



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 08:59 PM UTC

PDB ID : 5I4U / pdb_00005i4u
Title : The crystal structure of PI3Kdelta with compound 34
Authors : Somoza, J.R.; Villasenor, A.G.
Deposited on : 2016-02-12
Resolution : 2.37 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

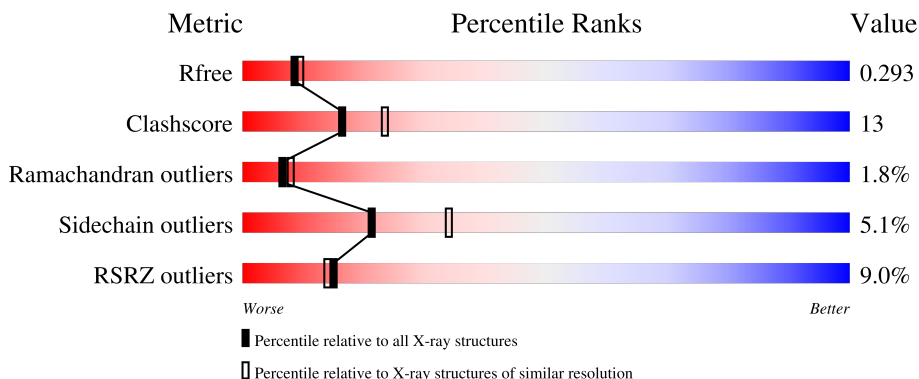
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	939	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6681 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.

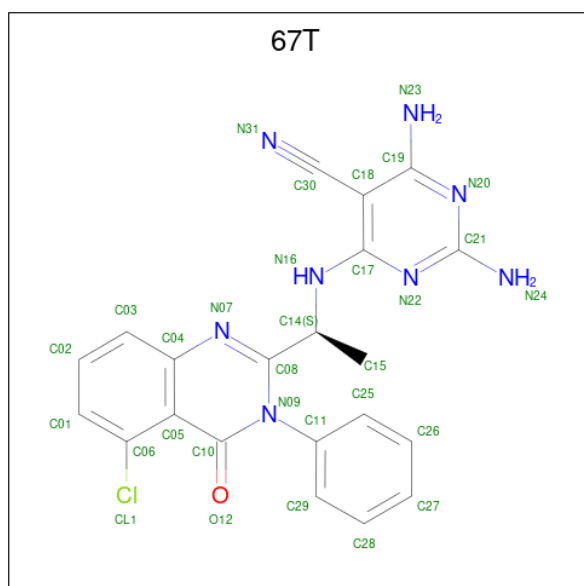
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic sub-unit delta isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	815	Total	C	N	O	S	0	0	0
			6566	4210	1115	1187	54			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	508	GLN	-	insertion	UNP O35904

- Molecule 2 is 2,4-diamino-6-[[[(1S)-1-(5-chloro-4-oxo-3-phenyl-3,4-dihydroquinazolin-2-yl)ethyl]amino]pyrimidine-5-carbonitrile (CCD ID: 67T) (formula: C₂₁H₁₇ClN₈O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			31	21	1	8	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	84	Total 84	O 84	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	64.27Å 143.48Å 221.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.89 – 2.37 45.89 – 2.37	Depositor EDS
% Data completeness (in resolution range)	93.4 (45.89-2.37) 89.0 (45.89-2.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.37Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.222 , 0.290 0.229 , 0.293	Depositor DCC
R_{free} test set	1999 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.4	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	0.93	EDS
Total number of atoms	6681	wwPDB-VP
Average B, all atoms (Å ²)	57.0	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 67T

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	0.59	1/6706 (0.0%)	0.91	13/9047 (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	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1009	GLU	N-CA	-5.03	1.40	1.46

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1010	GLU	N-CA-C	-9.68	101.14	113.72
1	A	1014	HIS	N-CA-C	-8.34	100.85	111.02
1	A	333	VAL	N-CA-C	7.93	119.57	108.23
1	A	1011	ALA	CA-C-N	7.36	131.12	120.38
1	A	1011	ALA	C-N-CA	7.36	131.12	120.38
1	A	1014	HIS	N-CA-CB	6.47	119.65	109.82
1	A	1009	GLU	N-CA-C	-6.20	97.08	107.80
1	A	996	GLN	CA-CB-CG	-5.66	102.79	114.10
1	A	1012	LEU	CA-CB-CG	5.28	134.79	116.30
1	A	1013	LYS	N-CA-C	-5.27	99.57	110.80
1	A	757	LYS	CA-C-N	-5.20	114.88	120.03
1	A	757	LYS	C-N-CA	-5.20	114.88	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	444	SER	N-CA-C	5.10	117.75	109.24

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1008	GLU	Peptide
1	A	1010	GLU	Peptide
1	A	1012	LEU	Peptide
1	A	333	VAL	Peptide

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	6566	0	6557	171	0
2	A	31	0	0	1	0
3	A	84	0	0	6	0
All	All	6681	0	6557	171	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 13.

All (171) 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:331:ARG:HD3	1:A:368:GLU:HG3	1.48	0.93
1:A:745:CYS:HB3	1:A:748:GLN:HE21	1.34	0.91
1:A:756:MET:HE2	1:A:781:GLY:HA3	1.52	0.90
1:A:367:SER:OG	1:A:368:GLU:OE2	1.90	0.88
1:A:512:ARG:HH21	1:A:538:VAL:HG22	1.39	0.86
1:A:331:ARG:HA	1:A:368:GLU:HA	1.57	0.86
1:A:1009:GLU:HG2	1:A:1011:ALA:C	2.03	0.84
1:A:1010:GLU:C	1:A:1012:LEU:H	1.85	0.84
1:A:888:VAL:HA	1:A:1001:SER:HB2	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1007:THR:HG22	1:A:1010:GLU:HB3	1.62	0.81
1:A:246:ARG:NH1	1:A:248:GLU:OE1	2.17	0.78
1:A:996:GLN:O	1:A:999:LYS:N	2.15	0.76
1:A:999:LYS:HG3	1:A:1000:ASP:N	2.03	0.74
1:A:786:GLN:NE2	1:A:914:HIS:O	2.23	0.72
1:A:512:ARG:HH22	1:A:531:VAL:HG13	1.55	0.72
1:A:549:LEU:HG	1:A:564:MET:HE1	1.72	0.71
1:A:386:ARG:HG3	1:A:387:MET:HE2	1.75	0.68
1:A:371:TRP:C	1:A:373:GLN:H	2.02	0.67
1:A:364:ASN:O	1:A:366:CYS:N	2.25	0.67
1:A:1010:GLU:HA	1:A:1012:LEU:HB2	1.77	0.67
1:A:333:VAL:HG11	1:A:367:SER:HA	1.76	0.66
1:A:512:ARG:HH12	1:A:531:VAL:HG22	1.59	0.66
1:A:955:ARG:NH2	3:A:1204:HOH:O	2.29	0.65
1:A:427:ASP:OD1	1:A:431:GLN:N	2.29	0.65
1:A:745:CYS:HB3	1:A:748:GLN:NE2	2.08	0.65
1:A:979:ALA:HA	1:A:995:ILE:HD11	1.79	0.64
1:A:245:GLY:HA3	1:A:768:ALA:HB2	1.79	0.64
1:A:1010:GLU:C	1:A:1012:LEU:N	2.56	0.63
1:A:512:ARG:NH1	1:A:512:ARG:HG3	2.14	0.62
1:A:331:ARG:HG3	1:A:332:LYS:HD3	1.80	0.62
1:A:512:ARG:NH2	1:A:538:VAL:HG22	2.13	0.62
1:A:333:VAL:O	1:A:334:ASN:ND2	2.33	0.61
1:A:999:LYS:CG	1:A:1000:ASP:N	2.63	0.61
1:A:138:ASP:OD2	1:A:428:TYR:OH	2.16	0.61
1:A:387:MET:HE3	1:A:590:CYS:HB3	1.83	0.60
1:A:933:ILE:HG12	3:A:1237:HOH:O	2.02	0.60
1:A:895:HIS:CE1	1:A:897:ASP:HB2	2.35	0.60
1:A:1013:LYS:HA	1:A:1016:ARG:CG	2.32	0.60
1:A:331:ARG:NH1	1:A:368:GLU:OE2	2.35	0.59
1:A:745:CYS:CB	1:A:748:GLN:HE21	2.12	0.59
1:A:419:ALA:HB3	1:A:441:MET:HE3	1.84	0.59
1:A:1010:GLU:HG3	1:A:1010:GLU:O	2.01	0.59
1:A:193:ASN:OD1	1:A:202:SER:OG	2.21	0.59
1:A:167:PHE:HZ	1:A:285:MET:HE1	1.68	0.58
1:A:271:THR:O	1:A:273:HIS:HD2	1.85	0.58
1:A:325:ILE:HD13	1:A:377:PHE:HE1	1.68	0.58
1:A:679:MET:O	1:A:683:MET:HG3	2.04	0.57
1:A:532:TRP:HZ3	1:A:564:MET:HE2	1.68	0.57
1:A:331:ARG:HG3	1:A:332:LYS:CD	2.35	0.57
1:A:340:LYS:HG2	1:A:362:GLU:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:957:ARG:HG3	1:A:1019:PHE:CE1	2.41	0.55
1:A:333:VAL:CG1	1:A:367:SER:HA	2.36	0.55
1:A:731:LEU:HD11	1:A:741:LEU:HD12	1.88	0.54
1:A:996:GLN:O	1:A:999:LYS:HB3	2.07	0.54
1:A:489:GLU:O	1:A:493:GLU:HG3	2.08	0.54
1:A:779:LYS:NZ	1:A:782:ASP:OD2	2.23	0.54
1:A:581:GLU:HB2	1:A:976:HIS:CD2	2.44	0.53
1:A:512:ARG:HG3	1:A:512:ARG:HH11	1.73	0.53
1:A:999:LYS:O	1:A:1003:ALA:N	2.42	0.53
1:A:610:GLN:O	1:A:792:GLN:NE2	2.40	0.52
1:A:321:GLN:OE1	1:A:321:GLN:N	2.34	0.52
1:A:335:ALA:C	1:A:365:VAL:HG11	2.34	0.52
1:A:1012:LEU:HD22	1:A:1013:LYS:HB3	1.91	0.52
1:A:167:PHE:CZ	1:A:285:MET:HE1	2.45	0.52
1:A:947:THR:O	1:A:948:ASN:ND2	2.43	0.52
1:A:553:THR:OG1	1:A:564:MET:HE3	2.10	0.52
1:A:364:ASN:C	1:A:366:CYS:H	2.16	0.52
1:A:188:ARG:HD3	1:A:189:ALA:O	2.10	0.51
1:A:594:SER:HB3	1:A:598:LYS:NZ	2.25	0.51
1:A:155:GLN:OE1	1:A:290:SER:HB3	2.10	0.51
1:A:713:GLU:O	1:A:717:MET:HG3	2.10	0.51
1:A:549:LEU:CG	1:A:564:MET:HE1	2.40	0.51
1:A:209:THR:HB	1:A:257:CYS:HB3	1.92	0.50
1:A:332:LYS:HB2	1:A:469:ALA:HA	1.92	0.50
1:A:1007:THR:HG22	1:A:1010:GLU:CB	2.36	0.50
1:A:856:LEU:O	1:A:860:LYS:HG3	2.11	0.50
1:A:848:ALA:HB1	1:A:853:ASP:HB2	1.94	0.49
1:A:349:HIS:O	1:A:352:GLU:HG3	2.12	0.49
1:A:929:ARG:NH2	1:A:1000:ASP:HB2	2.28	0.49
1:A:162:TRP:CD1	1:A:286:ARG:HG3	2.48	0.49
1:A:189:ALA:HA	1:A:208:SER:HA	1.94	0.49
1:A:339:MET:O	1:A:365:VAL:HG23	2.12	0.49
1:A:1013:LYS:HA	1:A:1016:ARG:HG2	1.95	0.49
1:A:331:ARG:HA	1:A:368:GLU:CA	2.37	0.49
1:A:157:LEU:HB3	1:A:161:GLU:HB2	1.95	0.49
1:A:270:LEU:HD22	1:A:770:SER:HB3	1.95	0.49
1:A:1007:THR:OG1	1:A:1008:GLU:N	2.47	0.48
1:A:594:SER:HB3	1:A:598:LYS:HZ3	1.79	0.48
1:A:915:PHE:HD1	1:A:916:LEU:HG	1.79	0.48
1:A:1009:GLU:O	1:A:1012:LEU:HB2	2.13	0.48
1:A:516:GLU:N	1:A:516:GLU:OE1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:ARG:NH2	1:A:430:ASP:OD1	2.34	0.48
1:A:802:LYS:C	1:A:804:GLU:H	2.22	0.48
1:A:890:GLY:O	1:A:915:PHE:HA	2.14	0.47
1:A:329:GLU:HB2	1:A:369:PRO:O	2.14	0.47
1:A:536:HIS:O	1:A:540:GLU:HG2	2.14	0.47
1:A:194:VAL:HG21	1:A:216:LEU:HD21	1.96	0.47
1:A:999:LYS:CG	1:A:1000:ASP:H	2.27	0.47
1:A:383:ASP:HB3	1:A:556:ASN:O	2.15	0.47
1:A:663:ARG:O	1:A:667:ILE:HG13	2.15	0.47
1:A:1007:THR:HG23	1:A:1008:GLU:HB2	1.97	0.47
1:A:325:ILE:HD13	1:A:377:PHE:CE1	2.49	0.47
1:A:349:HIS:O	1:A:352:GLU:CG	2.63	0.47
1:A:996:GLN:HG3	1:A:999:LYS:HB3	1.95	0.47
1:A:1016:ARG:C	1:A:1020:ASN:HD22	2.23	0.46
1:A:350:GLY:N	1:A:588:PRO:HG3	2.30	0.46
1:A:731:LEU:HD12	1:A:732:GLN:O	2.16	0.46
1:A:340:LYS:HG3	1:A:363:VAL:O	2.15	0.46
1:A:549:LEU:HG	1:A:564:MET:CE	2.44	0.45
1:A:188:ARG:HD3	1:A:188:ARG:C	2.41	0.45
1:A:1009:GLU:HG2	1:A:1012:LEU:N	2.32	0.45
1:A:512:ARG:NH2	1:A:531:VAL:HG13	2.28	0.45
1:A:991:CYS:HB2	1:A:993:LYS:H	1.81	0.45
1:A:123:LYS:NZ	3:A:1201:HOH:O	2.50	0.45
1:A:131:LEU:HD23	3:A:1209:HOH:O	2.16	0.45
1:A:915:PHE:CD1	1:A:916:LEU:HG	2.52	0.45
1:A:634:LEU:HD23	1:A:634:LEU:HA	1.80	0.44
1:A:859:LEU:HD21	1:A:901:ILE:HD11	1.99	0.44
1:A:289:GLN:HG2	1:A:677:HIS:CD2	2.52	0.44
1:A:696:ASN:O	1:A:700:LYS:HG3	2.16	0.44
1:A:371:TRP:C	1:A:373:GLN:N	2.74	0.44
1:A:535:ARG:HA	1:A:538:VAL:HG23	1.99	0.44
1:A:187:ASN:HB2	1:A:210:LYS:HG3	1.99	0.44
1:A:1018:LYS:NZ	3:A:1212:HOH:O	2.50	0.44
1:A:191:LEU:O	1:A:272:PRO:HD2	2.18	0.44
1:A:316:LEU:HB3	1:A:318:SER:OG	2.18	0.44
1:A:548:ARG:O	1:A:552:VAL:HG13	2.17	0.44
1:A:752:MET:HE3	2:A:1101:67T:C10	2.48	0.44
1:A:597:ILE:HD13	1:A:597:ILE:HA	1.80	0.43
1:A:349:HIS:CE1	1:A:588:PRO:HG2	2.53	0.43
1:A:340:LYS:CD	1:A:362:GLU:HB3	2.48	0.43
1:A:342:VAL:HB	1:A:395:TYR:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:671:TYR:OH	1:A:678:HIS:ND1	2.39	0.43
1:A:326:GLU:HB3	1:A:474:TYR:HB3	1.99	0.43
1:A:371:TRP:O	1:A:373:GLN:N	2.49	0.43
1:A:474:TYR:O	1:A:476:PRO:HD3	2.18	0.43
1:A:600:LEU:HA	1:A:600:LEU:HD23	1.81	0.42
1:A:754:SER:HB2	1:A:755:LYS:HG3	2.01	0.42
1:A:895:HIS:HE1	1:A:897:ASP:HB2	1.84	0.42
1:A:116:GLN:HB3	1:A:683:MET:SD	2.60	0.42
1:A:999:LYS:HG3	1:A:1000:ASP:OD1	2.20	0.42
1:A:356:LYS:HE3	1:A:356:LYS:HB2	1.78	0.42
1:A:364:ASN:C	1:A:366:CYS:N	2.76	0.42
1:A:691:LYS:HG3	1:A:724:TYR:CE2	2.54	0.42
1:A:783:ASP:OD1	1:A:785:ARG:HD3	2.20	0.42
1:A:915:PHE:CD1	1:A:915:PHE:C	2.98	0.42
1:A:996:GLN:O	1:A:997:TYR:C	2.63	0.42
1:A:187:ASN:HB3	1:A:209:THR:OG1	2.19	0.42
1:A:714:MET:HE3	1:A:714:MET:HB2	1.81	0.42
1:A:700:LYS:NZ	1:A:756:MET:HE3	2.35	0.41
1:A:317:TRP:HA	1:A:382:CYS:HB2	2.03	0.41
1:A:317:TRP:CZ3	1:A:494:LEU:HD22	2.55	0.41
1:A:347:LEU:HD23	1:A:347:LEU:HA	1.83	0.41
1:A:285:MET:HE2	1:A:285:MET:HB3	1.86	0.41
1:A:842:SER:O	1:A:843:ASN:HB3	2.19	0.41
1:A:891:ILE:HD13	1:A:912:PHE:CD1	2.55	0.41
1:A:752:MET:C	1:A:754:SER:H	2.29	0.41
1:A:841:LYS:HD2	1:A:844:MET:HE3	2.03	0.41
1:A:868:LEU:O	1:A:872:ILE:HG12	2.20	0.41
1:A:416:CYS:HA	1:A:417:PRO:HD3	1.87	0.41
1:A:594:SER:O	1:A:598:LYS:HG3	2.20	0.41
1:A:598:LYS:O	1:A:601:ARG:HG3	2.21	0.41
1:A:872:ILE:HB	3:A:1228:HOH:O	2.21	0.41
1:A:950:SER:O	1:A:954:GLU:HG2	2.21	0.41
1:A:361:SER:OG	1:A:373:GLN:NE2	2.54	0.40
1:A:1013:LYS:HA	1:A:1016:ARG:HG3	2.02	0.40
1:A:394:LEU:HD23	1:A:418:ILE:HB	2.03	0.40
1:A:800:LEU:HD22	1:A:970:HIS:CG	2.57	0.40
1:A:856:LEU:HG	1:A:860:LYS:CE	2.52	0.40
1:A:323:PHE:CE2	1:A:325:ILE:HD11	2.55	0.40
1:A:543:PRO:O	1:A:571:TRP:NE1	2.50	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	793/939 (84%)	734 (93%)	45 (6%)	14 (2%)	6 8

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	365	VAL
1	A	372	LYS
1	A	770	SER
1	A	913	GLY
1	A	915	PHE
1	A	1008	GLU
1	A	1011	ALA
1	A	1013	LYS
1	A	769	GLY
1	A	229	ARG
1	A	464	ASN
1	A	576	VAL
1	A	328	ILE
1	A	227	VAL

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	721/827 (87%)	684 (95%)	37 (5%)	21 34

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	VAL
1	A	110	LYS
1	A	163	LEU
1	A	188	ARG
1	A	200	GLU
1	A	201	GLU
1	A	250	LEU
1	A	325	ILE
1	A	333	VAL
1	A	352	GLU
1	A	356	LYS
1	A	365	VAL
1	A	366	CYS
1	A	367	SER
1	A	372	LYS
1	A	423	LEU
1	A	445	VAL
1	A	512	ARG
1	A	514	ILE
1	A	618	VAL
1	A	731	LEU
1	A	738	SER
1	A	748	GLN
1	A	770	SER
1	A	841	LYS
1	A	901	ILE
1	A	907	LEU
1	A	933	ILE
1	A	944	GLN
1	A	991	CYS
1	A	999	LYS
1	A	1006	LYS
1	A	1010	GLU
1	A	1013	LYS
1	A	1014	HIS
1	A	1016	ARG
1	A	1017	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	247	HIS
1	A	334	ASN

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Mol	Chain	Res	Type
1	A	748	GLN
1	A	940	HIS
1	A	943	GLN
1	A	948	ASN

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	67T	A	1101	-	34,34,34	1.21	2 (5%)	40,49,49	1.31	5 (12%)

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	67T	A	1101	-	-	0/10/14/14	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	67T	C18-C17	-3.25	1.38	1.42
2	A	1101	67T	C18-C19	-2.75	1.39	1.42

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	67T	C18-C17-N16	-3.69	118.64	120.94
2	A	1101	67T	C05-C06-CL1	2.52	122.86	119.62
2	A	1101	67T	C04-N07-C08	2.47	120.87	117.46
2	A	1101	67T	C25-C11-N09	2.35	122.46	119.65
2	A	1101	67T	C18-C19-N23	-2.19	119.32	121.65

There are no chirality outliers.

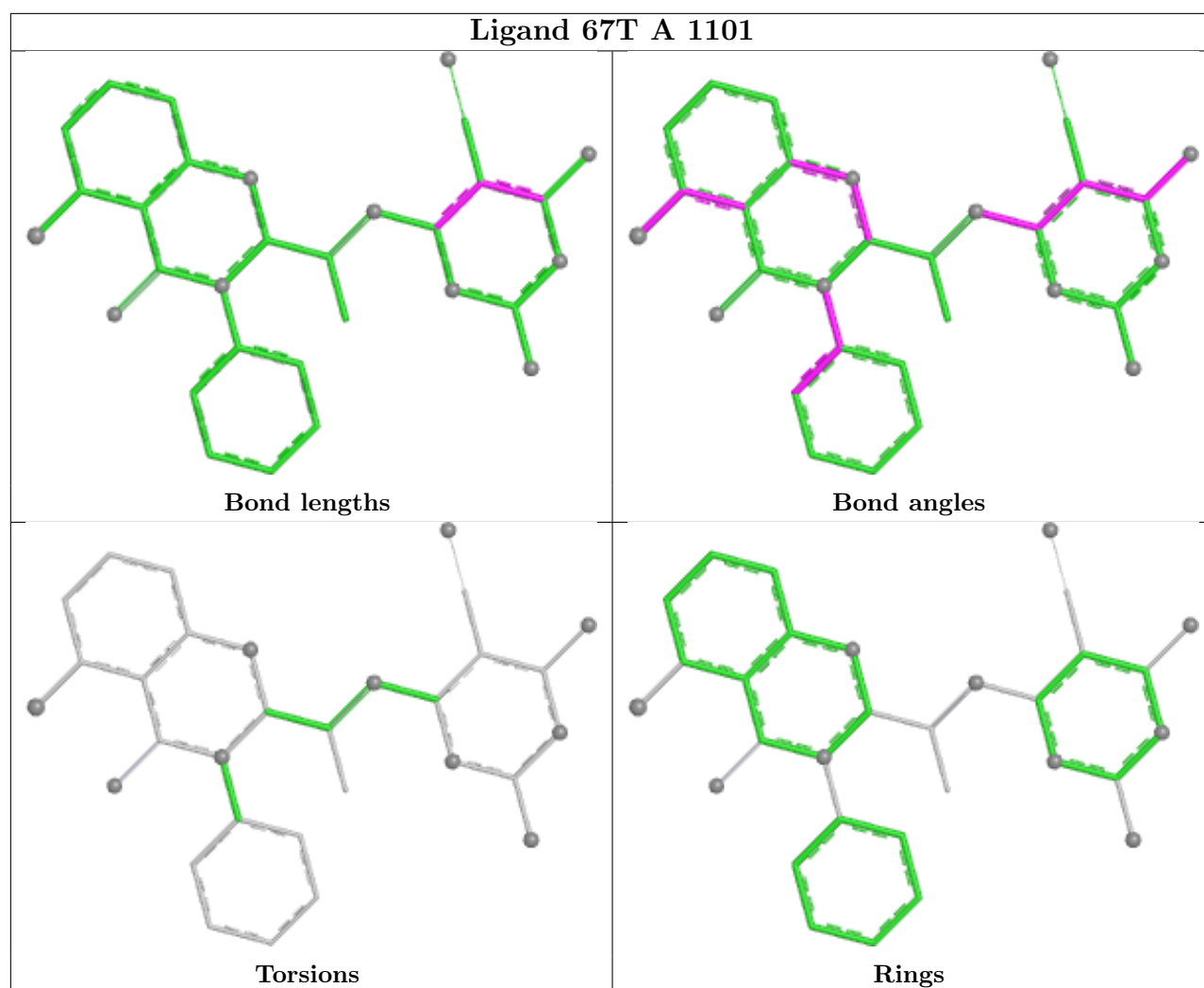
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	67T	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

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	815/939 (86%)	0.68	73 (8%) 15 14	32, 54, 82, 254	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	335	ALA	11.9
1	A	333	VAL	6.9
1	A	332	LYS	6.9
1	A	334	ASN	5.9
1	A	109	VAL	5.8
1	A	316	LEU	5.0
1	A	479	ALA	4.9
1	A	511	LEU	4.7
1	A	482	PRO	4.4
1	A	1000	ASP	4.2
1	A	1012	LEU	4.1
1	A	512	ARG	4.1
1	A	445	VAL	4.1
1	A	1011	ALA	3.9
1	A	915	PHE	3.8
1	A	365	VAL	3.8
1	A	367	SER	3.8
1	A	494	LEU	3.6
1	A	514	ILE	3.5
1	A	846	ALA	3.2
1	A	1008	GLU	3.2
1	A	1014	HIS	3.2
1	A	325	ILE	3.1
1	A	470	ALA	3.0
1	A	839	LEU	3.0
1	A	1023	LEU	2.9
1	A	474	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	452	LEU	2.8
1	A	317	TRP	2.8
1	A	936	TYR	2.8
1	A	331	ARG	2.8
1	A	366	CYS	2.8
1	A	1024	ARG	2.7
1	A	934	LEU	2.7
1	A	1007	THR	2.7
1	A	1010	GLU	2.7
1	A	153	HIS	2.6
1	A	1009	GLU	2.6
1	A	932	PHE	2.6
1	A	363	VAL	2.6
1	A	842	SER	2.6
1	A	468	ALA	2.6
1	A	381	VAL	2.5
1	A	228	PHE	2.5
1	A	173	PRO	2.4
1	A	1017	VAL	2.4
1	A	771	ALA	2.4
1	A	844	MET	2.4
1	A	398	VAL	2.4
1	A	516	GLU	2.4
1	A	933	ILE	2.3
1	A	323	PHE	2.3
1	A	343	VAL	2.3
1	A	1005	GLY	2.3
1	A	748	GLN	2.3
1	A	269	GLY	2.2
1	A	235	GLN	2.2
1	A	478	VAL	2.2
1	A	937	ASP	2.2
1	A	1001	SER	2.2
1	A	1015	PHE	2.1
1	A	230	GLN	2.1
1	A	358	VAL	2.1
1	A	469	ALA	2.1
1	A	513	GLU	2.1
1	A	929	ARG	2.1
1	A	847	THR	2.1
1	A	352	GLU	2.1
1	A	1025	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	350	GLY	2.1
1	A	339	MET	2.0
1	A	364	ASN	2.0
1	A	488	LEU	2.0

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](#)

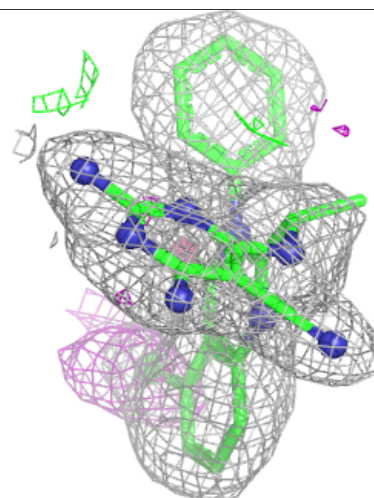
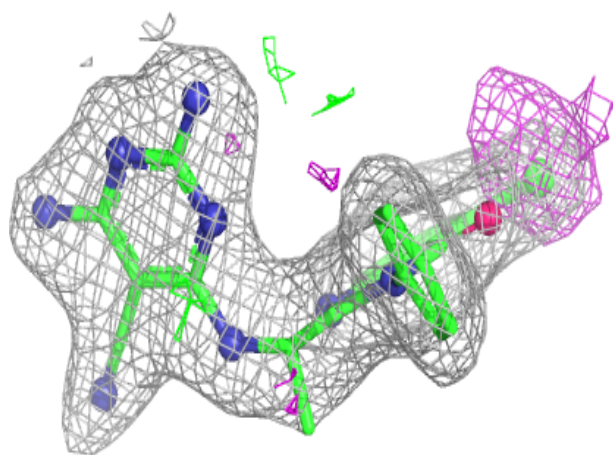
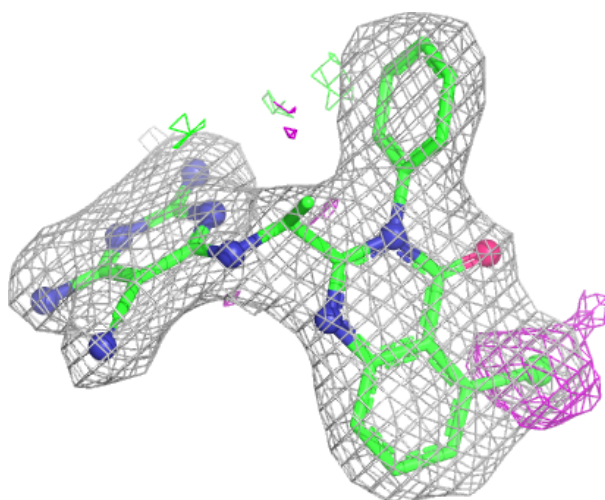
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	67T	A	1101	31/31	0.91	0.09	32,40,47,56	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.

Electron density around 67T A 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.