



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:35 PM UTC

PDB ID : 4TV3 / pdb_00004tv3
Title : Isolated p110a subunit of PI3Ka provides a platform for structure-based drug design
Authors : Chen, P.; Deng, Y.-L.; Bergqvist, S.; Falk, M.; Liu, W.; Timofeevski, S.
Deposited on : 2014-06-25
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

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

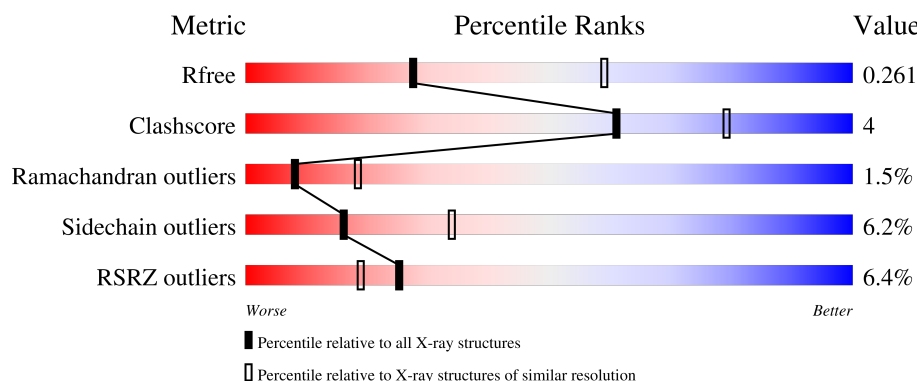
1 Overall quality at a glance

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	946	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6636 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.

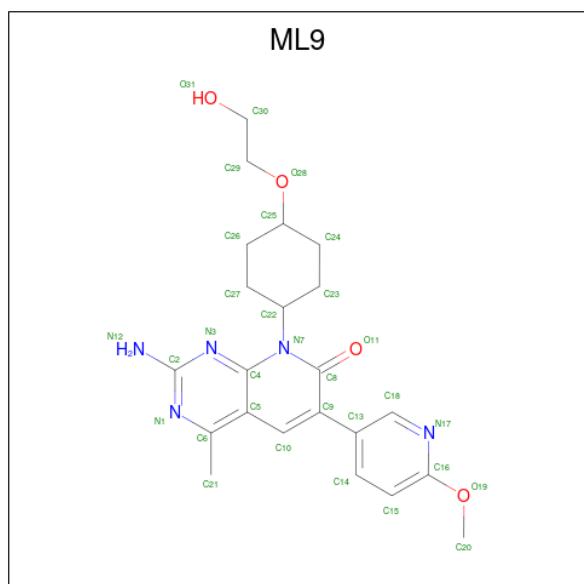
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic sub-unit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	879	Total	C	N	O	S	0	0	0
			6601	4231	1106	1206	58			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	GLY	-	expression tag	UNP P42336
A	104	SER	-	expression tag	UNP P42336

- Molecule 2 is 2-amino-8-[trans-4-(2-hydroxyethoxy)cyclohexyl]-6-(6-methoxypyridin-3-yl)-4-methylpyrido[2,3-d]pyrimidin-7(8H)-one (CCD ID: ML9) (formula: C₂₂H₂₇N₅O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			31	22	5	4		

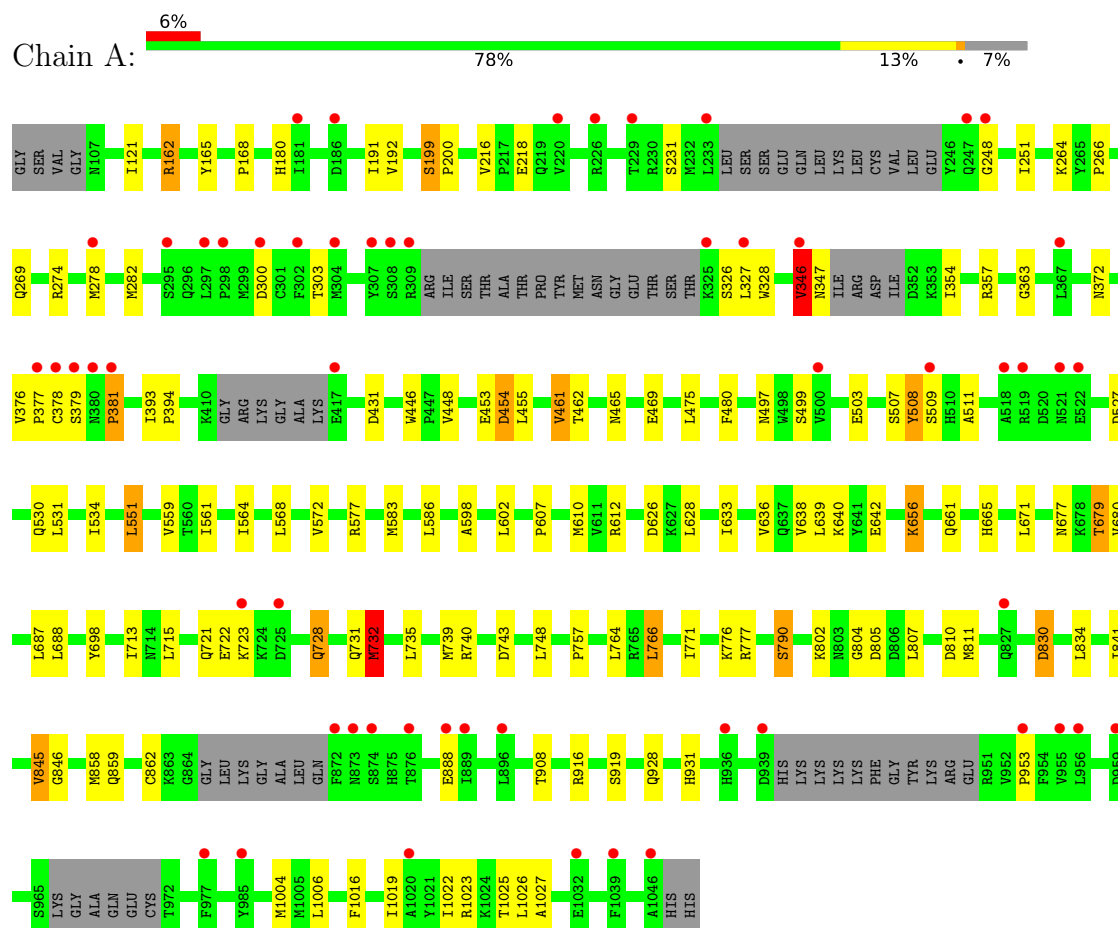
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		

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 alpha isoform



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.04Å 136.77Å 142.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.41 – 2.85 34.41 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.4 (34.41-2.85) 99.8 (34.41-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.85Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.208 , 0.250 0.221 , 0.261	Depositor DCC
R_{free} test set	1361 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	70.4	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 81.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6636	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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: ML9

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	0.92	3/6751 (0.0%)	1.39	29/9207 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	327	LEU	CA-C	8.08	1.57	1.52
1	A	633	ILE	CG1-CD1	5.35	1.72	1.51
1	A	732	MET	SD-CE	-5.15	1.66	1.79

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	507	SER	CA-C-N	10.58	140.74	121.70
1	A	507	SER	C-N-CA	10.58	140.74	121.70
1	A	377	PRO	CA-C-N	7.56	135.98	121.54
1	A	377	PRO	C-N-CA	7.56	135.98	121.54
1	A	1023	ARG	N-CA-C	-7.36	103.26	112.90
1	A	527	ASP	CA-CB-CG	6.34	118.94	112.60
1	A	743	ASP	CA-CB-CG	6.31	118.91	112.60
1	A	509	SER	N-CA-C	5.90	119.22	112.97
1	A	431	ASP	CA-CB-CG	5.85	118.45	112.60
1	A	888	GLU	CA-C-N	5.66	129.41	120.47
1	A	888	GLU	C-N-CA	5.66	129.41	120.47
1	A	598	ALA	CA-C-N	5.46	127.86	120.38
1	A	598	ALA	C-N-CA	5.46	127.86	120.38
1	A	830	ASP	CA-CB-CG	5.42	118.02	112.60
1	A	626	ASP	CA-CB-CG	5.22	117.82	112.60
1	A	454	ASP	CA-CB-CG	5.20	117.80	112.60
1	A	1016	PHE	CA-C-N	5.20	127.24	120.28
1	A	1016	PHE	C-N-CA	5.20	127.24	120.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	677	ASN	CA-CB-CG	5.19	117.79	112.60
1	A	346	VAL	CA-C-N	5.14	130.95	121.70
1	A	346	VAL	C-N-CA	5.14	130.95	121.70
1	A	790	SER	CA-C-N	5.14	127.88	120.38
1	A	790	SER	C-N-CA	5.14	127.88	120.38
1	A	766	LEU	CA-C-N	5.10	128.76	120.60
1	A	766	LEU	C-N-CA	5.10	128.76	120.60
1	A	497	ASN	CA-C-N	5.09	127.52	120.29
1	A	497	ASN	C-N-CA	5.09	127.52	120.29
1	A	671	LEU	CA-C-N	5.08	127.09	120.28
1	A	671	LEU	C-N-CA	5.08	127.09	120.28

There are no chirality outliers.

There are no planarity outliers.

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	6601	0	5945	53	0
2	A	31	0	27	0	0
3	A	4	0	0	0	0
All	All	6636	0	5972	53	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 (53) 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:568:LEU:HG	1:A:583:MET:HE1	1.58	0.85
1:A:807:LEU:HD12	1:A:846:GLY:HA3	1.60	0.83
1:A:180:HIS:CD2	1:A:830:ASP:HB2	2.26	0.70
1:A:739:MET:HG2	1:A:766:LEU:HD11	1.76	0.65
1:A:534:ILE:HG21	1:A:551:LEU:HD11	1.81	0.63
1:A:628:LEU:HD23	1:A:656:LYS:HG2	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:SER:HB2	1:A:200:PRO:CD	2.30	0.61
1:A:346:VAL:HG22	1:A:347:ASN:H	1.64	0.61
1:A:454:ASP:CG	1:A:455:LEU:H	2.09	0.60
1:A:739:MET:HE1	1:A:748:LEU:HD12	1.85	0.59
1:A:180:HIS:HD2	1:A:830:ASP:HB2	1.67	0.58
1:A:199:SER:HB2	1:A:200:PRO:HD2	1.86	0.56
1:A:807:LEU:CD1	1:A:846:GLY:HA3	2.35	0.55
1:A:266:PRO:HG2	1:A:269:GLN:HB2	1.90	0.53
1:A:461:VAL:HG21	1:A:679:THR:HG23	1.91	0.53
1:A:628:LEU:CD2	1:A:656:LYS:HG2	2.39	0.52
1:A:908:THR:HB	1:A:953:PRO:HG2	1.93	0.51
1:A:728:GLN:O	1:A:732:MET:HB2	2.10	0.51
1:A:269:GLN:HA	1:A:274:ARG:HH21	1.76	0.51
1:A:1022:ILE:O	1:A:1026:LEU:HB2	2.10	0.51
1:A:162:ARG:HH22	1:A:300:ASP:H	1.59	0.50
1:A:640:LYS:HE2	1:A:680:VAL:HG11	1.92	0.50
1:A:802:LYS:HE3	1:A:805:ASP:HB2	1.95	0.49
1:A:713:ILE:HG12	1:A:845:VAL:HG11	1.96	0.48
1:A:191:ILE:HG22	1:A:282:MET:SD	2.54	0.47
1:A:776:LYS:HE2	1:A:804:GLY:HA3	1.96	0.47
1:A:328:TRP:CD1	1:A:394:PRO:HB3	2.49	0.47
1:A:379:SER:O	1:A:381:PRO:HD3	2.14	0.47
1:A:121:ILE:HG12	1:A:688:LEU:HB3	1.97	0.46
1:A:916:ARG:HD3	1:A:931:HIS:ND1	2.31	0.45
1:A:531:LEU:HA	1:A:534:ILE:HD12	1.98	0.45
1:A:199:SER:CB	1:A:200:PRO:CD	2.94	0.45
1:A:858:MET:HE3	1:A:859:GLN:HG3	1.98	0.45
1:A:636:VAL:O	1:A:639:LEU:HB2	2.17	0.45
1:A:661:GLN:NE2	1:A:698:TYR:HB2	2.32	0.45
1:A:508:TYR:H	1:A:508:TYR:HD2	1.65	0.44
1:A:1006:LEU:HD21	1:A:1019:ILE:HD11	1.99	0.44
1:A:561:ILE:O	1:A:564:ILE:HG22	2.18	0.43
1:A:354:ILE:HD11	1:A:381:PRO:HB3	1.99	0.43
1:A:602:LEU:O	1:A:612:ARG:NH2	2.52	0.43
1:A:731:GLN:HB3	1:A:771:ILE:HD13	2.00	0.43
1:A:372:ASN:HD22	1:A:372:ASN:N	2.17	0.43
1:A:363:GLY:N	1:A:607:PRO:HG3	2.34	0.43
1:A:583:MET:HA	1:A:586:LEU:HD12	2.02	0.42
1:A:638:VAL:HG11	1:A:1004:MET:HG2	2.01	0.42
1:A:499:SER:O	1:A:503:GLU:HB2	2.21	0.41
1:A:572:VAL:HG21	1:A:583:MET:HG2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:GLU:OE2	1:A:248:GLY:HA3	2.21	0.41
1:A:612:ARG:NH1	1:A:642:GLU:CD	2.79	0.40
1:A:165:TYR:O	1:A:168:PRO:HD3	2.21	0.40
1:A:393:ILE:HD13	1:A:480:PHE:CZ	2.57	0.40
1:A:665:HIS:CG	1:A:757:PRO:HG3	2.56	0.40
1:A:446:TRP:CZ2	1:A:465:ASN:HA	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	863/946 (91%)	791 (92%)	59 (7%)	13 (2%)	8	18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	CYS
1	A	508	TYR
1	A	199	SER
1	A	381	PRO
1	A	453	GLU
1	A	511	ALA
1	A	722	GLU
1	A	862	CYS
1	A	264	LYS
1	A	723	LYS
1	A	231	SER
1	A	1027	ALA
1	A	346	VAL

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	624/860 (73%)	585 (94%)	39 (6%)	16	34

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	162	ARG
1	A	192	VAL
1	A	216	VAL
1	A	251	ILE
1	A	278	MET
1	A	303	THR
1	A	326	SER
1	A	357	ARG
1	A	376	VAL
1	A	448	VAL
1	A	461	VAL
1	A	462	THR
1	A	469	GLU
1	A	475	LEU
1	A	530	GLN
1	A	551	LEU
1	A	559	VAL
1	A	577	ARG
1	A	610	MET
1	A	656	LYS
1	A	679	THR
1	A	687	LEU
1	A	715	LEU
1	A	721	GLN
1	A	728	GLN
1	A	732	MET
1	A	735	LEU
1	A	740	ARG
1	A	764	LEU
1	A	777	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	790	SER
1	A	810	ASP
1	A	811	MET
1	A	834	LEU
1	A	841	ILE
1	A	845	VAL
1	A	919	SER
1	A	928	GLN
1	A	1025	THR

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	219	GLN
1	A	362	HIS
1	A	419	HIS
1	A	426	ASN
1	A	530	GLN
1	A	661	GLN
1	A	756	ASN
1	A	760	GLN
1	A	763	ASN
1	A	796	ASN
1	A	825	GLN
1	A	859	GLN
1	A	1000	ASN

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

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	ML9	A	1101	-	34,34,34	0.95	1 (2%)	42,48,48	1.07	4 (9%)

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	ML9	A	1101	-	-	1/14/24/24	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	ML9	C8-N7	4.98	1.44	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	ML9	C2-N1-C6	3.17	119.37	116.79
2	A	1101	ML9	C22-N7-C8	3.15	122.18	117.69
2	A	1101	ML9	C13-C9-C10	-2.38	119.30	121.99
2	A	1101	ML9	C5-C6-N1	-2.33	119.65	122.18

There are no chirality outliers.

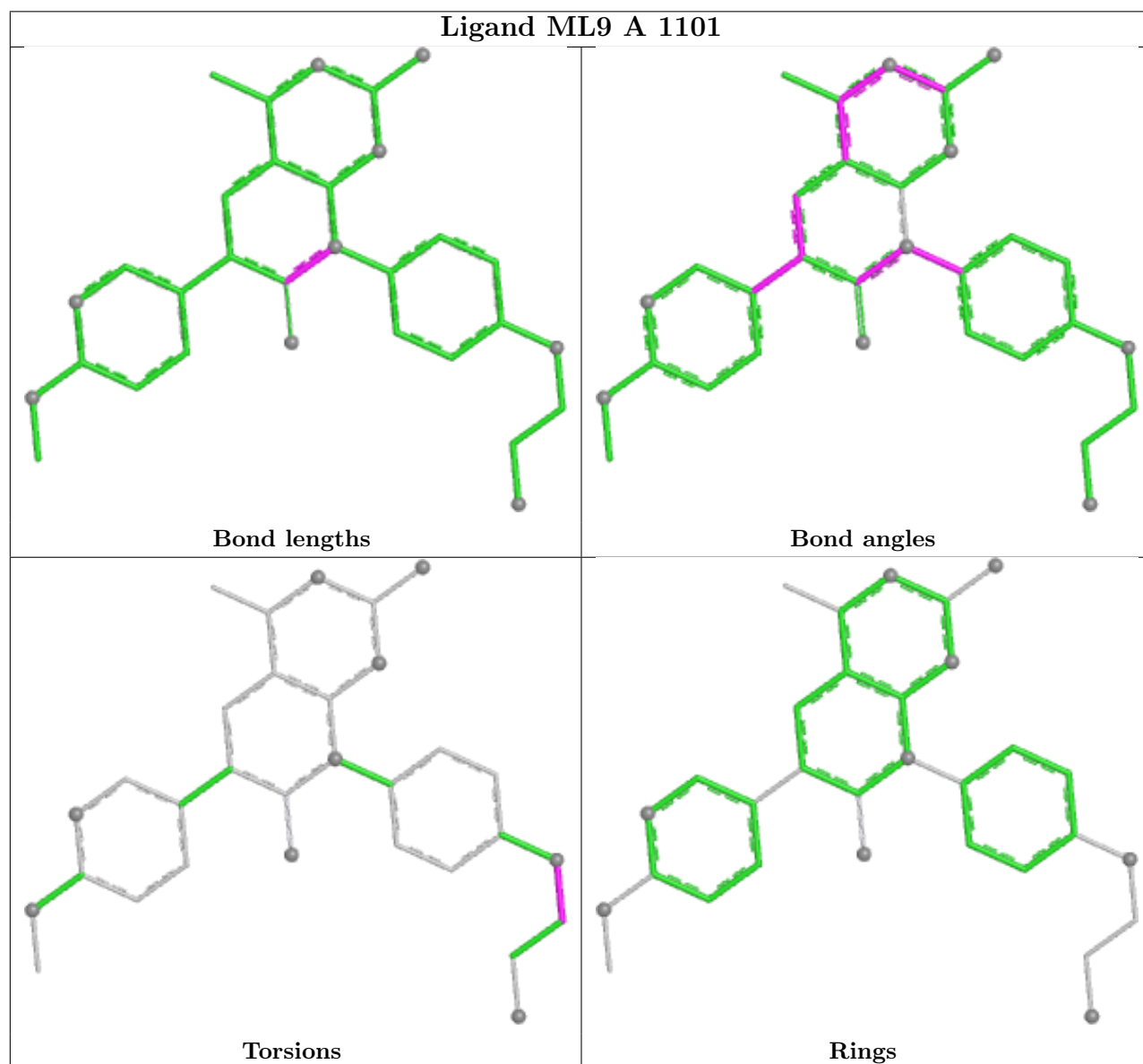
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	ML9	C30-C29-O28-C25

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	879/946 (92%)	0.39	56 (6%) 25 19	37, 70, 118, 162	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	380	ASN	5.2
1	A	233	LEU	4.7
1	A	939	ASP	4.4
1	A	307	TYR	4.2
1	A	985	TYR	4.0
1	A	959	ASP	3.9
1	A	873	ASN	3.4
1	A	725	ASP	3.3
1	A	1046	ALA	3.2
1	A	379	SER	3.1
1	A	300	ASP	3.0
1	A	876	THR	2.9
1	A	518	ALA	2.9
1	A	309	ARG	2.8
1	A	509	SER	2.7
1	A	888	GLU	2.7
1	A	302	PHE	2.7
1	A	346	VAL	2.6
1	A	1039	PHE	2.6
1	A	247	GLN	2.6
1	A	522	GLU	2.6
1	A	953	PRO	2.6
1	A	1032	GLU	2.5
1	A	377	PRO	2.5
1	A	827	GLN	2.5
1	A	977	PHE	2.5
1	A	278	MET	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	298	PRO	2.4
1	A	872	PHE	2.4
1	A	896	LEU	2.4
1	A	723	LYS	2.4
1	A	295	SER	2.3
1	A	955	VAL	2.3
1	A	378	CYS	2.3
1	A	229	THR	2.3
1	A	500	VAL	2.3
1	A	936	HIS	2.2
1	A	304	MET	2.2
1	A	367	LEU	2.2
1	A	417	GLU	2.2
1	A	521	ASN	2.2
1	A	519	ARG	2.2
1	A	874	SER	2.2
1	A	956	LEU	2.2
1	A	186	ASP	2.1
1	A	325	LYS	2.1
1	A	248	GLY	2.1
1	A	297	LEU	2.1
1	A	181	ILE	2.1
1	A	381	PRO	2.1
1	A	327	LEU	2.1
1	A	220	VAL	2.0
1	A	226	ARG	2.0
1	A	308	SER	2.0
1	A	889	ILE	2.0
1	A	1020	ALA	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 ⓘ

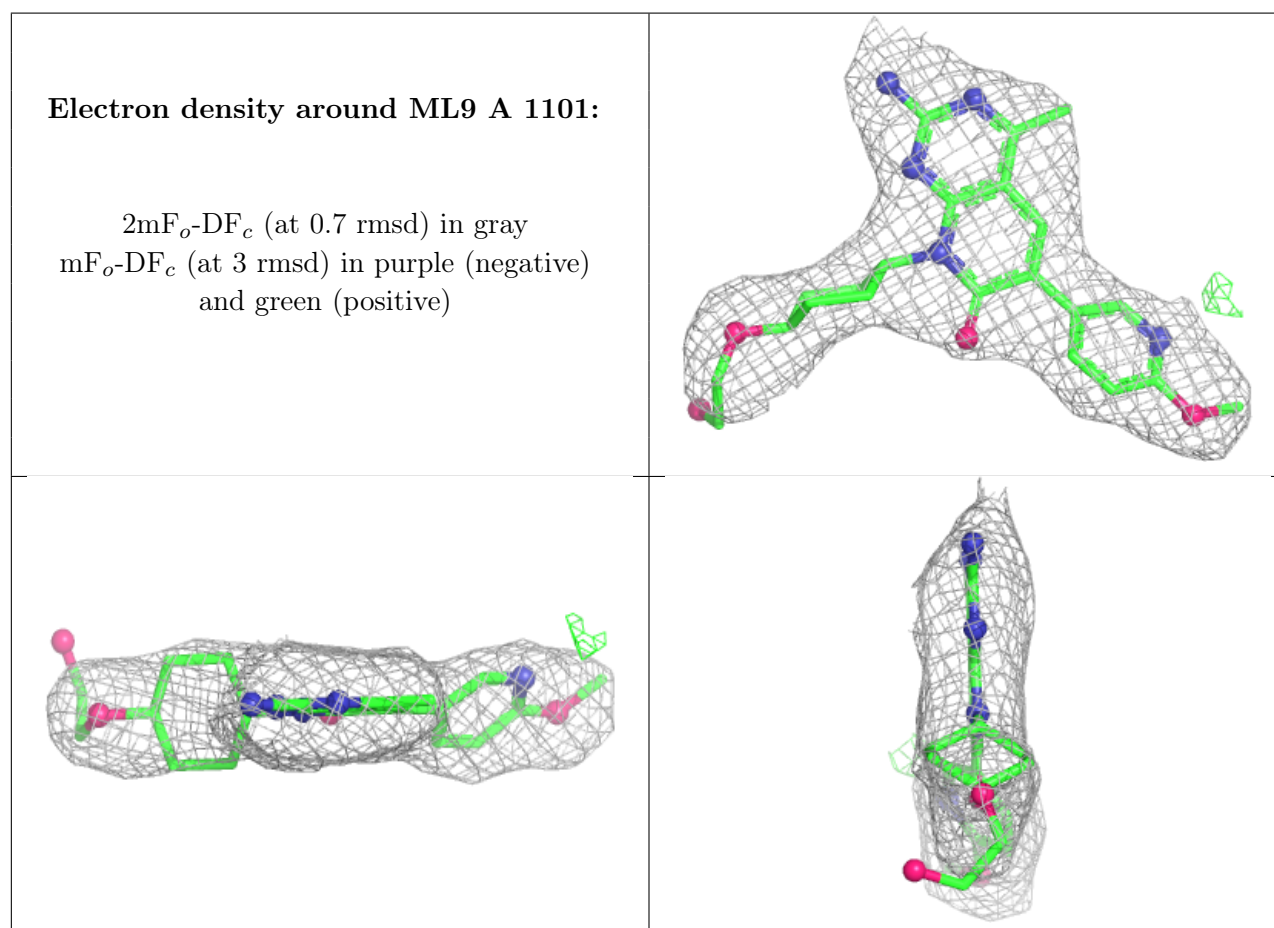
There are no oligosaccharides in this entry.

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	ML9	A	1101	31/31	0.94	0.10	62,69,91,97	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.