



wwPDB EM Validation Summary Report ⓘ

Jun 28, 2026 – 12:45 AM JST

PDB ID : 9VXY / pdb_00009vxy
EMDB ID : EMD-65445
Title : Cryo-EM Structure of Nipah Virus Polymerase in complex with GL22
Authors : Xue, L.; Gui, J.; Chang, T.; Pan, H.; Xiong, X.
Deposited on : 2025-07-20
Resolution : 2.87 Å(reported)

This is a wwPDB EM Validation Summary 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	: 4-5-2 with Phenix2.0
Buster-report	: wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	: 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	: NOT EXECUTED
MapQ	: FAILED
Ideal geometry (proteins)	: Engh & Huber (2001)
Ideal geometry (DNA, RNA)	: Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: 2.49

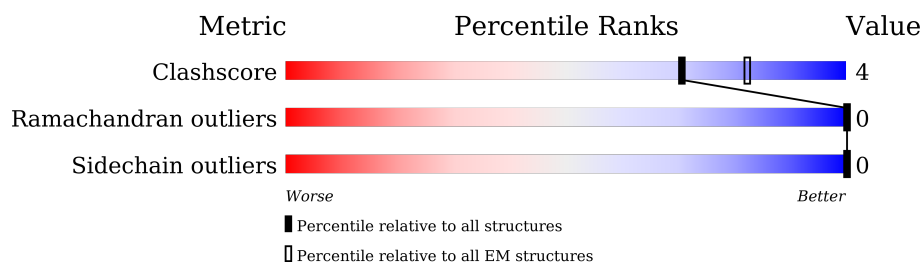
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.87 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	2244	
2	B	709	
2	C	709	
2	D	709	
2	E	709	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12815 atoms, of which 0 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1270	Total	C	N	O	S	0	0
			10226	6520	1749	1890	67		

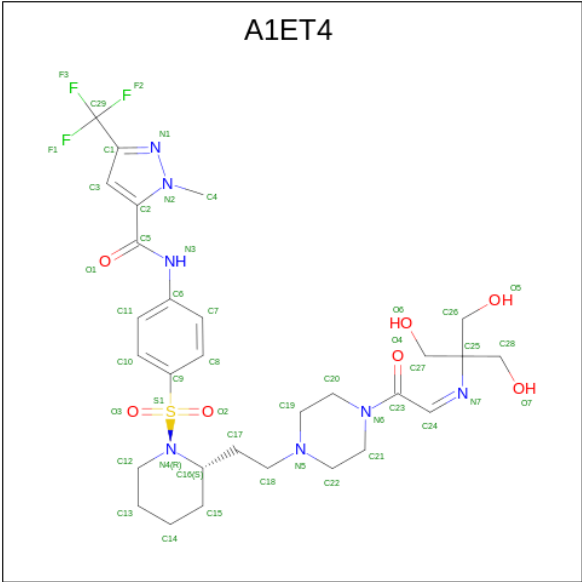
- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	148	Total	C	N	O	S	1	0
			1190	743	203	239	5		
2	C	51	Total	C	N	O	S	0	0
			404	256	69	75	4		
2	D	66	Total	C	N	O	S	0	0
			516	323	93	96	4		
2	E	55	Total	C	N	O	S	0	0
			430	272	75	79	4		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

- Molecule 4 is {N}-[4-[(2 {S})-2-[2-[4-[(2 {Z})-2-[2-(hydroxymethyl)-1,3-bis(oxidanyl)propa n-2-yl]iminoethanoyl]piperazin-1-yl]ethyl]piperidin-1-yl]sulfonylphenyl]-2-methyl-5-(trifluoro methyl)pyrazole-3-carboxamide (CCD ID: A1ET4) (formula: C₂₉H₄₀F₃N₇O₇S) (labeled as "Ligand of Interest" by depositor).

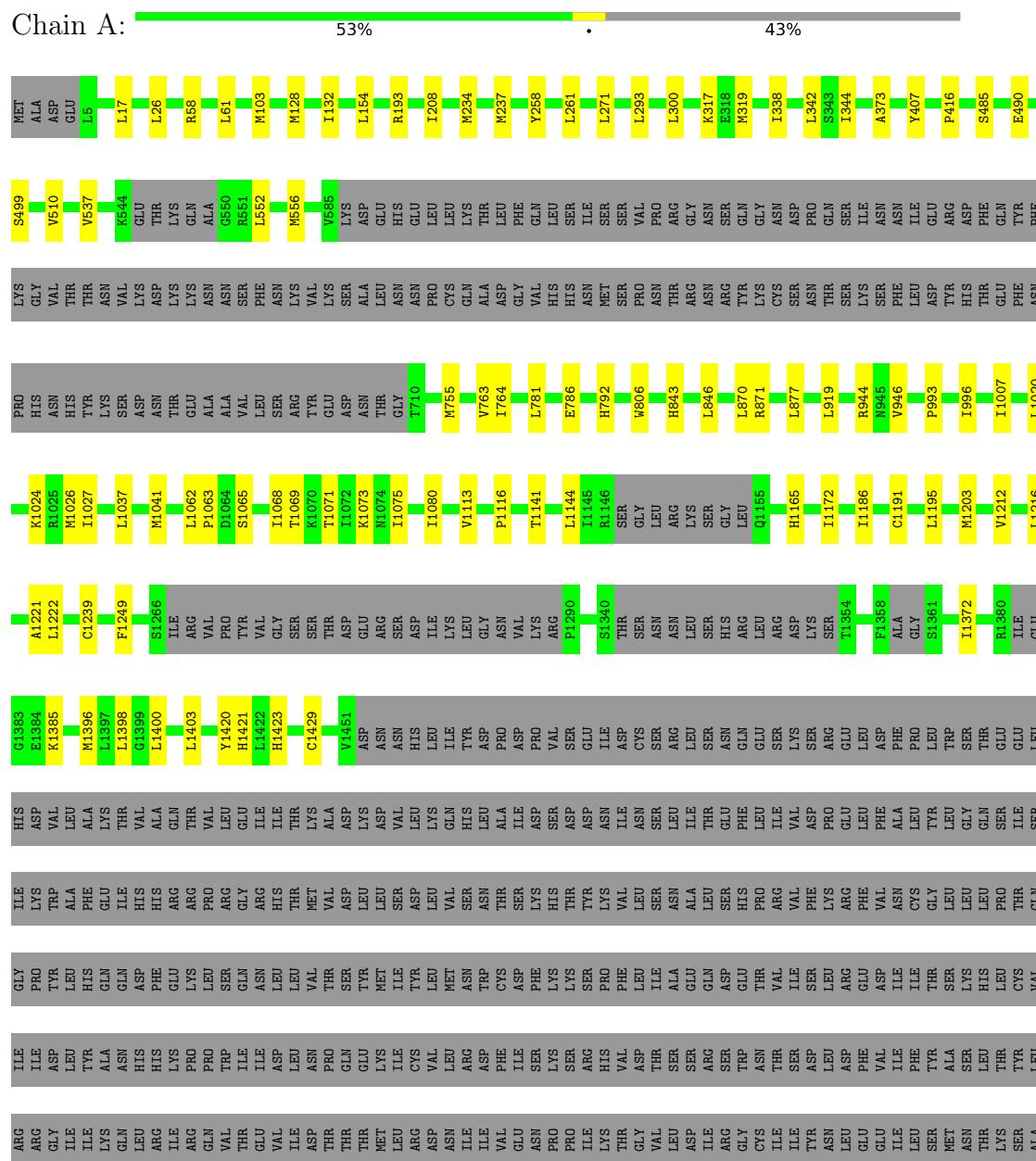


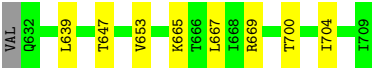
Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	N	O	S	
4	A	1	47	29	3	7	7	1	0

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.

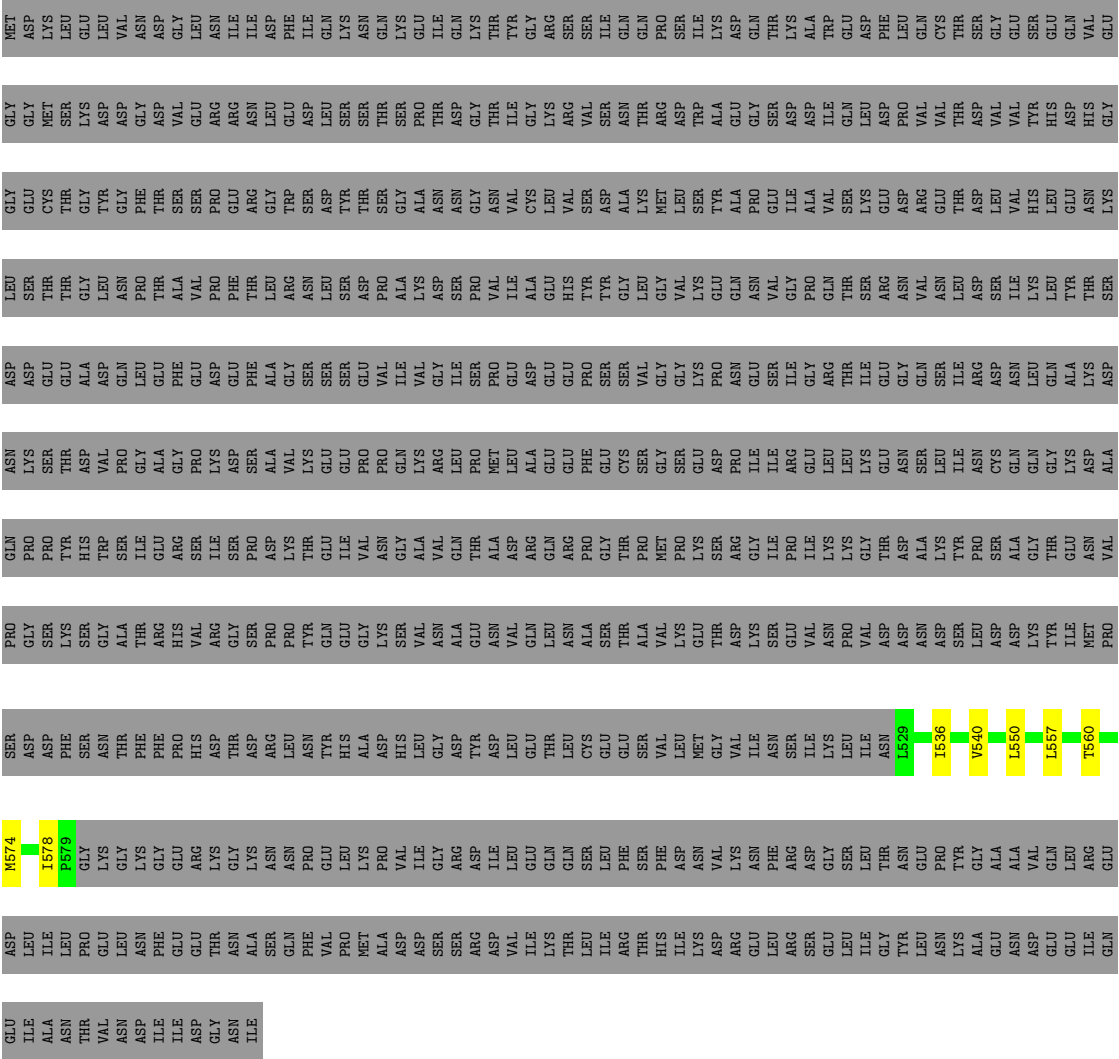
• Molecule 1: RNA-directed RNA polymerase L





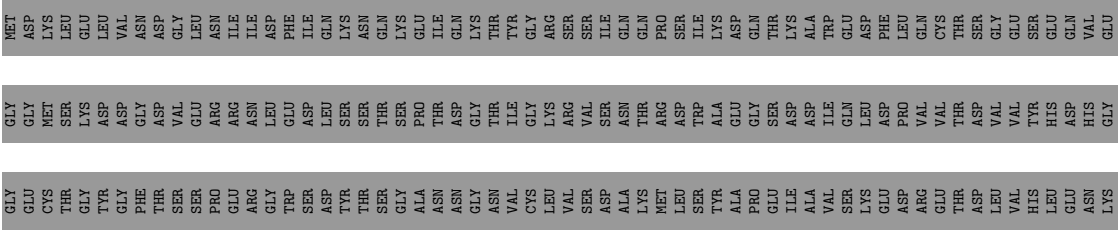
● Molecule 2: Phosphoprotein

Chain C: 6% . 93%



● Molecule 2: Phosphoprotein

Chain D: 7% . 91%



T562	A563	I567	E568	V572	S573	P579	K583	GLY	GLU	ARG	LYS	GLY	LYS	ASN	ASN	PRO	GLU	LEU	LYS	PRO	VAL	ILE	GLY	ARG	ASP	ILE	LEU	GLU	GLN	GLN	SER	LEU	PHE	SER	PHE	ASP	ASN	ASN	VAL	LYS	ASN	PHE	ARG	ASP	GLY	SER	LEU	ILE	GLY	TYR	ASN	PRO	GLU	TYR	LYS	ALA	GLU	ASN	ALA	VAL		
GLU	GLU	ILE	GLN	GLU	ILE	ALA	ASN	THR	VAL	ASN	ASP	ILE	ILE	ILE	ASP	GLY	ASN	ILE	ILE	ILE	ASP	GLU	THR	ASN	ALA	SER	GLN	PHE	VAL	PRO	MET	ALA	ASP	ASP	SER	SER	ARG	ASP	VAL	ILE	LYS	THR	LEU	ILE	ARG	GLU	LEU	ARG	SER	SER	GLU	LEU	ILE	GLY	TYR	LEU	ASN	LYS	ALA	GLU	ASN	ASP
GLU	GLU	ILE	GLN	GLU	ILE	ALA	ASN	THR	VAL	ASN	ASP	ILE	ILE	ILE	ASP	GLY	ASN	ILE	ILE	ILE	ASP	GLU	THR	ASN	ALA	SER	GLN	PHE	VAL	PRO	MET	ALA	ASP	ASP	SER	SER	ARG	ASP	VAL	ILE	LYS	THR	LEU	ILE	ARG	GLU	LEU	ARG	SER	SER	GLU	LEU	ILE	GLY	TYR	LEU	ASN	LYS	ALA	GLU	ASN	ASP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4977110	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k 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: ZN, A1ET4

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	0.13	0/10434	0.31	0/14098
2	B	0.15	0/1202	0.38	0/1619
2	C	0.18	0/407	0.41	0/547
2	D	0.17	0/520	0.36	0/694
2	E	0.19	0/433	0.41	0/579
All	All	0.14	0/12996	0.33	0/17537

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	10226	0	10262	53	0
2	B	1190	0	1213	24	0
2	C	404	0	435	11	0
2	D	516	0	554	11	0
2	E	430	0	467	11	0
3	A	2	0	0	0	0
4	A	47	0	0	0	0
All	All	12815	0	12931	91	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.

The worst 5 of 91 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)
2:D:552:SER:HA	2:D:555:ARG:HE	1.58	0.69
1:A:26:LEU:HD22	1:A:234:MET:HE1	1.77	0.66
2:B:544:PRO:HA	2:B:547:ILE:HG22	1.76	0.66
2:D:549:LYS:HG2	2:E:550:LEU:HB3	1.77	0.66
1:A:58:ARG:HH12	1:A:490:GLU:HG3	1.61	0.66

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 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	1254/2244 (56%)	1224 (98%)	30 (2%)	0	100	100
2	B	143/709 (20%)	141 (99%)	2 (1%)	0	100	100
2	C	49/709 (7%)	49 (100%)	0	0	100	100
2	D	64/709 (9%)	64 (100%)	0	0	100	100
2	E	53/709 (8%)	52 (98%)	1 (2%)	0	100	100
All	All	1563/5080 (31%)	1530 (98%)	33 (2%)	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 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	1140/2046 (56%)	1140 (100%)	0	100	100
2	B	139/625 (22%)	139 (100%)	0	100	100
2	C	48/625 (8%)	48 (100%)	0	100	100
2	D	59/625 (9%)	59 (100%)	0	100	100
2	E	50/625 (8%)	50 (100%)	0	100	100
All	All	1436/4546 (32%)	1436 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	539	GLN
2	E	535	HIS
2	E	570	HIS
1	A	778	HIS
1	A	1164	HIS

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 ⓘ

Of 3 ligands modelled in this entry, 2 are 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	$\# Z > 2$
4	A1ET4	A	2303	-	50,50,50	0.67	0	69,73,73	0.59	2 (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
4	A1ET4	A	2303	-	-	6/49/71/71	1/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2303	A1ET4	C1-N1-N2	2.47	106.59	104.36
4	A	2303	A1ET4	C2-C3-C1	2.29	105.93	103.64

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2303	A1ET4	O4-C23-C24-N7
4	A	2303	A1ET4	C23-C24-N7-C25
4	A	2303	A1ET4	C24-C23-N6-C21
4	A	2303	A1ET4	O1-C5-N3-C6
4	A	2303	A1ET4	C2-C5-N3-C6

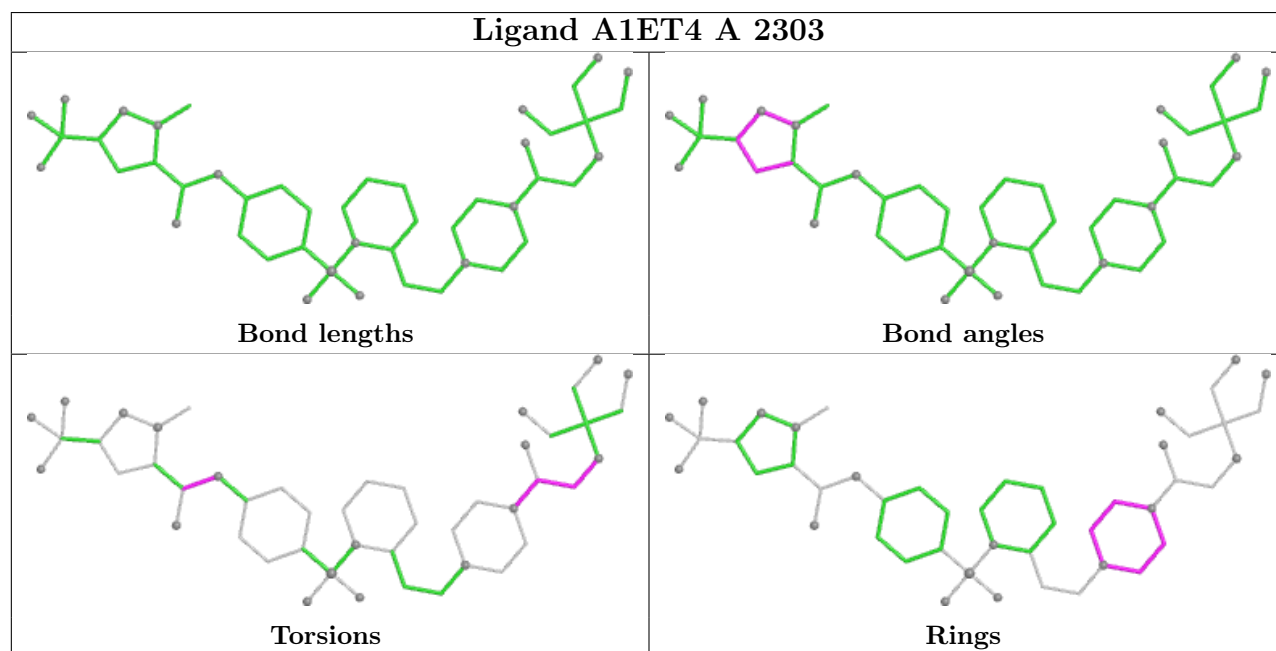
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2303	A1ET4	C19-C20-C21-C22-N5-N6

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.