



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:59 AM UTC

PDB ID : 1KHZ / pdb_00001khz
Title : Structure of the ADPR-ase in complex with AMPCPR and Mg
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Deposited on : 2001-12-01
Resolution : 2.04 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

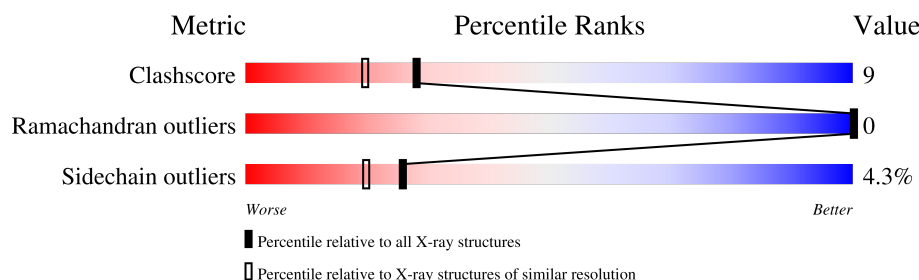
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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))
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	209	
1	B	209	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3519 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 ADP-ribose pyrophosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1643	1037	288	313	5			
1	B	202	Total	C	N	O	S	0	0	0
			1613	1017	285	307	4			

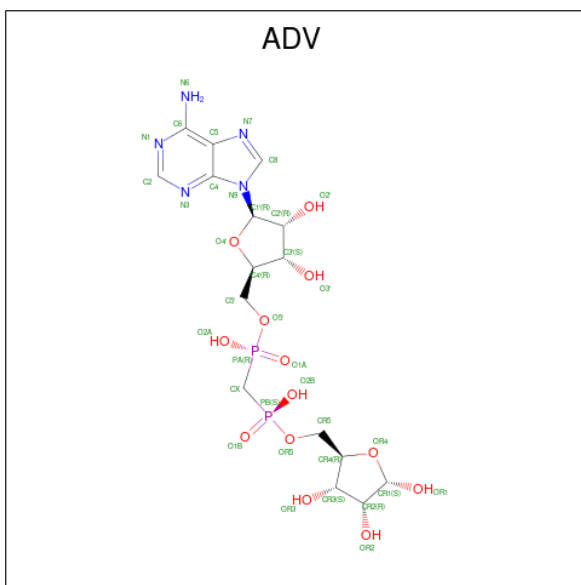
- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Mg	0	0
			3	3		

- Molecule 4 is ALPHA-BETA METHYLENE ADP-RIBOSE (CCD ID: ADV) (formula: C₁₆H₂₅N₅O₁₃P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			36	16	5	13	2		

- Molecule 5 is water.

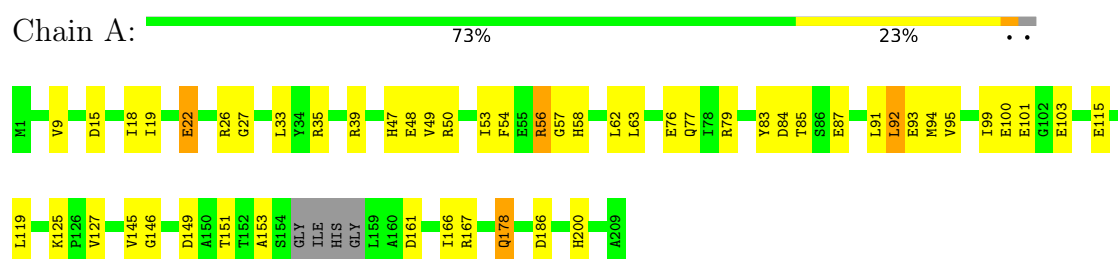
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	106	Total O 106 106	0	0
5	B	117	Total O 117 117	0	0

3 Residue-property plots [i](#)

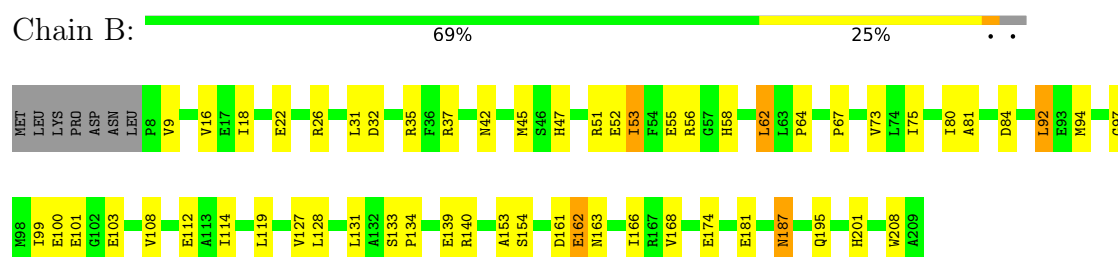
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

Note EDS was not executed.

• Molecule 1: ADP-ribose pyrophosphatase



• Molecule 1: ADP-ribose pyrophosphatase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.10Å 67.40Å 96.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.64 – 2.04	Depositor
% Data completeness (in resolution range)	95.5 (26.64-2.04)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.196 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3519	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADV, MG, CL

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	0.50	0/1674	1.00	6/2265 (0.3%)
1	B	0.52	0/1645	1.01	13/2226 (0.6%)
All	All	0.51	0/3319	1.00	19/4491 (0.4%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	57	GLY	N-CA-C	9.84	121.45	111.21
1	A	47	HIS	N-CA-C	-7.27	100.31	110.35
1	B	133	SER	CA-C-N	7.03	128.62	119.84
1	B	133	SER	C-N-CA	7.03	128.62	119.84
1	B	47	HIS	N-CA-C	-6.93	101.88	110.41
1	A	93	GLU	N-CA-C	6.32	118.15	109.18
1	A	95	VAL	N-CA-C	-6.09	101.72	109.58
1	B	162	GLU	N-CA-C	-5.62	106.59	113.50
1	A	83	TYR	N-CA-C	5.51	116.97	111.07
1	B	139	GLU	N-CA-C	5.45	118.22	110.10
1	B	201	HIS	N-CA-C	5.35	117.11	111.28
1	B	195	GLN	N-CA-C	-5.32	105.65	111.82
1	B	154	SER	N-CA-C	5.29	116.56	108.42
1	B	42	ASN	N-CA-C	-5.23	106.14	112.88
1	B	84	ASP	N-CA-C	5.21	118.73	112.38
1	B	114	ILE	N-CA-C	-5.20	105.77	110.82
1	B	53	ILE	N-CA-C	5.18	115.37	108.11
1	B	187	ASN	N-CA-C	-5.10	101.39	109.96
1	A	84	ASP	N-CA-C	5.00	118.64	112.54

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	1643	0	1618	35	0
1	B	1613	0	1580	31	0
2	A	1	0	0	0	0
3	B	3	0	0	0	0
4	B	36	0	22	0	0
5	A	106	0	0	4	0
5	B	117	0	0	2	0
All	All	3519	0	3220	58	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 9.

All (58) 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:9:VAL:HG12	1:B:92:LEU:HD13	1.58	0.86
1:B:26:ARG:C	1:B:26:ARG:HD3	2.02	0.84
1:A:100:GLU:HB2	1:A:103:GLU:OE2	1.83	0.78
1:A:186:ASP:OD2	1:B:140:ARG:NH2	2.19	0.74
1:B:119:LEU:HD21	1:B:153:ALA:HB2	1.70	0.72
1:B:26:ARG:HD3	1:B:26:ARG:O	1.90	0.70
1:A:127:VAL:HG21	1:A:145:VAL:HG13	1.80	0.62
1:A:149:ASP:OD1	1:A:151:THR:HB	1.99	0.62
1:A:35:ARG:HH12	1:A:50:ARG:HE	1.46	0.62
1:A:178:GLN:HG2	5:A:443:HOH:O	2.00	0.61
1:B:100:GLU:HB2	1:B:103:GLU:OE2	2.02	0.59
1:A:53:ILE:HD12	1:B:81:ALA:HB2	1.86	0.58
1:A:19:ILE:HD12	1:A:48:GLU:HG3	1.86	0.58
1:A:58:HIS:ND1	1:A:99:ILE:HD12	2.19	0.57
1:A:27:GLY:HA2	5:A:467:HOH:O	2.04	0.57
1:A:77:GLN:HB3	1:A:166:ILE:HD13	1.88	0.55
1:A:58:HIS:CE1	5:A:466:HOH:O	2.60	0.54
1:A:15:ASP:HB3	1:A:39:ARG:HG3	1.89	0.53
1:A:9:VAL:CG1	1:B:92:LEU:HD13	2.36	0.53
1:B:127:VAL:HG12	1:B:128:LEU:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ARG:HG2	1:A:26:ARG:HH11	1.75	0.52
1:A:35:ARG:HH12	1:A:50:ARG:NE	2.07	0.52
1:B:64:PRO:HB2	1:B:73:VAL:HB	1.90	0.51
1:A:54:PHE:CE2	1:A:56:ARG:HG3	2.46	0.50
1:B:22:GLU:OE2	1:B:35:ARG:HD3	2.12	0.50
1:A:119:LEU:HD21	1:A:153:ALA:HB2	1.93	0.49
1:A:127:VAL:CG2	1:A:145:VAL:HG13	2.42	0.49
1:B:37:ARG:HB3	1:B:45:MET:HE3	1.93	0.49
1:A:76:GLU:HG3	1:B:9:VAL:HG22	1.95	0.49
1:A:22:GLU:OE2	1:A:35:ARG:NE	2.38	0.48
1:A:62:LEU:HD11	1:A:146:GLY:HA3	1.94	0.48
1:A:94:MET:HA	5:A:431:HOH:O	2.15	0.47
1:B:101:GLU:HG2	1:B:101:GLU:O	2.14	0.47
1:B:187:ASN:HB2	5:B:464:HOH:O	2.15	0.46
1:B:52:GLU:C	1:B:53:ILE:HD12	2.40	0.46
1:A:18:ILE:CD1	1:B:80:ILE:HD11	2.45	0.46
1:A:77:GLN:HG3	1:A:79:ARG:HD3	1.98	0.45
1:B:94:MET:HE2	1:B:94:MET:HA	1.97	0.45
1:B:62:LEU:HD23	1:B:64:PRO:HG3	1.97	0.45
1:A:115:GLU:O	1:A:161:ASP:HB2	2.17	0.45
1:B:99:ILE:HA	1:B:108:VAL:HG21	1.98	0.44
1:A:167:ARG:NH2	5:B:412:HOH:O	2.49	0.44
1:A:26:ARG:HG2	1:A:26:ARG:NH1	2.33	0.44
1:B:32:ASP:OD2	1:B:55:GLU:HG3	2.18	0.43
1:B:62:LEU:O	1:B:64:PRO:HD3	2.18	0.43
1:A:92:LEU:HD12	1:A:92:LEU:HA	1.87	0.43
1:B:97:GLY:HA3	1:B:112:GLU:CD	2.43	0.43
1:B:162:GLU:O	1:B:163:ASN:HB2	2.18	0.43
1:A:125:LYS:HB3	1:A:145:VAL:CG2	2.49	0.43
1:A:63:LEU:HD13	1:A:94:MET:SD	2.60	0.42
1:B:75:ILE:HB	1:B:166:ILE:CG2	2.49	0.42
1:B:131:LEU:CB	1:B:134:PRO:HG3	2.50	0.42
1:B:16:VAL:HG12	1:B:18:ILE:HD12	2.02	0.41
1:A:22:GLU:HG3	1:A:33:LEU:HB3	2.03	0.41
1:A:85:THR:HG21	1:B:58:HIS:CE1	2.56	0.41
1:A:200:HIS:HE1	1:B:181:GLU:OE1	2.04	0.41
1:B:67:PRO:HG3	1:B:208:TRP:HE3	1.84	0.41
1:B:31:LEU:HD12	1:B:31:LEU:HA	1.86	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 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	201/209 (96%)	193 (96%)	8 (4%)	0	100	100
1	B	200/209 (96%)	192 (96%)	8 (4%)	0	100	100
All	All	401/418 (96%)	385 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	175/177 (99%)	167 (95%)	8 (5%)	24	18
1	B	170/177 (96%)	163 (96%)	7 (4%)	27	21
All	All	345/354 (98%)	330 (96%)	15 (4%)	26	20

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

Mol	Chain	Res	Type
1	A	22	GLU
1	A	49	VAL
1	A	56	ARG
1	A	87	GLU
1	A	91	LEU
1	A	92	LEU
1	A	101	GLU
1	A	178	GLN

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Mol	Chain	Res	Type
1	B	51	ARG
1	B	56	ARG
1	B	62	LEU
1	B	92	LEU
1	B	161	ASP
1	B	168	VAL
1	B	174	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	200	HIS
1	B	14	ASN
1	B	44	GLN
1	B	178	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 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	ADV	B	402	3	35,39,39	2.71	16 (45%)	50,60,60	1.14	4 (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
4	ADV	B	402	3	-	3/22/54/54	0/4/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	ADV	OR4-CR4	5.90	1.58	1.45
4	B	402	ADV	PA-O2A	-5.35	1.43	1.56
4	B	402	ADV	OR4-CR1	4.87	1.49	1.43
4	B	402	ADV	PA-O1A	-4.62	1.40	1.51
4	B	402	ADV	C4-N3	4.20	1.42	1.34
4	B	402	ADV	OR5-CR5	4.08	1.60	1.44
4	B	402	ADV	C2-N1	3.61	1.40	1.33
4	B	402	ADV	PB-O2B	-3.55	1.47	1.56
4	B	402	ADV	C1'-N9	3.31	1.55	1.46
4	B	402	ADV	O4'-C1'	3.19	1.49	1.42
4	B	402	ADV	O2'-C2'	3.16	1.50	1.43
4	B	402	ADV	C2'-C3'	3.04	1.61	1.53
4	B	402	ADV	OR2-CR2	-2.86	1.35	1.43
4	B	402	ADV	CR5-CR4	2.73	1.59	1.51
4	B	402	ADV	CR1-CR2	2.63	1.55	1.52
4	B	402	ADV	C6-N1	2.27	1.42	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	402	ADV	CR1-CR2-CR3	3.53	106.64	102.29
4	B	402	ADV	C4'-O4'-C1'	2.49	114.96	109.47
4	B	402	ADV	CR5-CR4-CR3	-2.45	106.40	115.21
4	B	402	ADV	OR1-CR1-OR4	-2.30	108.19	111.12

There are no chirality outliers.

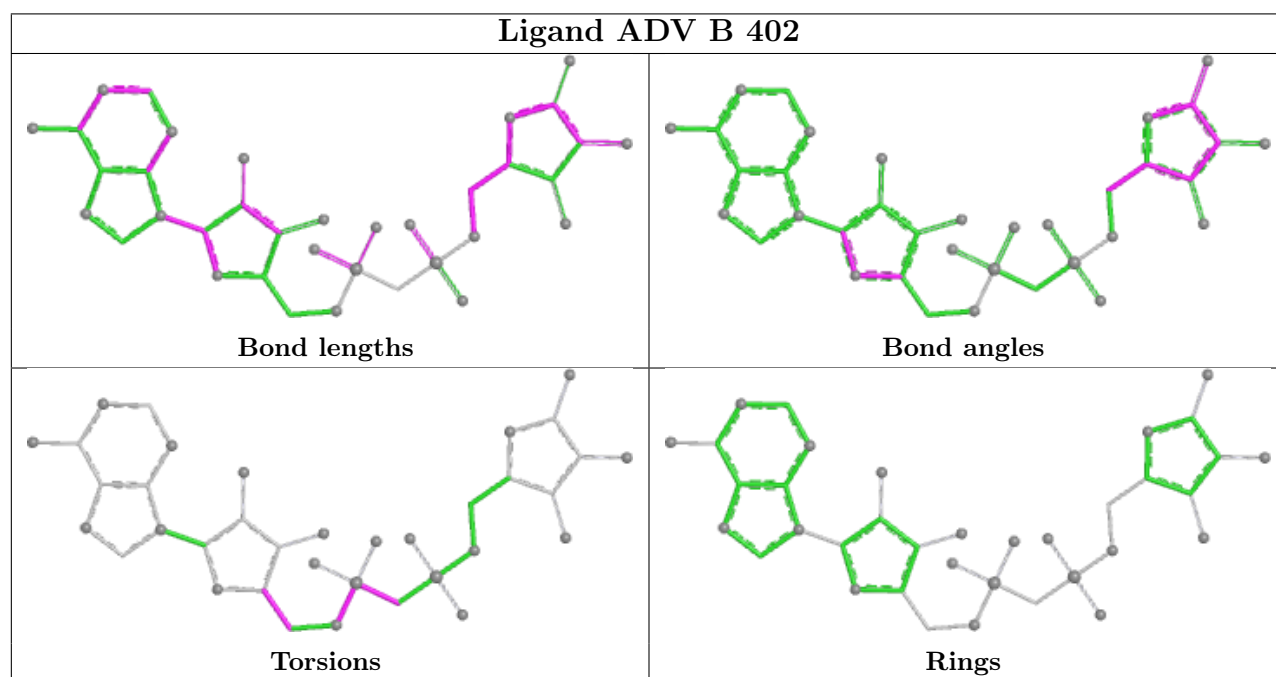
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	402	ADV	C5'-O5'-PA-CX
4	B	402	ADV	PB-CX-PA-O2A
4	B	402	ADV	C3'-C4'-C5'-O5'

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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.