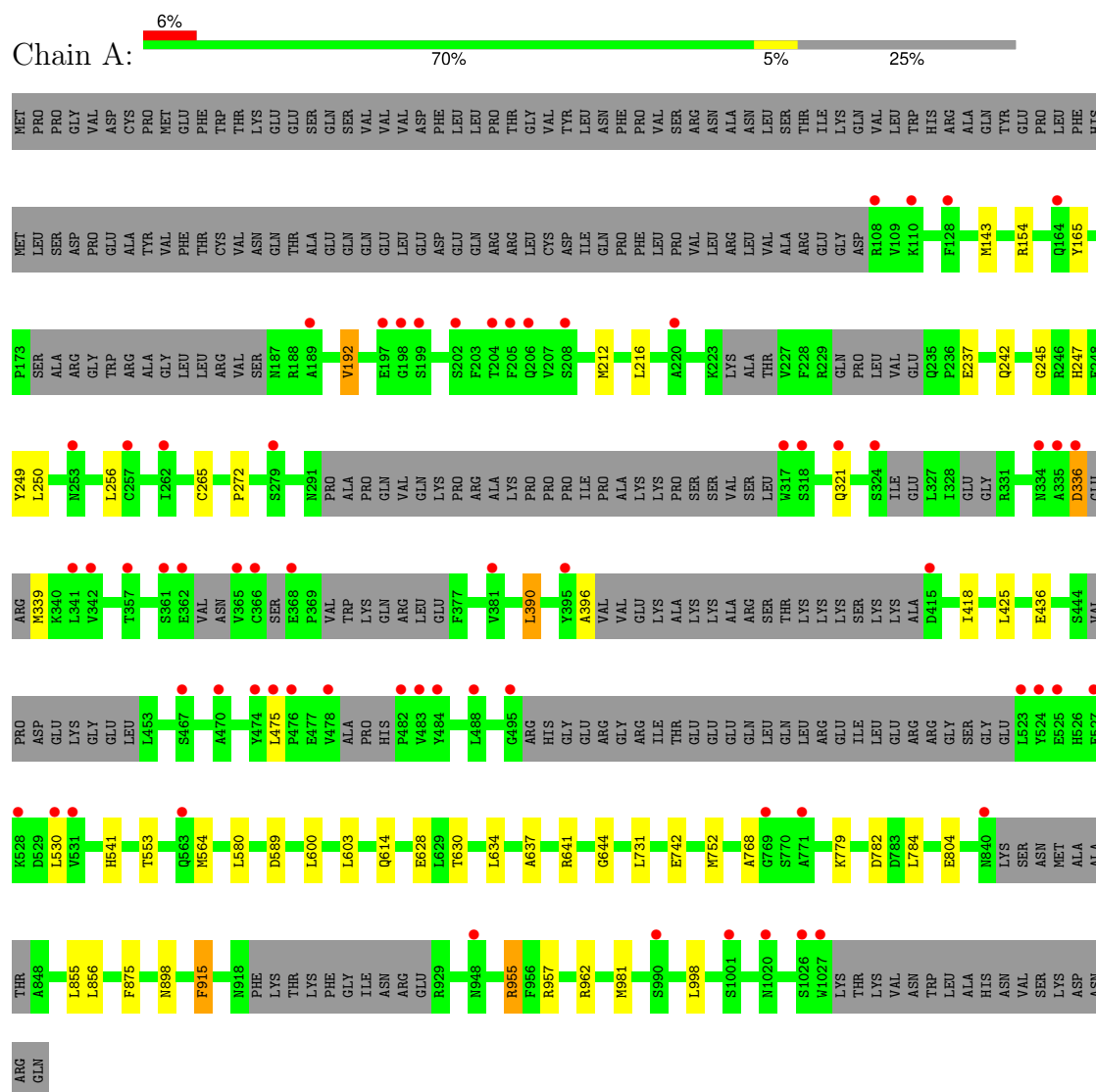
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	232	Total	O	0	0
			232	232		

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: 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	141.46Å 64.32Å 116.64Å 90.00° 103.20° 90.00°	Depositor
Resolution (Å)	65.95 – 2.85 65.95 – 2.85	Depositor EDS
% Data completeness (in resolution range)	97.8 (65.95-2.85) 97.8 (65.95-2.85)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.61 (at 2.86Å)	Xtriage
Refinement program	BUSTER-TNT	Depositor
R, R_{free}	0.229 , 0.271 0.237 , 0.288	Depositor DCC
R_{free} test set	1181 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	45.8	Xtriage
Anisotropy	0.695	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 80.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5917	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% 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: 6CY

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	0.74	0/5763	1.36	9/7833 (0.1%)

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	2

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	915	PHE	CA-CB-CG	7.73	121.53	113.80
1	A	955	ARG	N-CA-C	-5.93	104.89	111.36
1	A	589	ASP	CA-C-N	5.59	127.77	120.28
1	A	589	ASP	C-N-CA	5.59	127.77	120.28
1	A	541	HIS	N-CA-C	5.18	116.73	111.14
1	A	957	ARG	CA-C-N	5.04	125.68	119.99
1	A	957	ARG	C-N-CA	5.04	125.68	119.99
1	A	875	PHE	CA-C-N	5.03	127.32	120.54
1	A	875	PHE	C-N-CA	5.03	127.32	120.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	321	GLN	Mainchain

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Mol	Chain	Res	Type	Group
1	A	475	LEU	Peptide

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	5648	0	4949	15	0
2	A	37	0	0	1	0
3	A	232	0	0	0	0
All	All	5917	0	4949	15	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 1.

All (15) 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	1.78	0.65
1:A:336:ASP:HB3	1:A:339:MET:HB2	1.90	0.54
1:A:553:THR:HG21	1:A:564:MET:HG2	1.92	0.51
1:A:779:LYS:HE3	1:A:782:ASP:HB2	1.92	0.51
1:A:614:GLN:HG3	1:A:981:MET:HG2	1.94	0.50
1:A:600:LEU:HD22	1:A:603:LEU:HD11	1.96	0.46
1:A:396:ALA:HB2	1:A:418:ILE:HD11	1.98	0.45
1:A:752:MET:HG2	2:A:1101:6CY:O16	2.18	0.44
1:A:630:THR:O	1:A:634:LEU:HB2	2.18	0.42
1:A:216:LEU:HD22	1:A:256:LEU:HD21	2.01	0.42
1:A:154:ARG:HD2	1:A:165:TYR:CZ	2.55	0.41
1:A:637:ALA:HB1	1:A:644:GLY:HA2	2.03	0.41
1:A:192:VAL:HG13	1:A:272:PRO:HB2	2.02	0.41
1:A:390:LEU:HD12	1:A:425:LEU:HD21	2.01	0.41
1:A:242:GLN:HG3	1:A:249:TYR:CZ	2.57	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	751/1044 (72%)	725 (96%)	25 (3%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	742	GLU

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	487/925 (53%)	463 (95%)	24 (5%)	22	45

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	MET
1	A	192	VAL
1	A	212	MET
1	A	237	GLU
1	A	247	HIS
1	A	250	LEU
1	A	265	CYS
1	A	336	ASP
1	A	390	LEU
1	A	436	GLU

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Mol	Chain	Res	Type
1	A	530	LEU
1	A	580	LEU
1	A	628	GLU
1	A	641	ARG
1	A	731	LEU
1	A	784	LEU
1	A	804	GLU
1	A	855	LEU
1	A	856	LEU
1	A	898	ASN
1	A	915	PHE
1	A	955	ARG
1	A	962	ARG
1	A	998	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	193	ASN
1	A	278	HIS
1	A	610	GLN
1	A	677	HIS
1	A	721	GLN
1	A	730	HIS
1	A	773	ASN
1	A	836	ASN
1	A	838	GLN
1	A	898	ASN
1	A	943	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 [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	6CY	A	1101	-	41,41,41	1.24	3 (7%)	58,58,58	2.31	18 (31%)

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	6CY	A	1101	-	-	3/23/34/34	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	6CY	C27-N28	3.78	1.36	1.32
2	A	1101	6CY	O51-C45	3.61	1.40	1.35
2	A	1101	6CY	C29-N31	2.23	1.35	1.32

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	6CY	C33-C27-N28	-6.52	118.73	123.04
2	A	1101	6CY	C46-C45-N44	-6.10	119.00	123.71
2	A	1101	6CY	N31-C29-N28	-6.08	120.42	128.67
2	A	1101	6CY	C58-C56-N1	4.85	124.37	118.24
2	A	1101	6CY	O51-C45-C46	4.85	119.72	115.97
2	A	1101	6CY	C17-C15-N8	4.41	124.17	118.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	6CY	C29-N31-C32	4.25	120.27	115.43
2	A	1101	6CY	O16-C15-C17	-3.65	113.06	120.29
2	A	1101	6CY	C29-N28-C27	3.07	122.49	117.79
2	A	1101	6CY	C47-C46-C45	2.96	119.44	117.58
2	A	1101	6CY	C2-C5-N8	-2.71	105.02	110.42
2	A	1101	6CY	C12-N1-C2	2.54	117.86	112.68
2	A	1101	6CY	C41-C42-N44	-2.49	120.32	124.28
2	A	1101	6CY	C42-N44-C45	2.42	122.34	116.51
2	A	1101	6CY	O57-C56-C58	-2.35	112.82	122.03
2	A	1101	6CY	C45-C46-C49	2.29	122.65	120.16
2	A	1101	6CY	C9-N8-C5	2.19	117.16	112.68
2	A	1101	6CY	C20-C27-C33	2.09	125.85	122.37

There are no chirality outliers.

All (3) torsion outliers are listed below:

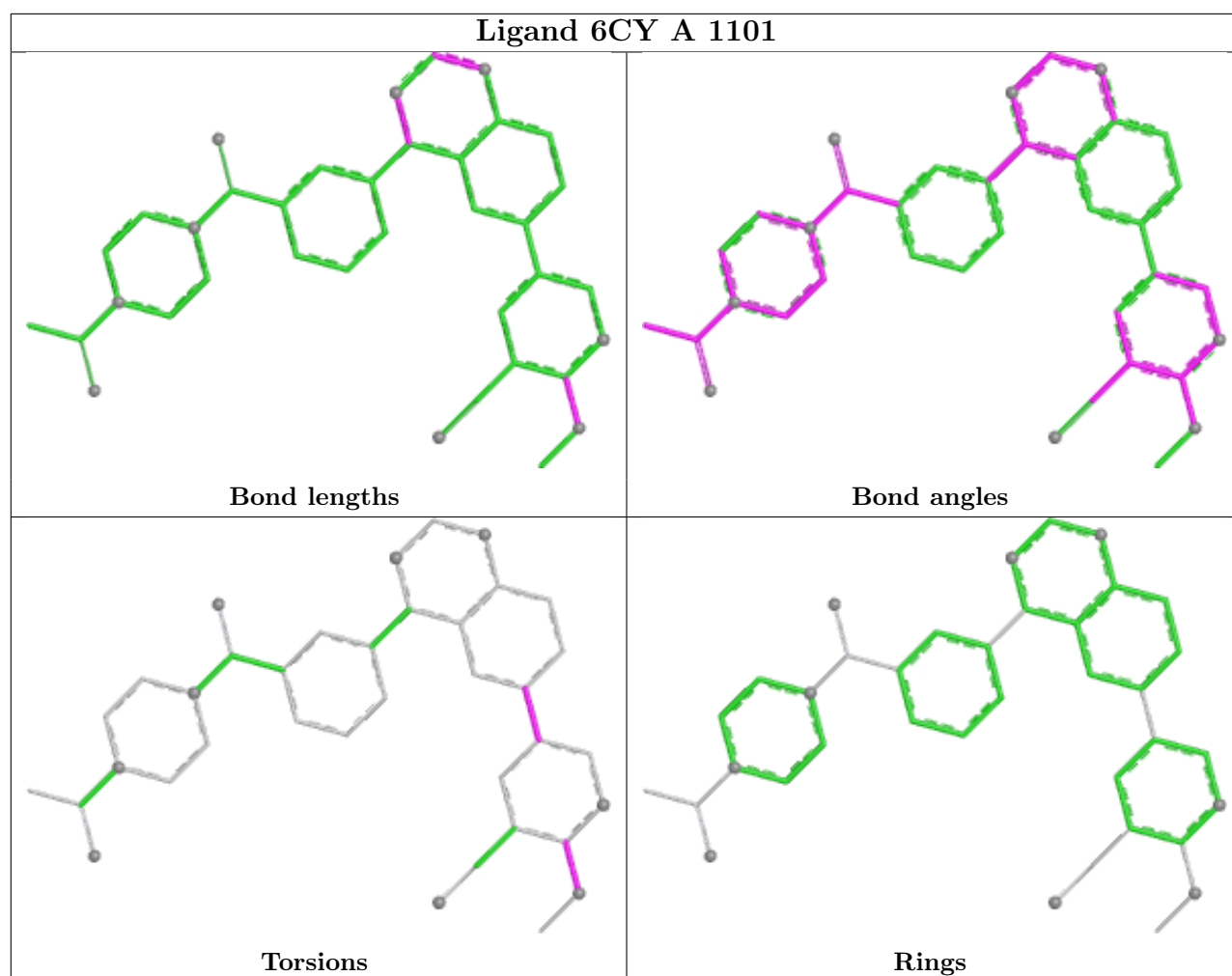
Mol	Chain	Res	Type	Atoms
2	A	1101	6CY	C46-C45-O51-C52
2	A	1101	6CY	N44-C45-O51-C52
2	A	1101	6CY	C37-C36-C41-C47

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	6CY	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, 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	785/1044 (75%)	0.67	64 (8%)	17 13	20, 51, 83, 109	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1027	TRP	5.4
1	A	318	SER	4.7
1	A	335	ALA	4.5
1	A	771	ALA	4.4
1	A	317	TRP	4.0
1	A	365	VAL	3.7
1	A	361	SER	3.6
1	A	478	VAL	3.6
1	A	948	ASN	3.5
1	A	524	TYR	3.4
1	A	484	TYR	3.2
1	A	523	LEU	3.2
1	A	253	ASN	3.1
1	A	189	ALA	3.1
1	A	362	GLU	3.0
1	A	206	GLN	2.9
1	A	528	LYS	2.9
1	A	202	SER	2.8
1	A	205	PHE	2.8
1	A	198	GLY	2.7
1	A	467	SER	2.7
1	A	474	TYR	2.7
1	A	395	TYR	2.7
1	A	381	VAL	2.7
1	A	366	CYS	2.6
1	A	368	GLU	2.6
1	A	257	CYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	475	LEU	2.6
1	A	357	THR	2.6
1	A	527	GLU	2.6
1	A	204	THR	2.5
1	A	336	ASP	2.5
1	A	334	ASN	2.5
1	A	208	SER	2.5
1	A	495	GLY	2.4
1	A	197	GLU	2.4
1	A	199	SER	2.4
1	A	341	LEU	2.4
1	A	128	PHE	2.4
1	A	1001	SER	2.4
1	A	769	GLY	2.3
1	A	279	SER	2.3
1	A	531	VAL	2.3
1	A	1020	ASN	2.3
1	A	530	LEU	2.3
1	A	563	GLN	2.3
1	A	110	LYS	2.2
1	A	342	VAL	2.2
1	A	321	GLN	2.2
1	A	415	ASP	2.2
1	A	488	LEU	2.2
1	A	840	ASN	2.1
1	A	476	PRO	2.1
1	A	1026	SER	2.1
1	A	262	ILE	2.1
1	A	482	PRO	2.1
1	A	108	ARG	2.1
1	A	990	SER	2.1
1	A	483	VAL	2.1
1	A	220	ALA	2.1
1	A	164	GLN	2.0
1	A	470	ALA	2.0
1	A	324	SER	2.0
1	A	525	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](#)

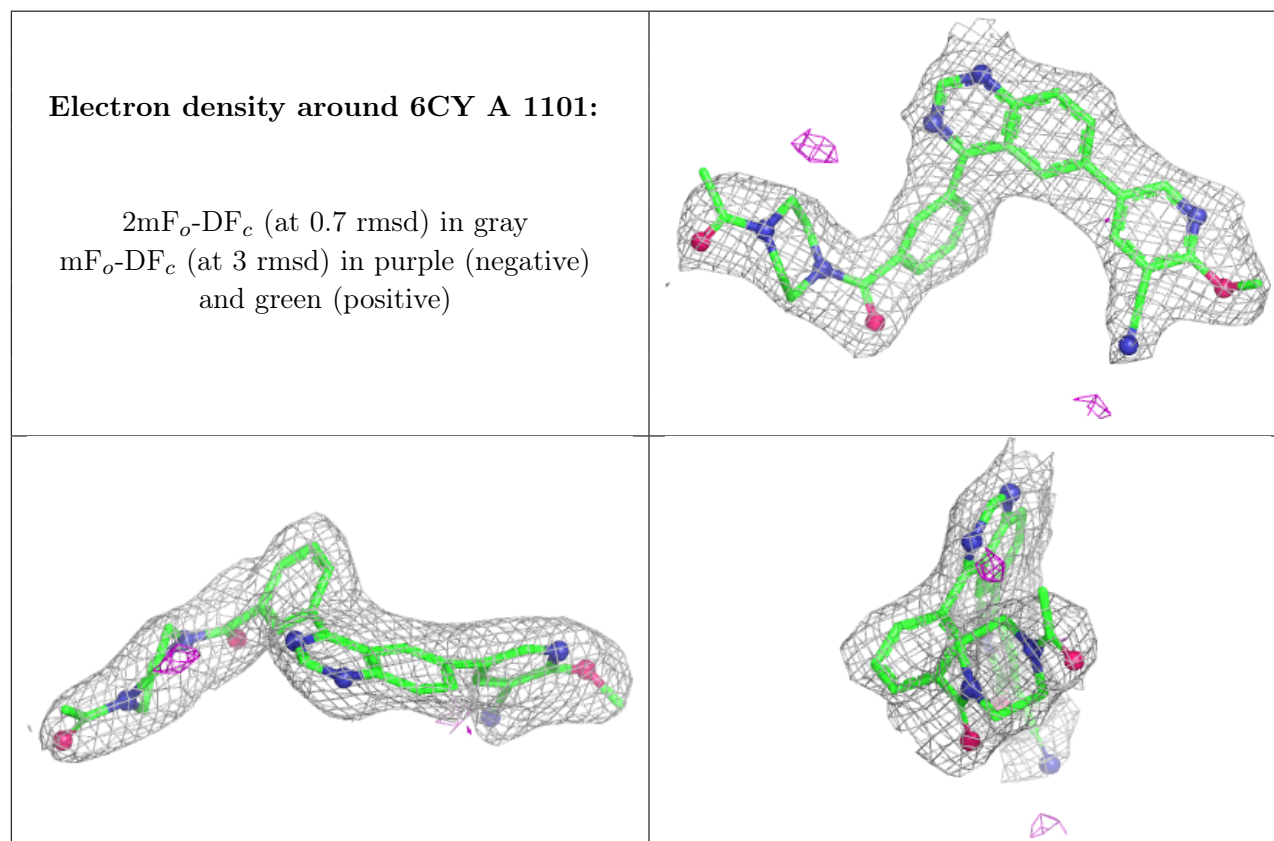
There are no oligosaccharides in this entry.

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	6CY	A	1101	37/37	0.93	0.10	29,33,40,41	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.