



Full wwPDB EM Validation Report ⓘ

Aug 25, 2024 – 12:07 AM JST

PDB ID : 8Z1L
EMDB ID : EMD-39729
Title : Cryo-EM structure of human norepinephrine transporter NET in the presence of the antidepressant atomoxetine in an outward-open state at resolution of 3.4 angstrom.
Authors : Tan, J.; Xiao, Y.; Kong, F.; Lei, J.; Yuan, Y.; Yan, C.
Deposited on : 2024-04-11
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.38.2

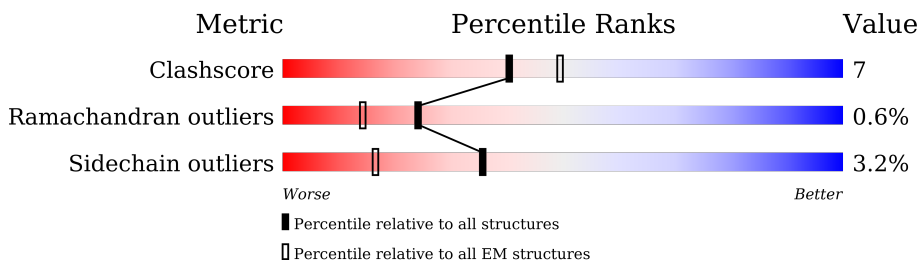
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	617	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8805 atoms, of which 4386 are hydrogens and 0 are deuteriums.

In the tables below, 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.

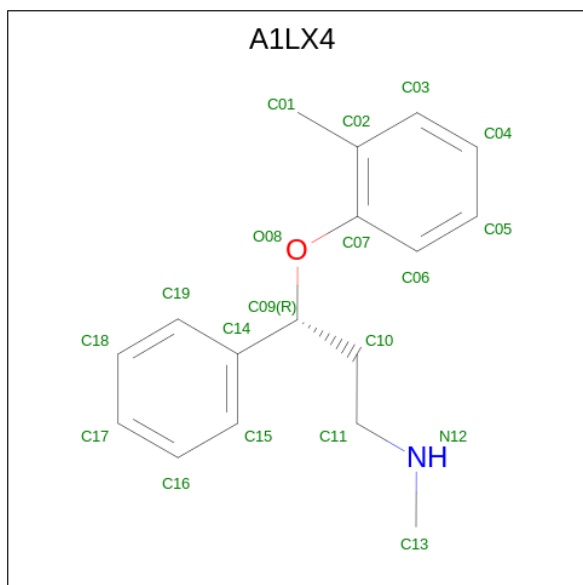
- Molecule 1 is a protein called Sodium-dependent noradrenaline transporter.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	549	8785	2955	4386	684	740	20	0	0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Cl	0
			1	1	

- Molecule 3 is (3R)-N-methyl-3-(2-methylphenoxy)-3-phenyl-propan-1-amine (three-letter code: A1LX4) (formula: C₁₇H₂₁NO) (labeled as "Ligand of Interest" by depositor).



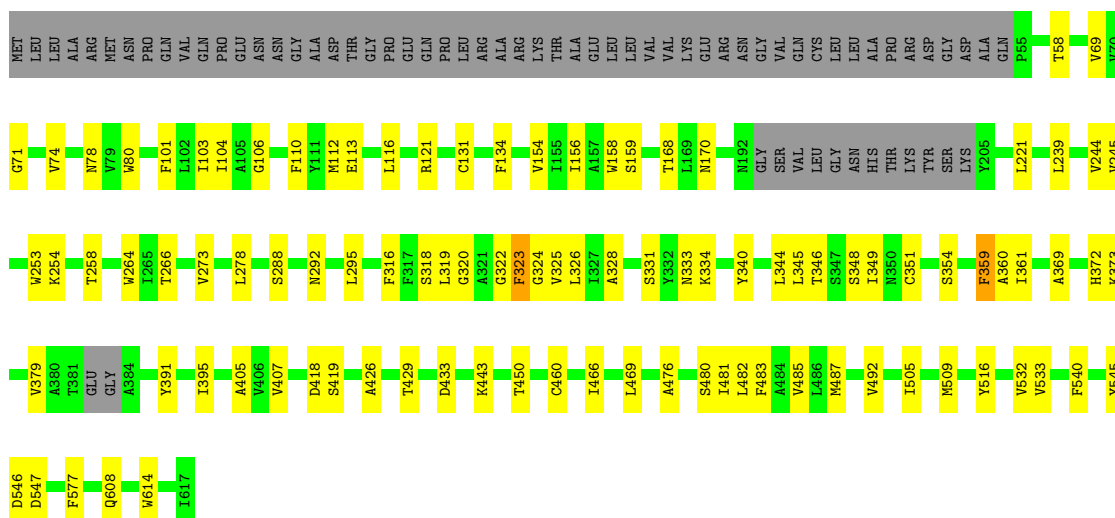
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	A	1	19	17	1	1	0

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. 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. 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: Sodium-dependent noradrenaline transporter

Chain A: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	197643	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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: CL, A1LX4

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	0.28	0/4542	0.46	0/6195

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	4399	4386	4385	60	0
2	A	1	0	0	0	0
3	A	19	0	0	0	0
All	All	4419	4386	4385	60	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 7.

All (60) 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:482:LEU:HD21	1:A:532:VAL:HG12	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:GLN:O	1:A:614:TRP:NE1	2.32	0.63
1:A:395:ILE:HD12	1:A:405:ALA:HB2	1.83	0.59
1:A:78:ASN:CG	1:A:354:SER:HG	2.07	0.58
1:A:476:ALA:O	1:A:480:SER:OG	2.21	0.58
1:A:482:LEU:HD23	1:A:533:VAL:HA	1.85	0.58
1:A:103:ILE:O	1:A:516:TYR:OH	2.22	0.56
1:A:278:LEU:HD13	1:A:360:ALA:HB2	1.89	0.55
1:A:316:PHE:CZ	1:A:485:VAL:HG21	2.42	0.55
1:A:322:GLY:O	1:A:324:GLY:N	2.40	0.54
1:A:121:ARG:NH2	1:A:333:ASN:O	2.39	0.53
1:A:361:ILE:HD13	1:A:391:TYR:OH	2.08	0.53
1:A:168:THR:OG1	1:A:170:ASN:O	2.23	0.52
1:A:316:PHE:HZ	1:A:485:VAL:HG21	1.75	0.51
1:A:110:PHE:CZ	1:A:326:LEU:HD11	2.46	0.51
1:A:113:GLU:OE2	1:A:322:GLY:HA2	2.11	0.50
1:A:69:VAL:HG12	1:A:346:THR:HG21	1.93	0.50
1:A:469:LEU:C	1:A:469:LEU:HD23	2.32	0.50
1:A:113:GLU:OE2	1:A:322:GLY:N	2.45	0.49
1:A:487:MET:HA	1:A:487:MET:CE	2.42	0.49
1:A:545:TYR:O	1:A:547:ASP:N	2.45	0.49
1:A:154:VAL:HG21	1:A:460:CYS:HB2	1.95	0.48
1:A:395:ILE:CD1	1:A:405:ALA:HB2	2.43	0.48
1:A:158:TRP:CH2	1:A:469:LEU:HD13	2.48	0.47
1:A:373:LYS:HA	1:A:373:LYS:HE2	1.96	0.47
1:A:322:GLY:O	1:A:323:PHE:C	2.53	0.46
1:A:116:LEU:HD11	1:A:492:VAL:HG21	1.97	0.46
1:A:273:VAL:HG13	1:A:407:VAL:HG12	1.98	0.46
1:A:369:ALA:HB2	1:A:379:VAL:HG11	1.97	0.46
1:A:106:GLY:HA3	1:A:319:LEU:HD12	1.97	0.46
1:A:323:PHE:HA	1:A:481:ILE:HD11	1.98	0.46
1:A:131:CYS:HG	1:A:134:PHE:HE1	1.64	0.45
1:A:273:VAL:HG22	1:A:407:VAL:HG13	1.97	0.45
1:A:323:PHE:CD2	1:A:481:ILE:CD1	2.99	0.45
1:A:156:ILE:HG21	1:A:244:VAL:HG21	1.99	0.45
1:A:288:SER:O	1:A:292:ASN:OD1	2.36	0.44
1:A:325:VAL:HA	1:A:426:ALA:HB2	1.99	0.44
1:A:372:HIS:O	1:A:372:HIS:ND1	2.51	0.44
1:A:254:LYS:HB2	1:A:258:THR:HG21	1.98	0.44
1:A:239:LEU:HD23	1:A:239:LEU:O	2.18	0.44
1:A:481:ILE:O	1:A:485:VAL:HG23	2.18	0.43
1:A:221:LEU:HD11	1:A:466:ILE:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:ILE:HG23	1:A:509:MET:CE	2.48	0.43
1:A:106:GLY:CA	1:A:319:LEU:HD12	2.49	0.43
1:A:328:ALA:HB1	1:A:429:THR:HG21	2.01	0.43
1:A:487:MET:HA	1:A:487:MET:HE2	2.02	0.42
1:A:112:MET:SD	1:A:492:VAL:HG11	2.59	0.42
1:A:113:GLU:OE2	1:A:322:GLY:CA	2.67	0.42
1:A:71:GLY:CA	1:A:418:ASP:OD2	2.67	0.42
1:A:266:THR:HG22	1:A:418:ASP:HB2	2.02	0.42
1:A:273:VAL:HG13	1:A:407:VAL:CG1	2.49	0.42
1:A:74:VAL:O	1:A:74:VAL:HG23	2.18	0.41
1:A:156:ILE:CG2	1:A:244:VAL:HG21	2.51	0.41
1:A:221:LEU:HD21	1:A:466:ILE:CG2	2.51	0.41
1:A:245:VAL:HG13	1:A:450:THR:HG23	2.03	0.41
1:A:295:LEU:HD11	1:A:359:PHE:HE1	1.85	0.41
1:A:340:TYR:CE1	1:A:344:LEU:HD11	2.56	0.41
1:A:101:PHE:HA	1:A:104:ILE:HG22	2.02	0.40
1:A:318:SER:O	1:A:320:GLY:N	2.54	0.40
1:A:345:LEU:O	1:A:349:ILE:HD12	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	543/617 (88%)	522 (96%)	18 (3%)	3 (1%)	22 50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	323	PHE
1	A	546	ASP
1	A	58	THR

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 PDB entries followed by that with respect to all EM entries.

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	464/519 (89%)	449 (97%)	15 (3%)	34 59

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	TRP
1	A	159	SER
1	A	253	TRP
1	A	264	TRP
1	A	331	SER
1	A	334	LYS
1	A	348	SER
1	A	351	CYS
1	A	359	PHE
1	A	419	SER
1	A	433	ASP
1	A	443	LYS
1	A	483	PHE
1	A	540	PHE
1	A	577	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	181	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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
3	A1LX4	A	702	-	20,20,20	4.16	13 (65%)	23,25,25	1.21	2 (8%)

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
3	A1LX4	A	702	-	-	3/12/12/12	0/2/2/2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	A1LX4	C15-C14	8.25	1.52	1.39
3	A	702	A1LX4	C18-C19	6.60	1.52	1.38
3	A	702	A1LX4	C03-C02	5.90	1.52	1.39
3	A	702	A1LX4	C06-C07	5.62	1.51	1.39
3	A	702	A1LX4	C05-C04	5.28	1.52	1.38
3	A	702	A1LX4	C16-C17	5.24	1.51	1.38
3	A	702	A1LX4	O08-C09	-4.89	1.40	1.44
3	A	702	A1LX4	C19-C14	-4.49	1.31	1.39
3	A	702	A1LX4	C07-C02	-4.34	1.30	1.39
3	A	702	A1LX4	C04-C03	-3.75	1.31	1.38
3	A	702	A1LX4	C05-C06	-3.52	1.31	1.38
3	A	702	A1LX4	C16-C15	-3.43	1.31	1.38
3	A	702	A1LX4	C18-C17	-2.64	1.31	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	A1LX4	O08-C09-C10	2.59	109.32	105.18
3	A	702	A1LX4	C10-C11-N12	-2.43	107.77	111.79

There are no chirality outliers.

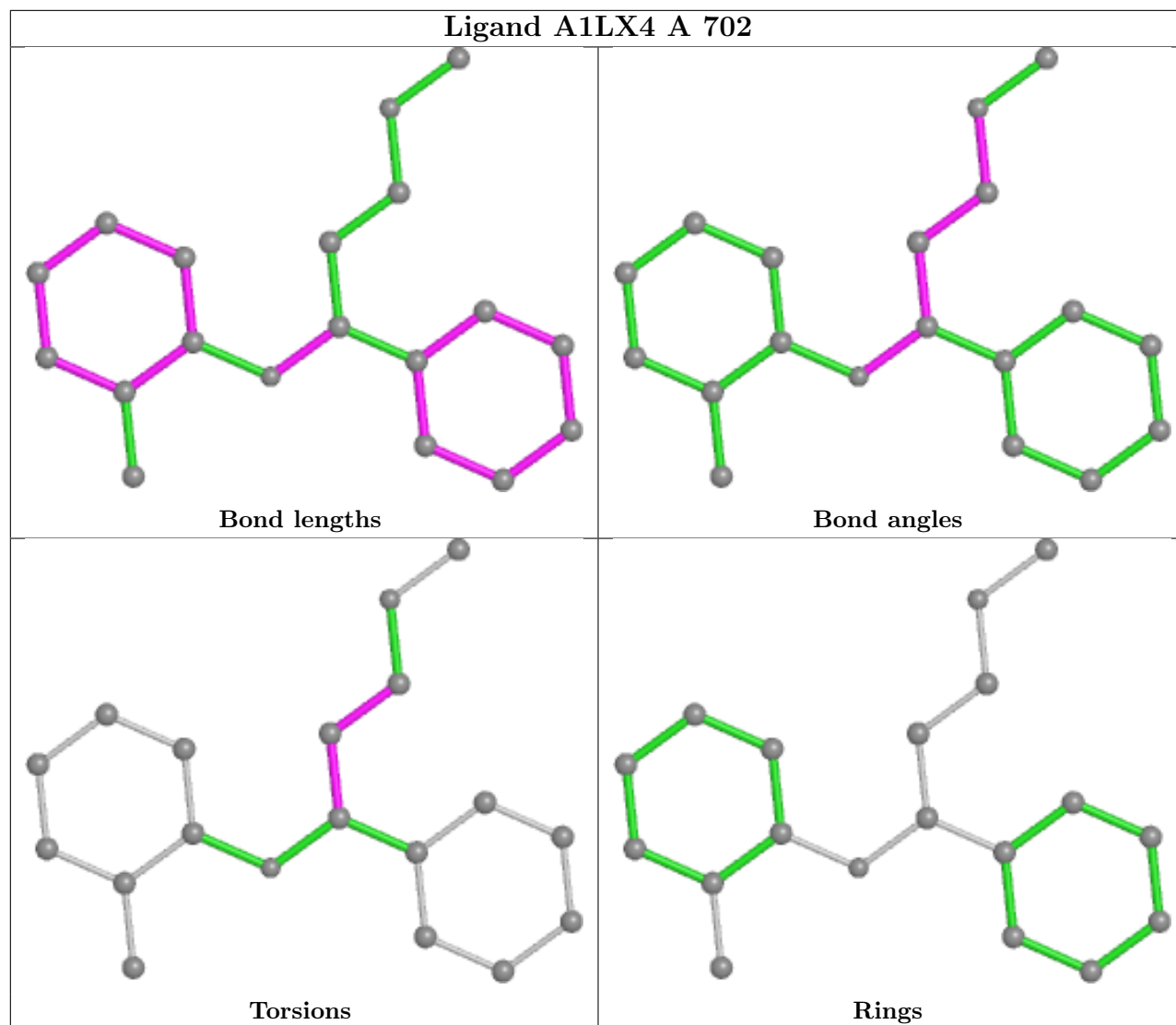
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	702	A1LX4	O08-C09-C10-C11
3	A	702	A1LX4	C14-C09-C10-C11
3	A	702	A1LX4	C09-C10-C11-N12

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.