



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:44 AM UTC

PDB ID : 8EXV / pdb_00008exv
Title : Crystal structure of PI3K-alpha in complex with compound 32
Authors : Kiefer, J.R.; Eigenbrot, C.; Staben, S.T.; Hanan, E.J.; Wallweber, H.J.A.;
Ultsch, M.; Braun, M.G.; Friedman, L.S.; Purkey, H.E.
Deposited on : 2022-10-25
Resolution : 2.48 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

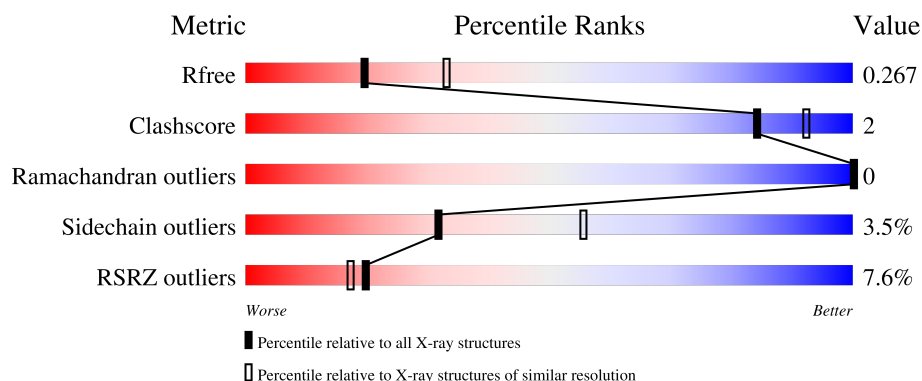
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	1080	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7450 atoms, of which 2 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	895	Total	C	N	O	S	0	3	0
			7348	4691	1263	1331	63			

There are 34 discrepancies between the modelled and reference sequences:

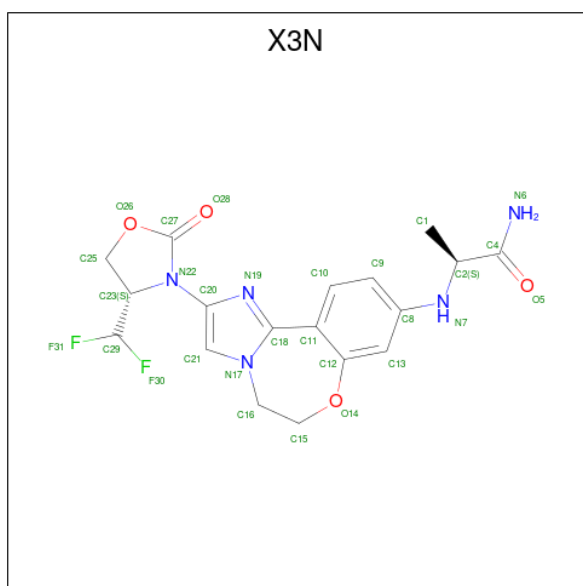
Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP P42336
A	-26	SER	-	expression tag	UNP P42336
A	-25	TYR	-	expression tag	UNP P42336
A	-24	TYR	-	expression tag	UNP P42336
A	-23	HIS	-	expression tag	UNP P42336
A	-22	HIS	-	expression tag	UNP P42336
A	-21	HIS	-	expression tag	UNP P42336
A	-20	HIS	-	expression tag	UNP P42336
A	-19	HIS	-	expression tag	UNP P42336
A	-18	HIS	-	expression tag	UNP P42336
A	-17	ASP	-	expression tag	UNP P42336
A	-16	TYR	-	expression tag	UNP P42336
A	-15	ASP	-	expression tag	UNP P42336
A	-14	ILE	-	expression tag	UNP P42336
A	-13	PRO	-	expression tag	UNP P42336
A	-12	THR	-	expression tag	UNP P42336
A	-11	THR	-	expression tag	UNP P42336
A	-10	GLU	-	expression tag	UNP P42336
A	-9	ASN	-	expression tag	UNP P42336
A	-8	LEU	-	expression tag	UNP P42336
A	-7	TYR	-	expression tag	UNP P42336
A	-6	PHE	-	expression tag	UNP P42336
A	-5	GLN	-	expression tag	UNP P42336
A	-4	GLY	-	expression tag	UNP P42336
A	-3	ALA	-	expression tag	UNP P42336
A	-2	MET	-	expression tag	UNP P42336

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P42336
A	99	GLU	-	insertion	UNP P42336
A	100	ASN	-	insertion	UNP P42336
A	101	LEU	-	insertion	UNP P42336
A	102	TYR	-	insertion	UNP P42336
A	103	PHE	-	insertion	UNP P42336
A	104	GLN	-	insertion	UNP P42336
A	105	GLY	-	insertion	UNP P42336

- Molecule 2 is N 2 -{(4S,11aP)-2-[(4S)-4-(difluoromethyl)-2-oxo-1,3-oxazolidin-3-yl]-5,6-dihydroimidazo[1,2-d][1,4]benzoxazepin-9-yl}-L-alaninamide (CCD ID: X3N) (formula: C₁₈H₁₉F₂N₅O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	
			31	18	2	2	5	4	0

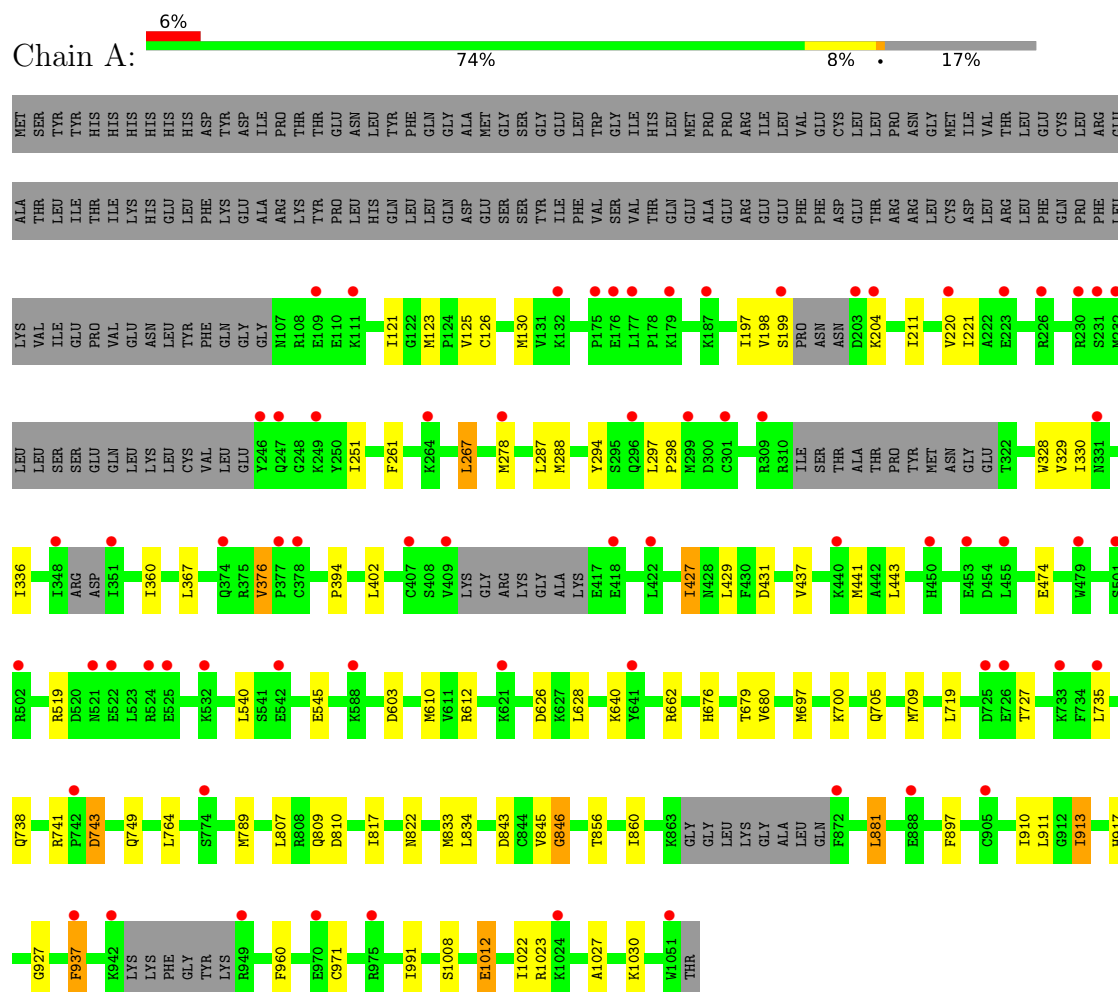
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O		
			71	71	0	0

3 Residue-property plots

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	58.72Å 133.72Å 141.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.63 – 2.48 48.63 – 2.48	Depositor EDS
% Data completeness (in resolution range)	92.9 (48.63-2.48) 93.4 (48.63-2.48)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 2.48Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.205 , 0.258 0.207 , 0.267	Depositor DCC
R_{free} test set	943 reflections (2.51%)	wwPDB-VP
Wilson B-factor (Å ²)	48.3	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.2	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	0.94	EDS
Total number of atoms	7450	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% 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: X3N

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	0.84	0/7513	1.28	17/10144 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	376	VAL	CB-CA-C	6.69	115.89	109.33
1	A	743	ASP	CA-CB-CG	6.46	119.06	112.60
1	A	937	PHE	CA-CB-CG	6.19	119.99	113.80
1	A	603	ASP	CA-CB-CG	6.17	118.77	112.60
1	A	917	HIS	CA-C-N	5.74	128.76	120.38
1	A	917	HIS	C-N-CA	5.74	128.76	120.38
1	A	626	ASP	CA-CB-CG	5.70	118.30	112.60
1	A	610	MET	CA-C-N	5.64	127.78	120.56
1	A	610	MET	C-N-CA	5.64	127.78	120.56
1	A	519	ARG	CA-C-N	5.46	129.87	121.19
1	A	519	ARG	C-N-CA	5.46	129.87	121.19
1	A	846	GLY	N-CA-C	5.41	118.48	110.42
1	A	261	PHE	CA-CB-CG	5.39	119.19	113.80
1	A	1008	SER	N-CA-C	-5.19	101.97	109.59
1	A	431	ASP	CA-CB-CG	5.07	117.67	112.60
1	A	612	ARG	CA-C-N	5.03	125.56	119.98
1	A	612	ARG	C-N-CA	5.03	125.56	119.98

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	7348	0	7325	34	0
2	A	29	2	0	0	0
3	A	71	0	0	1	0
All	All	7448	2	7325	34	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.

All (34) 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:719:LEU:HD11	1:A:735:LEU:HD13	1.74	0.70
1:A:540:LEU:HB2	1:A:1023:ARG:HD2	1.74	0.69
1:A:298:PRO:HG2	1:A:697:MET:HE2	1.79	0.64
1:A:807:LEU:HD12	1:A:846:GLY:HA3	1.80	0.62
1:A:328:TRP:HA	1:A:394:PRO:HB3	1.82	0.61
1:A:881:LEU:HD21	1:A:927:GLY:HA2	1.85	0.59
1:A:640:LYS:HE2	1:A:680:VAL:HG11	1.89	0.55
1:A:662:ARG:HD3	3:A:1208:HOH:O	2.12	0.49
1:A:204:LYS:HD3	1:A:789:MET:HE3	1.95	0.49
1:A:360:ILE:HG22	1:A:367:LEU:HD12	1.94	0.49
1:A:126:CYS:O	1:A:130:MET:HG2	2.13	0.48
1:A:294:TYR:HA	1:A:297:LEU:HD12	1.96	0.47
1:A:911:LEU:HB2	1:A:913:ILE:HD12	1.97	0.46
1:A:738:GLN:HE22	1:A:741:ARG:HH11	1.62	0.46
1:A:211:ILE:HD13	1:A:220:VAL:HG22	1.98	0.46
1:A:1027:ALA:HB1	1:A:1030:LYS:HD2	1.96	0.45
1:A:676:HIS:CG	1:A:843:ASP:HB2	2.51	0.45
1:A:705:GLN:O	1:A:709:MET:HG2	2.17	0.45
1:A:749:GLN:HG2	1:A:764:LEU:H	1.81	0.45
1:A:881:LEU:HD23	1:A:881:LEU:HA	1.86	0.44
1:A:221:ILE:HG23	1:A:287:LEU:HD11	2.00	0.44
1:A:298:PRO:HB2	1:A:697:MET:HG3	2.00	0.44
1:A:910:ILE:HD13	1:A:991:ILE:HG21	1.98	0.43
1:A:897:PHE:HZ	1:A:960:PHE:HD1	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ILE:HG22	1:A:123:MET:HG2	2.00	0.43
1:A:856:THR:O	1:A:860:ILE:HG12	2.19	0.43
1:A:697:MET:SD	1:A:700:LYS:HD2	2.59	0.42
1:A:817:ILE:HG23	1:A:833:MET:HE3	2.01	0.42
1:A:427:ILE:HD12	1:A:443:LEU:HD22	2.02	0.42
1:A:336:ILE:HD13	1:A:402:LEU:HD22	2.02	0.41
1:A:429:LEU:O	1:A:437:VAL:HG23	2.20	0.41
1:A:809:GLN:HE22	1:A:1012:GLU:CG	2.34	0.41
1:A:809:GLN:HE22	1:A:1012:GLU:HG3	1.84	0.41
1:A:220:VAL:HG21	1:A:267:LEU:HD13	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	882/1080 (82%)	850 (96%)	32 (4%)	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	A	822/983 (84%)	793 (96%)	29 (4%)	32	55

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	VAL
1	A	197	ILE
1	A	198	VAL
1	A	199	SER
1	A	251	ILE
1	A	267	LEU
1	A	278	MET
1	A	288	MET
1	A	329	VAL
1	A	330	ILE
1	A	376	VAL
1	A	427	ILE
1	A	441	MET
1	A	474	GLU
1	A	545	GLU
1	A	628	LEU
1	A	679	THR
1	A	727	THR
1	A	743	ASP
1	A	810	ASP
1	A	822	ASN
1	A	834	LEU
1	A	845	VAL
1	A	881	LEU
1	A	913	ILE
1	A	937	PHE
1	A	971	CYS
1	A	1012	GLU
1	A	1022	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	189	GLN
1	A	384	ASN
1	A	556	HIS
1	A	661	GLN
1	A	676	HIS
1	A	738	GLN
1	A	763	ASN
1	A	918	ASN

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Mol	Chain	Res	Type
1	A	994	HIS

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	X3N	A	1101	-	30,32,32	1.33	3 (10%)	36,47,47	2.74	11 (30%)

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	X3N	A	1101	-	-	1/13/39/39	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	X3N	C18-N17	3.95	1.39	1.36
2	A	1101	X3N	C27-N22	-2.34	1.35	1.39
2	A	1101	X3N	F30-C29	2.29	1.41	1.36

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	X3N	C21-C20-N19	-9.46	106.57	112.77
2	A	1101	X3N	C20-N22-C27	5.79	130.00	122.95
2	A	1101	X3N	O26-C27-N22	5.32	113.15	108.78
2	A	1101	X3N	C25-C23-N22	5.10	104.37	100.09
2	A	1101	X3N	N17-C18-N19	-4.34	106.12	111.67
2	A	1101	X3N	C20-C21-N17	3.99	107.58	104.39
2	A	1101	X3N	F31-C29-F30	3.25	111.80	105.53
2	A	1101	X3N	C15-O14-C12	3.21	121.45	116.13
2	A	1101	X3N	C23-N22-C27	-3.13	107.44	111.03
2	A	1101	X3N	O26-C25-C23	-2.79	102.48	105.63
2	A	1101	X3N	O28-C27-N22	-2.66	125.63	128.62

There are no chirality outliers.

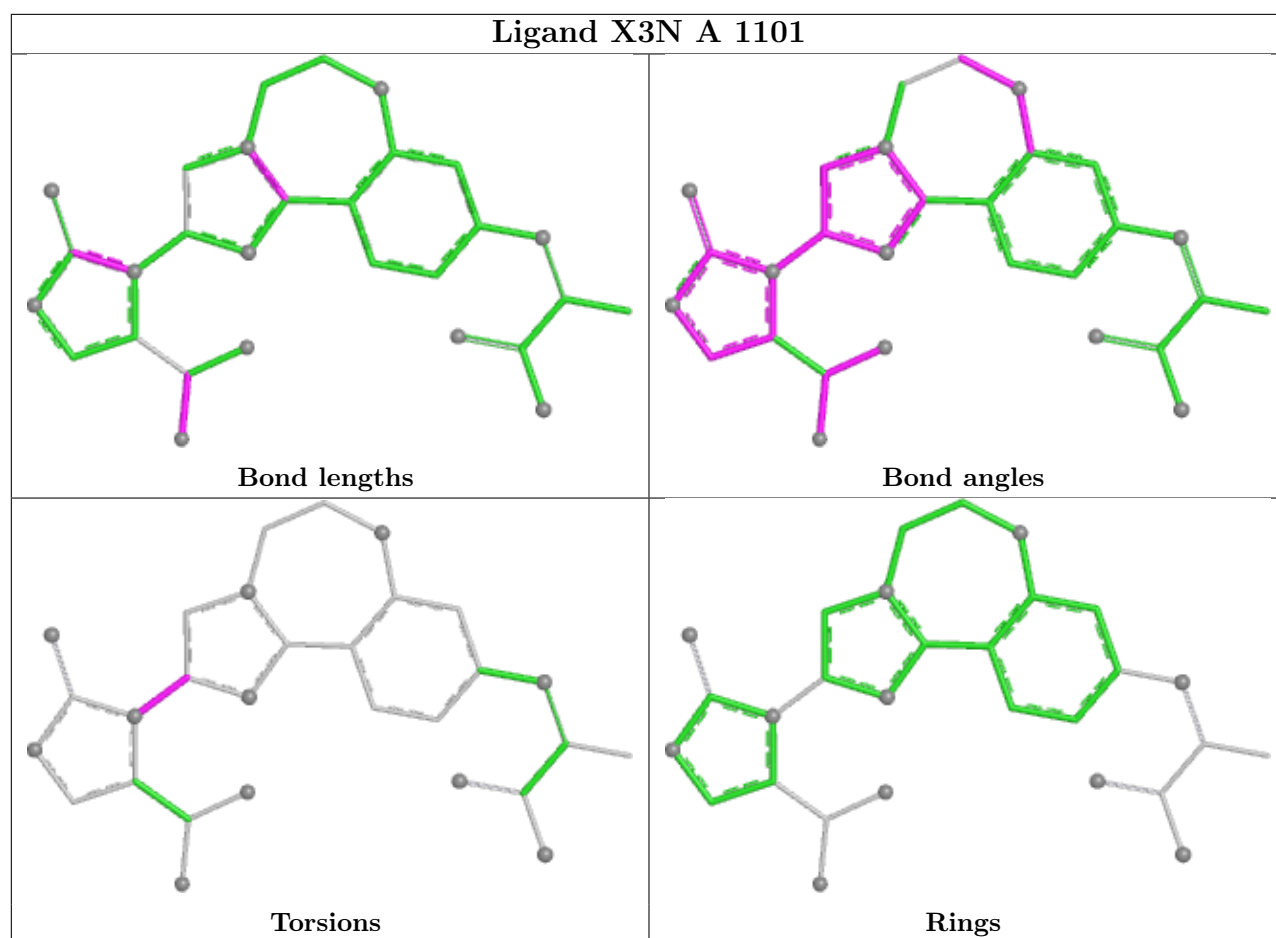
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	X3N	N19-C20-N22-C23

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	895/1080 (82%)	0.57	68 (7%)	20 17	20, 55, 92, 132	40 (4%)

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	TYR	12.2
1	A	348	ILE	9.4
1	A	524	ARG	7.8
1	A	230	ARG	7.7
1	A	179	LYS	6.7
1	A	203	ASP	6.6
1	A	176	GLU	6.6
1	A	888	GLU	6.5
1	A	450	HIS	6.4
1	A	226	ARG	6.2
1	A	309	ARG	6.1
1	A	187	LYS	6.0
1	A	247	GLN	5.8
1	A	109	GLU	5.6
1	A	975	ARG	5.6
1	A	249	LYS	5.3
1	A	522	GLU	5.1
1	A	132	LYS	5.1
1	A	374	GLN	5.0
1	A	970	GLU	4.9
1	A	521	ASN	4.8
1	A	278	MET	4.7
1	A	733	LYS	4.6
1	A	199	SER	4.6
1	A	220	VAL	4.4
1	A	453	GLU	4.3
1	A	725	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	621	LYS	4.3
1	A	111	LYS	4.2
1	A	525	GLU	3.9
1	A	455	LEU	3.5
1	A	440	LYS	3.5
1	A	532	LYS	3.4
1	A	231	SER	3.4
1	A	378	CYS	3.2
1	A	409	VAL	3.1
1	A	479	TRP	3.1
1	A	726	GLU	3.0
1	A	264	LYS	2.9
1	A	542	GLU	2.8
1	A	204	LYS	2.8
1	A	641	TYR	2.8
1	A	418	GLU	2.8
1	A	177	LEU	2.7
1	A	942	LYS	2.7
1	A	502	ARG	2.7
1	A	588	LYS	2.6
1	A	232	MET	2.6
1	A	331	ASN	2.5
1	A	1024	LYS	2.5
1	A	774	SER	2.5
1	A	905	CYS	2.4
1	A	175	PRO	2.4
1	A	223	GLU	2.4
1	A	872	PHE	2.4
1	A	377	PRO	2.3
1	A	351	ILE	2.3
1	A	735	LEU	2.3
1	A	742	PRO	2.3
1	A	501	SER	2.3
1	A	407	CYS	2.3
1	A	299	MET	2.2
1	A	937	PHE	2.2
1	A	301	CYS	2.2
1	A	1051	TRP	2.2
1	A	296	GLN	2.1
1	A	422	LEU	2.0
1	A	949	ARG	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](#)

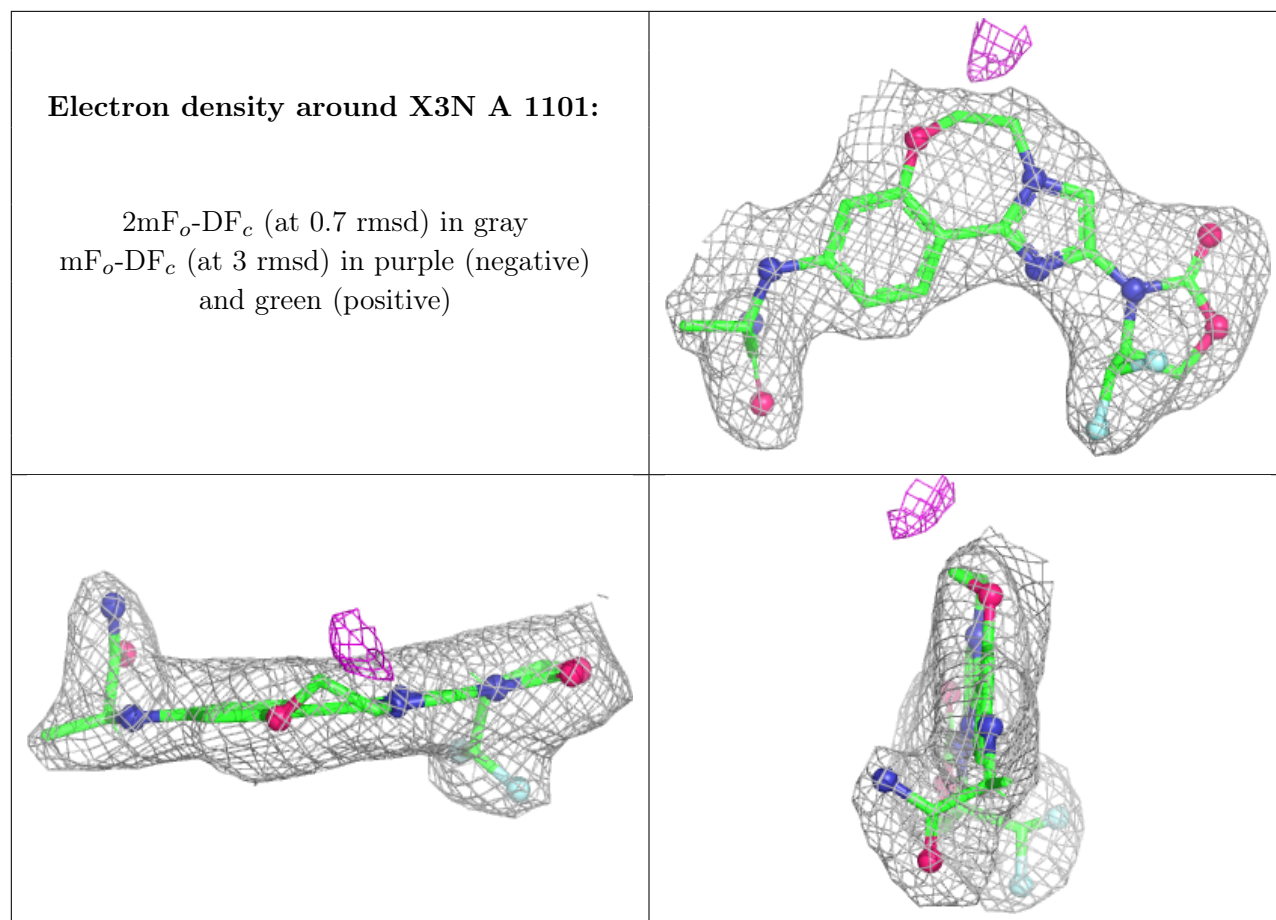
There are no oligosaccharides in this entry.

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	X3N	A	1101	29/29	0.95	0.07	36,42,54,59	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.