



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 04:13 AM EDT

PDB ID : 7MLK
Title : Crystal structure of human PI3Ka (p110a subunit) with MMV085400 bound to the active site determined at 2.9 angstroms resolution
Authors : Krake, S.H.; Martinez, P.D.G.; Poggi, M.L.; Ferreira, M.S.; Aguiar, A.C.C.; Souza, G.E.; Wenlock, M.; Jones, B.; Steinbrecher, T.; Day, T.; McPhail, J.; Burke, J.; Yeo, T.; Mok, S.; Uhlemann, A.C.; Fidock, D.A.; Chen, P.; Grodsky, N.; Deng, Y.L.; Guido, R.V.C.; Campbell, S.F.; Willis, P.A.; Dias, L.C.
Deposited on : 2021-04-28
Resolution : 2.91 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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)

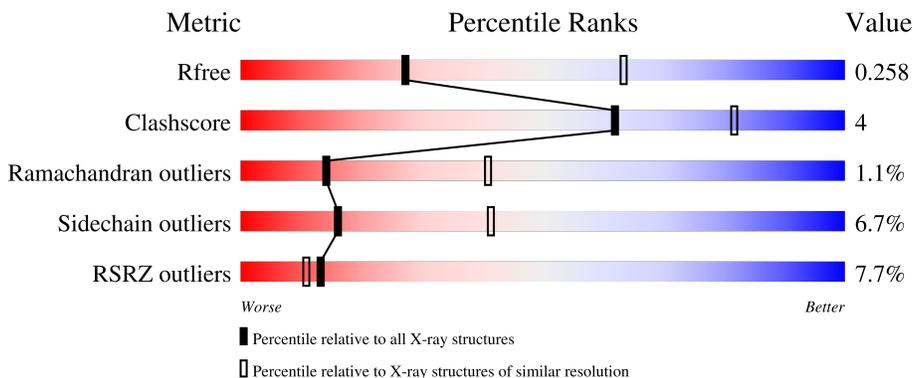
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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	968	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.35.1

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7270 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 subunit alpha isoform.

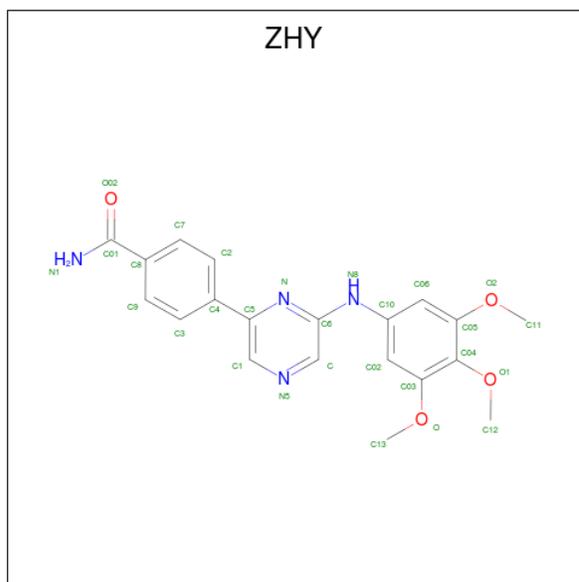
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	888	7242	4627	1244	1310	61	0	1	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	MET	-	initiating methionine	UNP P42336
A	82	ALA	-	expression tag	UNP P42336
A	83	SER	-	expression tag	UNP P42336
A	84	HIS	-	expression tag	UNP P42336
A	85	HIS	-	expression tag	UNP P42336
A	86	HIS	-	expression tag	UNP P42336
A	87	HIS	-	expression tag	UNP P42336
A	88	HIS	-	expression tag	UNP P42336
A	89	HIS	-	expression tag	UNP P42336
A	90	ASP	-	expression tag	UNP P42336
A	91	TYR	-	expression tag	UNP P42336
A	92	ASP	-	expression tag	UNP P42336
A	93	GLY	-	expression tag	UNP P42336
A	94	ALA	-	expression tag	UNP P42336
A	95	THR	-	expression tag	UNP P42336
A	96	THR	-	expression tag	UNP P42336
A	97	GLU	-	expression tag	UNP P42336
A	98	ASN	-	expression tag	UNP P42336
A	99	LEU	-	expression tag	UNP P42336
A	100	TYR	-	expression tag	UNP P42336
A	101	PHE	-	expression tag	UNP P42336
A	102	GLN	-	expression tag	UNP P42336
A	103	GLY	-	expression tag	UNP P42336
A	104	SER	-	expression tag	UNP P42336

- Molecule 2 is 4-[6-(3,4,5-trimethoxyanilino)pyrazin-2-yl]benzamide (three-letter code: ZHY)

(formula: C₂₀H₂₀N₄O₄) (labeled as "Ligand of Interest" by depositor).

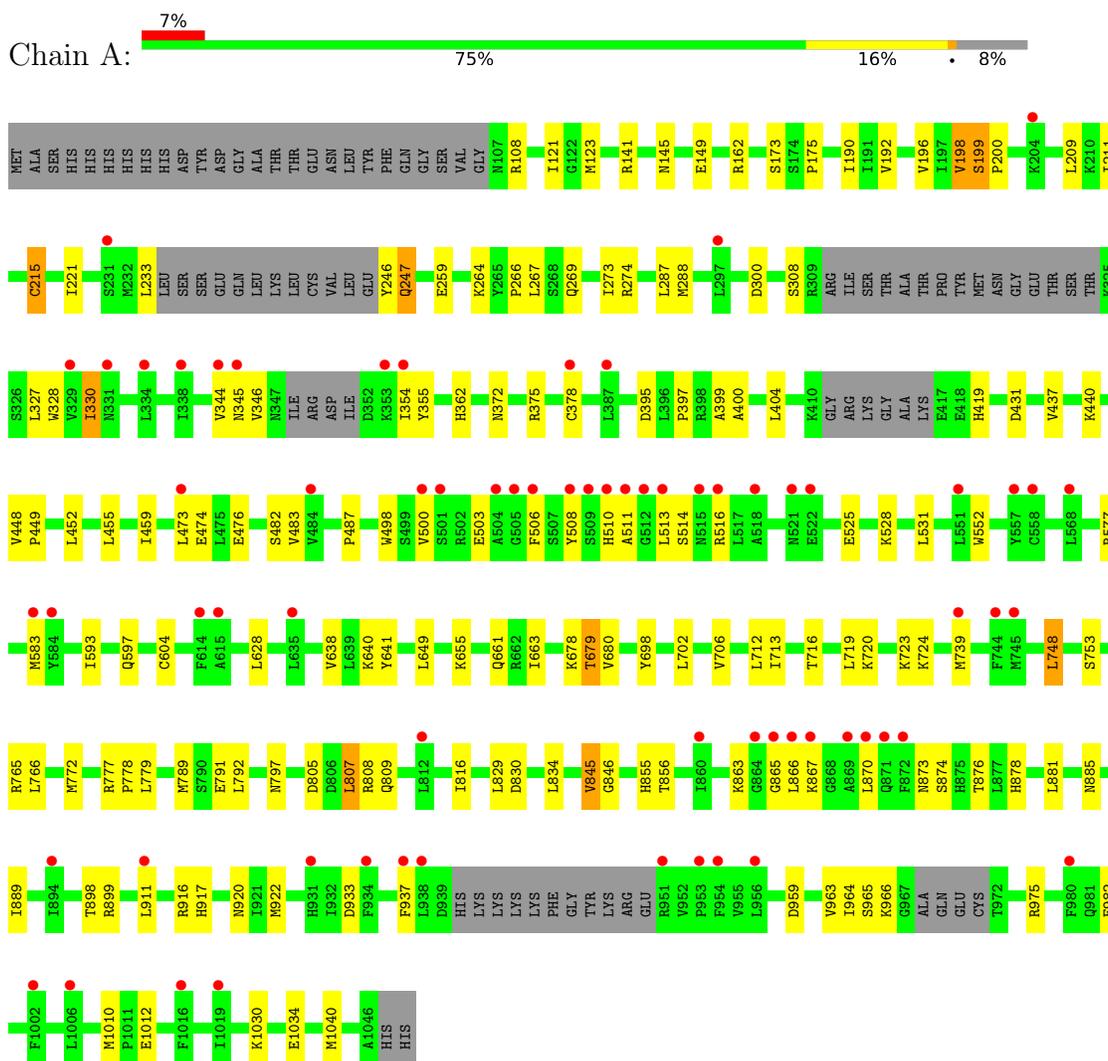


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	28	20	4	4	0	0

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	58.85Å 134.79Å 141.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	97.75 – 2.91 97.75 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.1 (97.75-2.91) 99.4 (97.75-2.91)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.91Å)	Xtrriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.205 , 0.242 0.221 , 0.258	Depositor DCC
R_{free} test set	1281 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	88.1	Xtrriage
Anisotropy	0.548	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 78.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.020 for -h,l,k	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7270	wwPDB-VP
Average B, all atoms (Å ²)	105.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.47	0/7403	0.66	0/10001

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	7242	0	7230	64	0
2	A	28	0	0	0	0
All	All	7270	0	7230	64	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 (64) 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:878:HIS:HD2	1:A:963:VAL:HA	1.47	0.80
1:A:898:THR:HG22	1:A:964:ILE:HG12	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:SER:HB2	1:A:200:PRO:HD2	1.68	0.74
1:A:149:GLU:HB3	1:A:655:LYS:HE3	1.73	0.69
1:A:1030:LYS:HB3	1:A:1034:GLU:HB3	1.74	0.69
1:A:679:THR:HG22	1:A:680:VAL:HG13	1.83	0.61
1:A:772:MET:HB2	1:A:778:PRO:HD2	1.84	0.59
1:A:354:ILE:HG12	1:A:378:CYS:HB3	1.85	0.59
1:A:878:HIS:CD2	1:A:963:VAL:HA	2.36	0.57
1:A:867:LYS:HE3	1:A:873:ASN:H	1.71	0.56
1:A:789:MET:HB3	1:A:792:LEU:HD12	1.88	0.56
1:A:809:GLN:HG3	1:A:937:PHE:CE2	2.41	0.55
1:A:330:ILE:H	1:A:330:ILE:HD12	1.73	0.54
1:A:807:LEU:HD13	1:A:846:GLY:HA3	1.90	0.54
1:A:199:SER:CB	1:A:200:PRO:HD2	2.36	0.53
1:A:449:PRO:HD2	1:A:452:LEU:HD13	1.91	0.52
1:A:712:LEU:HD21	1:A:748:LEU:HD21	1.91	0.52
1:A:196:VAL:HG12	1:A:198:VAL:HG22	1.91	0.52
1:A:661:GLN:NE2	1:A:698:TYR:HB2	2.25	0.51
1:A:190:ILE:HG12	1:A:192:VAL:HG23	1.92	0.51
1:A:716:THR:O	1:A:720:LYS:HG2	2.10	0.51
1:A:917:HIS:H	1:A:920:ASN:HB2	1.75	0.51
1:A:440:LYS:HG2	1:A:476:GLU:HG3	1.91	0.51
1:A:816:ILE:HG21	1:A:911:LEU:HD21	1.94	0.50
1:A:211:ILE:HG12	1:A:215:CYS:SG	2.52	0.50
1:A:506:PHE:HA	1:A:510:HIS:HB3	1.93	0.49
1:A:267:LEU:HG	1:A:273:ILE:HG13	1.95	0.49
1:A:638:VAL:HG23	1:A:649:LEU:HD21	1.94	0.49
1:A:404:LEU:HD13	1:A:473:LEU:HD23	1.95	0.48
1:A:514:SER:C	1:A:516:ARG:H	2.17	0.48
1:A:516:ARG:HB3	1:A:552:TRP:CD1	2.49	0.48
1:A:713:ILE:HG12	1:A:845:VAL:HG11	1.95	0.47
1:A:199:SER:HB2	1:A:200:PRO:CD	2.41	0.47
1:A:525:GLU:HA	1:A:528:LYS:HB2	1.97	0.47
1:A:516:ARG:HB3	1:A:552:TRP:HD1	1.79	0.47
1:A:628:LEU:HD23	1:A:663:ILE:HD13	1.95	0.47
1:A:175:PRO:HA	1:A:274:ARG:HH22	1.82	0.45
1:A:362:HIS:CE1	1:A:399:ALA:HB3	2.52	0.45
1:A:355:TYR:HE2	1:A:372:ASN:HD22	1.65	0.45
1:A:141:ARG:HG2	1:A:308:SER:HA	1.99	0.44
1:A:528:LYS:HA	1:A:531:LEU:HD12	1.99	0.44
1:A:498:TRP:C	1:A:500:VAL:H	2.21	0.43
1:A:885:ASN:HB3	1:A:889:ILE:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:808:ARG:HB3	1:A:1010:MET:HE2	1.99	0.43
1:A:344:VAL:HG12	1:A:378:CYS:HB2	2.01	0.43
1:A:640:LYS:HE2	1:A:680:VAL:HG11	2.01	0.42
1:A:638:VAL:HA	1:A:641:TYR:CD2	2.54	0.42
1:A:856:THR:HA	1:A:922:MET:HG2	2.01	0.42
1:A:266:PRO:HG2	1:A:269:GLN:HB2	2.02	0.42
1:A:221:ILE:HG23	1:A:287:LEU:HD11	2.02	0.42
1:A:419:HIS:HB3	1:A:455:LEU:HD21	2.01	0.41
1:A:830:ASP:HB3	1:A:899:ARG:NH1	2.35	0.41
1:A:552:TRP:HZ3	1:A:583:MET:HE2	1.86	0.41
1:A:916:ARG:HA	1:A:920:ASN:HD22	1.86	0.41
1:A:397:PRO:HD2	1:A:400:ALA:HB2	2.03	0.41
1:A:506:PHE:HA	1:A:510:HIS:CB	2.51	0.41
1:A:593:ILE:HD12	1:A:597:GLN:HB2	2.03	0.41
1:A:162:ARG:HH12	1:A:300:ASP:H	1.69	0.41
1:A:395:ASP:HA	1:A:577:ARG:HB3	2.03	0.41
1:A:863:LYS:HE3	1:A:876:THR:HG23	2.03	0.40
1:A:327:LEU:HD22	1:A:487:PRO:HA	2.04	0.40
1:A:702:LEU:O	1:A:706:VAL:HG23	2.21	0.40
1:A:121:ILE:HG22	1:A:123:MET:HG2	2.03	0.40
1:A:199:SER:CB	1:A:200:PRO:CD	2.99	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	875/968 (90%)	806 (92%)	59 (7%)	10 (1%)	14 41

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	511	ALA
1	A	199	SER
1	A	264	LYS
1	A	346	VAL
1	A	933	ASP
1	A	966	LYS
1	A	865	GLY
1	A	247	GLN
1	A	330	ILE
1	A	482	SER

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	807/879 (92%)	753 (93%)	54 (7%)	16 41

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	ARG
1	A	145	ASN
1	A	173	SER
1	A	198	VAL
1	A	209	LEU
1	A	215	CYS
1	A	233	LEU
1	A	246	TYR
1	A	247	GLN
1	A	259	GLU
1	A	288	MET
1	A	328	TRP
1	A	345	ASN
1	A	375	ARG
1	A	431	ASP
1	A	437	VAL
1	A	448	VAL

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Mol	Chain	Res	Type
1	A	459	ILE
1	A	474	GLU
1	A	483	VAL
1	A	503	GLU
1	A	508	TYR
1	A	513	LEU
1	A	604	CYS
1	A	678	LYS
1	A	679	THR
1	A	719	LEU
1	A	723	LYS
1	A	724	LYS
1	A	739	MET
1	A	748	LEU
1	A	753	SER
1	A	765	ARG
1	A	766	LEU
1	A	777	ARG
1	A	779	LEU
1	A	791	GLU
1	A	797	ASN
1	A	805	ASP
1	A	807	LEU
1	A	829	LEU
1	A	834	LEU
1	A	845	VAL
1	A	855	HIS
1	A	866	LEU
1	A	870	LEU
1	A	874	SER
1	A	881	LEU
1	A	959	ASP
1	A	965	SER
1	A	975	ARG
1	A	982	GLU
1	A	1012	GLU
1	A	1040	MET

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	213	HIS

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Mol	Chain	Res	Type
1	A	370	ASN
1	A	372	ASN
1	A	419	HIS
1	A	630	GLN
1	A	701	HIS
1	A	759	HIS
1	A	796	ASN
1	A	822	ASN
1	A	827	GLN
1	A	871	GLN
1	A	920	ASN
1	A	981	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	ZHY	A	1101	-	30,30,30	0.26	0	41,41,41	0.58	1 (2%)

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	ZHY	A	1101	-	-	0/18/18/18	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	ZHY	C-C6-N	-2.30	120.68	121.94

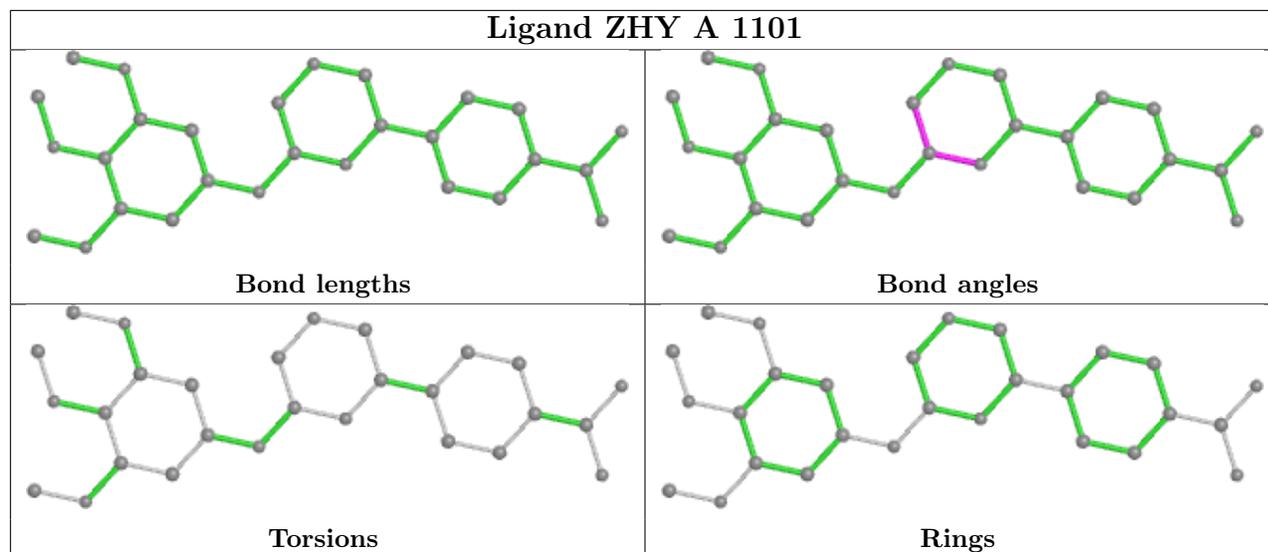
There are no chirality outliers.

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, 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	888/968 (91%)	0.62	68 (7%) 13 11	57, 100, 158, 203	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	953	PRO	9.2
1	A	504	ALA	9.2
1	A	510	HIS	9.1
1	A	511	ALA	9.0
1	A	512	GLY	8.7
1	A	513	LEU	7.4
1	A	509	SER	7.0
1	A	505	GLY	6.4
1	A	865	GLY	6.0
1	A	506	PHE	5.7
1	A	508	TYR	5.1
1	A	954	PHE	5.0
1	A	231	SER	4.9
1	A	864	GLY	4.9
1	A	501	SER	4.9
1	A	870	LEU	4.8
1	A	951	ARG	4.6
1	A	956	LEU	4.2
1	A	869	ALA	4.0
1	A	500	VAL	3.8
1	A	872	PHE	3.7
1	A	1016	PHE	3.6
1	A	518	ALA	3.5
1	A	1002	PHE	3.4
1	A	937	PHE	3.2
1	A	568	LEU	3.2
1	A	871	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	911	LEU	3.0
1	A	558	CYS	3.0
1	A	516	ARG	3.0
1	A	354	ILE	3.0
1	A	1019	ILE	2.9
1	A	584	TYR	2.8
1	A	557	TYR	2.8
1	A	980	PHE	2.7
1	A	521	ASN	2.6
1	A	860	ILE	2.6
1	A	938	LEU	2.6
1	A	867	LYS	2.5
1	A	522	GLU	2.5
1	A	484	VAL	2.5
1	A	551	LEU	2.5
1	A	635	LEU	2.5
1	A	344	VAL	2.5
1	A	331	ASN	2.5
1	A	745	MET	2.4
1	A	1006	LEU	2.4
1	A	345	ASN	2.3
1	A	387	LEU	2.3
1	A	515	ASN	2.3
1	A	353	LYS	2.3
1	A	739	MET	2.3
1	A	866	LEU	2.3
1	A	894	ILE	2.3
1	A	615	ALA	2.3
1	A	744	PHE	2.3
1	A	934	PHE	2.3
1	A	334	LEU	2.2
1	A	931	HIS	2.1
1	A	473	LEU	2.1
1	A	812	LEU	2.1
1	A	583	MET	2.1
1	A	378	CYS	2.1
1	A	329	VAL	2.1
1	A	204	LYS	2.1
1	A	338	ILE	2.0
1	A	614	PHE	2.0
1	A	297	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](#)

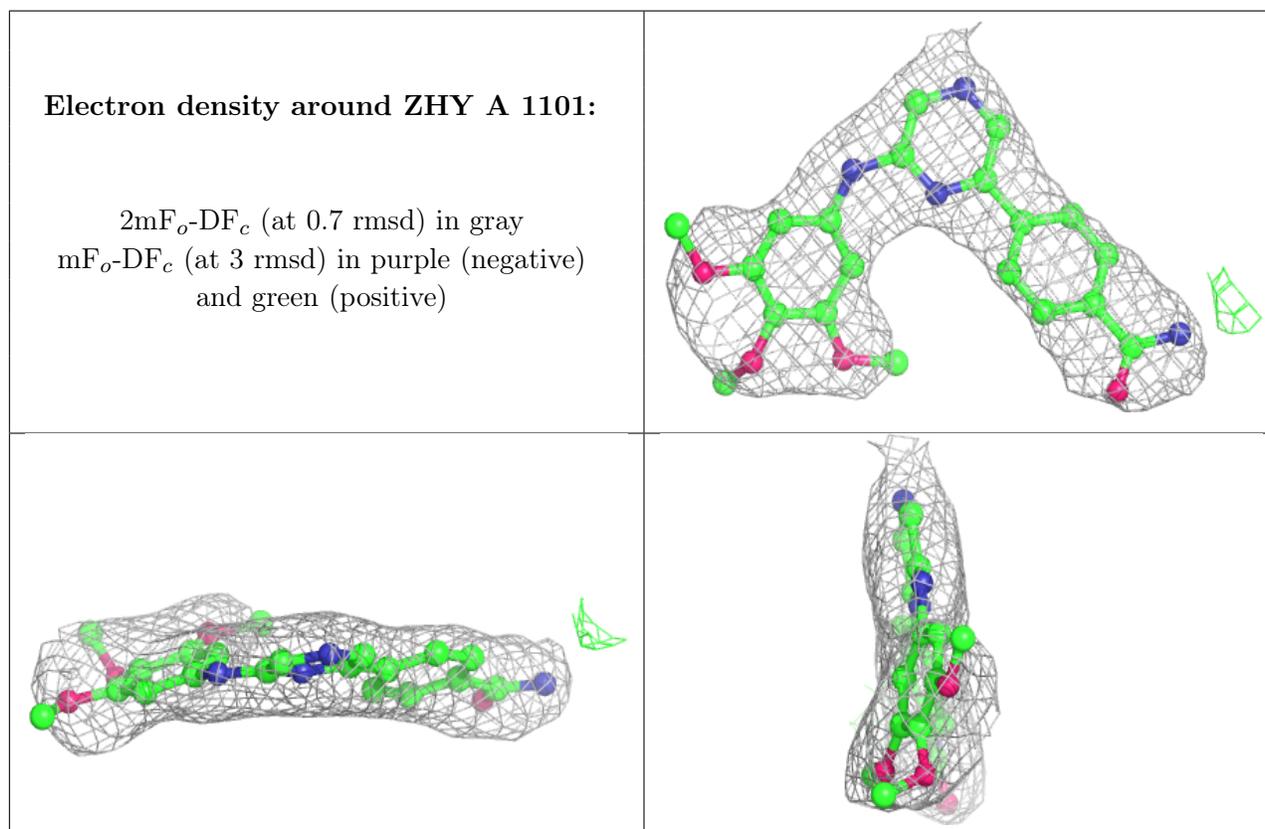
There are no monosaccharides in this entry.

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, 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(\AA^2)	Q<0.9
2	ZHY	A	1101	28/28	0.94	0.30	76,82,98,100	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.