



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2023 – 03:08 AM EDT

PDB ID : 6P04
Title : Binary structure of the E52D mutant of ANT-4" with Neomycin
Authors : Selvaraj, B.; Cuneo, M.J.
Deposited on : 2019-05-16
Resolution : 2.30 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 : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : **FAILED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

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 2.30 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4395 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.

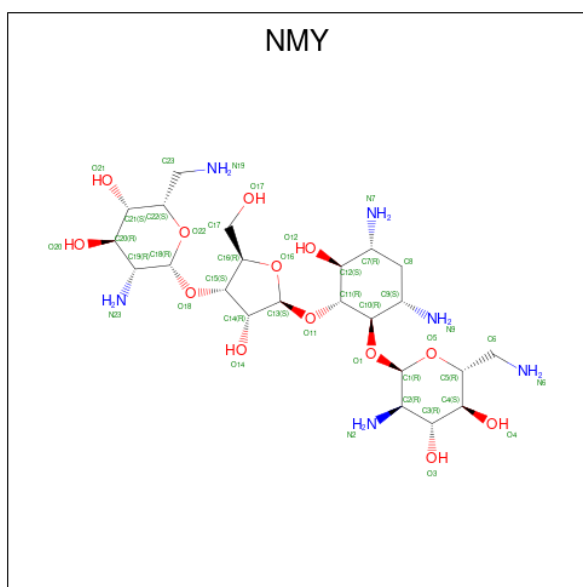
- Molecule 1 is a protein called Kanamycin nucleotidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	252	2100	1332	341	413	14	0	11	0
1	B	252	2067	1313	338	401	15	0	7	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P05058
A	-1	SER	-	expression tag	UNP P05058
A	0	HIS	-	expression tag	UNP P05058
A	52	ASP	GLU	engineered mutation	UNP P05058
B	-2	GLY	-	expression tag	UNP P05058
B	-1	SER	-	expression tag	UNP P05058
B	0	HIS	-	expression tag	UNP P05058
B	52	ASP	GLU	engineered mutation	UNP P05058

- Molecule 2 is NEOMYCIN (three-letter code: NMY) (formula: $C_{23}H_{46}N_6O_{13}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	42	23	6	13	0	0
2	A	1	42	23	6	13	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	65	65	65	0	0
4	B	78	78	78	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics i

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.70Å 98.45Å 101.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.23 – 2.30	Depositor
% Data completeness (in resolution range)	97.7 (49.23-2.30)	Depositor
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.29Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.195 , 0.236	Depositor
Wilson B-factor (Å ²)	34.7	Xtrriage
Anisotropy	0.637	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.027 for -h,l,k	Xtrriage
Total number of atoms	4395	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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
2	NMY	A	301	3	45,45,45	3.92	17 (37%)	63,67,67	1.26	7 (11%)
2	NMY	A	300	-	45,45,45	3.93	17 (37%)	63,67,67	1.28	8 (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	NMY	A	301	3	-	5/18/94/94	0/4/4/4
2	NMY	A	300	-	-	5/18/94/94	0/4/4/4

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	NMY	C13-C14	-14.45	1.34	1.52
2	A	300	NMY	C13-C14	-14.42	1.34	1.52
2	A	300	NMY	O16-C13	12.95	1.64	1.41
2	A	301	NMY	O16-C13	12.91	1.64	1.41
2	A	300	NMY	C23-C22	-7.74	1.41	1.52
2	A	301	NMY	C23-C22	-7.74	1.41	1.52
2	A	301	NMY	C6-C5	-7.00	1.42	1.52
2	A	300	NMY	C6-C5	-6.94	1.42	1.52
2	A	300	NMY	O16-C16	-5.95	1.31	1.45
2	A	301	NMY	C3-C2	-5.95	1.46	1.53
2	A	301	NMY	O16-C16	-5.87	1.31	1.45
2	A	300	NMY	C3-C2	-5.79	1.46	1.53
2	A	300	NMY	C2-N2	4.69	1.54	1.47
2	A	300	NMY	O22-C22	4.68	1.55	1.44
2	A	301	NMY	C2-N2	4.65	1.54	1.47
2	A	301	NMY	O22-C22	4.59	1.55	1.44
2	A	300	NMY	O5-C5	4.16	1.54	1.44
2	A	301	NMY	O5-C5	4.06	1.54	1.44
2	A	300	NMY	C19-N23	3.74	1.53	1.47
2	A	301	NMY	C19-N23	3.67	1.52	1.47
2	A	300	NMY	C20-C19	-3.03	1.49	1.53
2	A	301	NMY	C15-C16	2.90	1.60	1.52
2	A	300	NMY	O18-C15	-2.84	1.36	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	NMY	O5-C1	2.69	1.48	1.41
2	A	301	NMY	O18-C15	-2.65	1.37	1.43
2	A	301	NMY	O5-C1	2.64	1.48	1.41
2	A	301	NMY	C20-C19	-2.62	1.50	1.53
2	A	300	NMY	C15-C16	2.59	1.59	1.52
2	A	300	NMY	O22-C18	2.41	1.48	1.41
2	A	301	NMY	O22-C18	2.27	1.47	1.41
2	A	300	NMY	O3-C3	2.26	1.48	1.43
2	A	301	NMY	O14-C14	2.21	1.48	1.43
2	A	300	NMY	O14-C14	2.21	1.48	1.43
2	A	301	NMY	O3-C3	2.16	1.48	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	NMY	C13-O11-C11	-4.10	107.83	117.96
2	A	301	NMY	C13-O11-C11	-3.66	108.92	117.96
2	A	300	NMY	O22-C22-C21	-2.92	104.39	109.69
2	A	301	NMY	C1-O1-C10	-2.89	110.82	117.96
2	A	301	NMY	C21-C20-C19	2.66	115.65	111.07
2	A	300	NMY	O11-C13-O16	-2.52	108.70	111.43
2	A	301	NMY	O22-C22-C21	-2.43	105.29	109.69
2	A	301	NMY	O11-C13-C14	2.39	112.91	107.96
2	A	300	NMY	C18-O18-C15	-2.25	112.39	117.96
2	A	301	NMY	C8-C9-C10	2.24	115.20	109.53
2	A	300	NMY	C1-O1-C10	-2.12	112.72	117.96
2	A	300	NMY	O5-C5-C6	2.05	109.82	106.01
2	A	300	NMY	C18-C19-C20	2.03	115.53	110.21
2	A	301	NMY	C18-O18-C15	-2.03	112.95	117.96
2	A	300	NMY	O11-C13-C14	2.02	112.15	107.96

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	NMY	O22-C22-C23-N19
2	A	301	NMY	C21-C22-C23-N19
2	A	301	NMY	O22-C22-C23-N19
2	A	300	NMY	O16-C16-C17-O17
2	A	300	NMY	O5-C1-O1-C10
2	A	300	NMY	C15-C16-C17-O17
2	A	301	NMY	C15-C16-C17-O17

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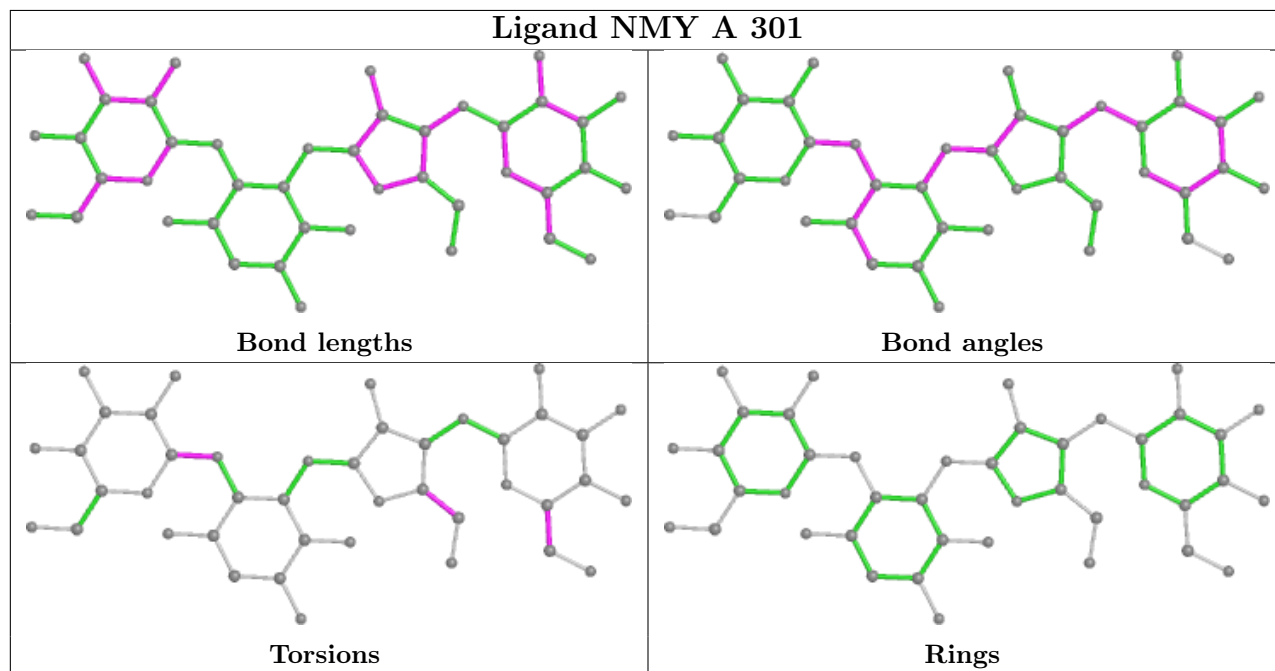
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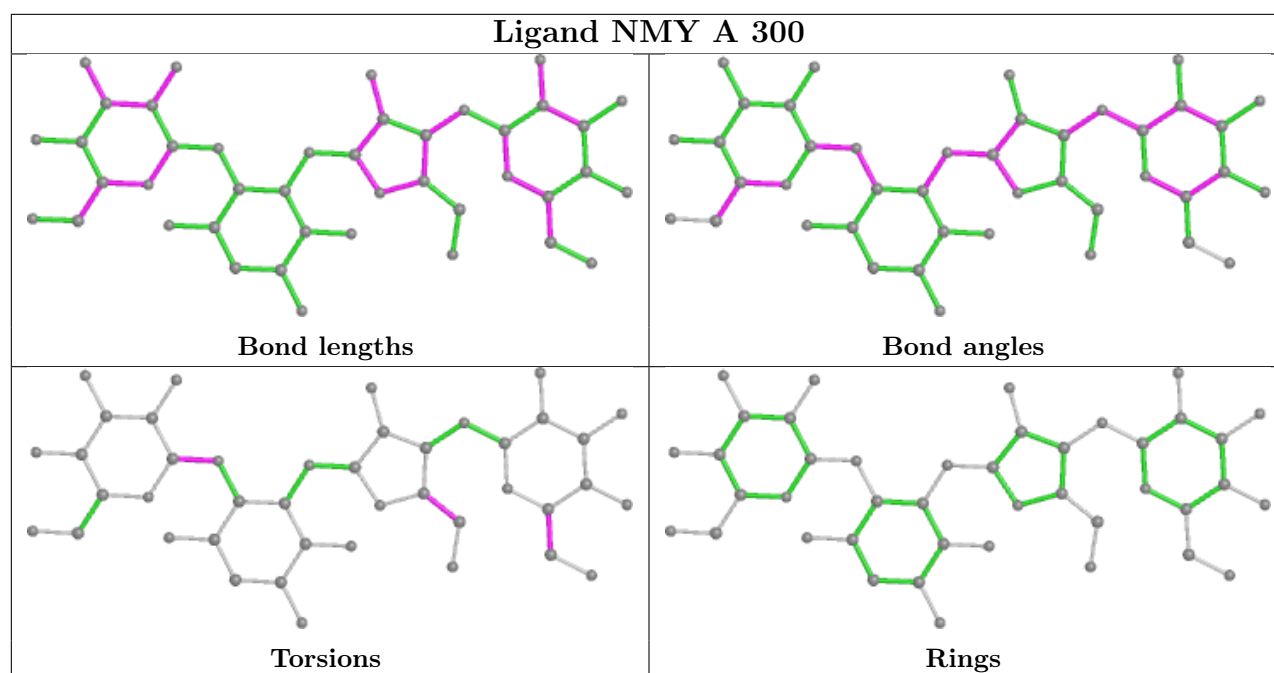
Mol	Chain	Res	Type	Atoms
2	A	301	NMY	O5-C1-O1-C10
2	A	301	NMY	O16-C16-C17-O17
2	A	300	NMY	C21-C22-C23-N19

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.





4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

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5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.