



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:53 AM UTC

PDB ID : 1JDV / pdb_00001jdv
Title : CRYSTAL STRUCTURE OF 5'-DEOXY-5'-METHYLTHIOADENOSINE PHOSPHORYLASE COMPLEXED WITH ADENOSINE AND SULFATE ION
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Deposited on : 2001-06-15
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure 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/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

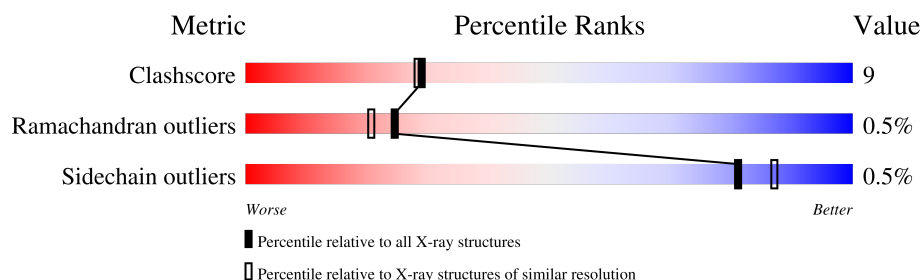
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	236	79% 16% . .
1	B	236	76% 19% . .
1	C	236	78% 21% .
1	D	236	78% 18% .
1	E	236	72% 22% . .
1	F	236	79% 19% .

2 Entry composition [i](#)

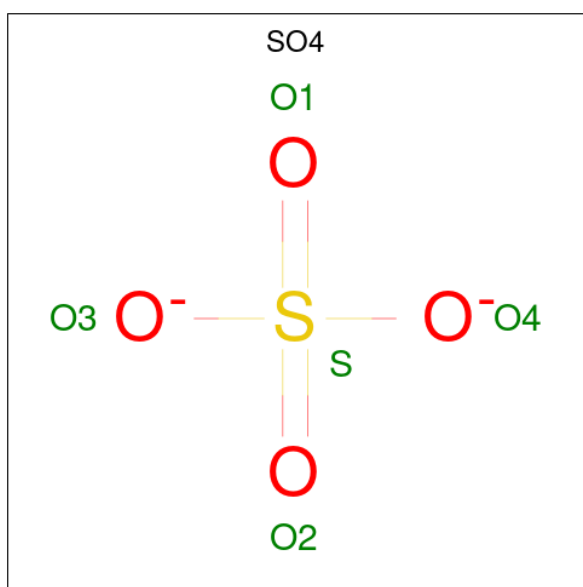
There are 4 unique types of molecules in this entry. The entry contains 10994 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 5'-METHYLTHIOADENOSINE PHOSPHORYLASE.

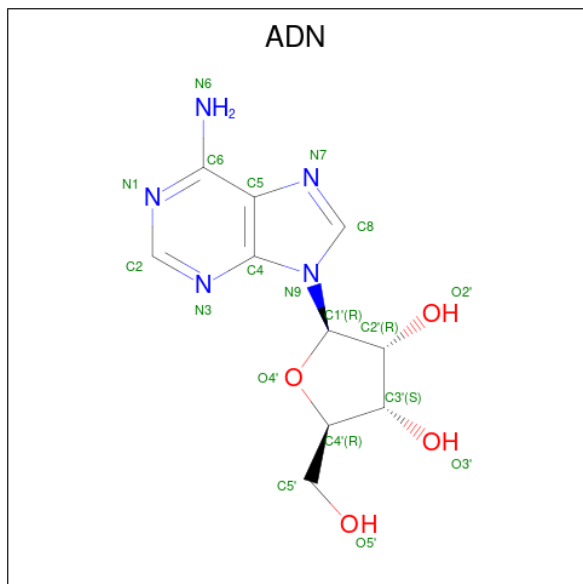
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1743	1115	289	334	5			
1	B	227	Total	C	N	O	S	0	0	0
			1743	1115	289	334	5			
1	C	235	Total	C	N	O	S	0	0	0
			1806	1157	299	345	5			
1	D	227	Total	C	N	O	S	0	0	0
			1743	1115	289	334	5			
1	E	227	Total	C	N	O	S	0	0	0
			1743	1115	289	334	5			
1	F	235	Total	C	N	O	S	0	0	0
			1806	1157	299	345	5			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

- Molecule 3 is ADENOSINE (CCD ID: ADN) (formula: $C_{10}H_{13}N_5O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 19 10 5 4	0	0
3	B	1	Total C N O 19 10 5 4	0	0
3	D	1	Total C N O 19 10 5 4	0	0
3	E	1	Total C N O 19 10 5 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	52	Total 52	O 52	0	0
4	B	48	Total 48	O 48	0	0
4	C	49	Total 49	O 49	0	0
4	D	55	Total 55	O 55	0	0
4	E	51	Total 51	O 51	0	0
4	F	49	Total 49	O 49	0	0

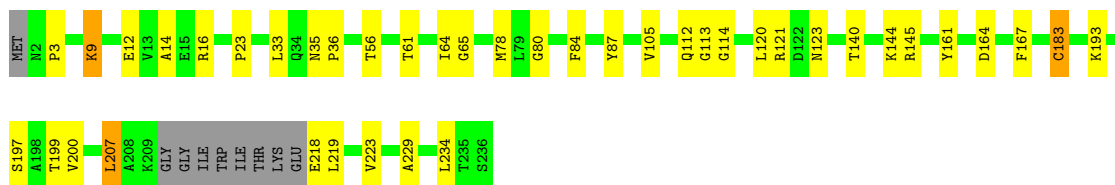
3 Residue-property plots

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.

Note EDS was not executed.

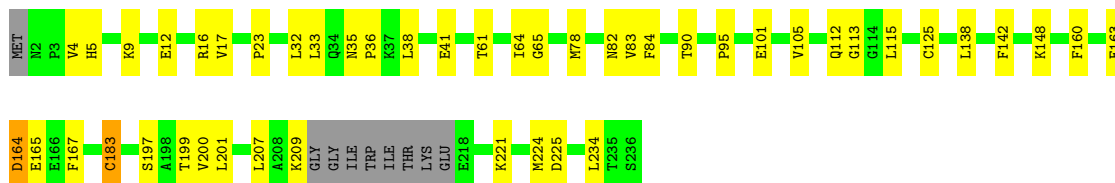
• Molecule 1: 5'-METHYLTHIOADENOSINE PHOSPHORYLASE

Chain A: 



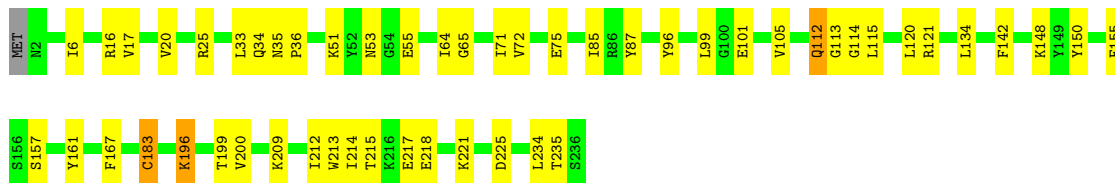
• Molecule 1: 5'-METHYLTHIOADENOSINE PHOSPHORYLASE

Chain B: 



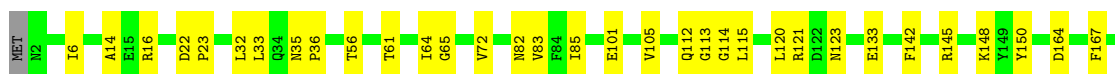
• Molecule 1: 5'-METHYLTHIOADENOSINE PHOSPHORYLASE

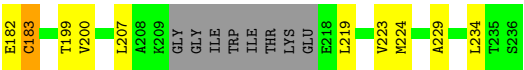
Chain C: 



• Molecule 1: 5'-METHYLTHIOADENOSINE PHOSPHORYLASE

Chain D: 

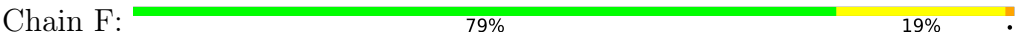




• Molecule 1: 5'-METHYLTHIOADENOSINE PHOSPHORYLASE



• Molecule 1: 5'-METHYLTHIOADENOSINE PHOSPHORYLASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.00Å 87.50Å 102.00Å 90.00° 119.99° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.246	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10994	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

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: SO4, ADN

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	0.43	0/1773	0.92	6/2401 (0.2%)
1	B	0.40	0/1773	0.90	5/2401 (0.2%)
1	C	0.39	0/1839	0.89	6/2492 (0.2%)
1	D	0.43	0/1773	0.93	5/2401 (0.2%)
1	E	0.39	0/1773	0.89	5/2401 (0.2%)
1	F	0.39	0/1839	0.89	5/2492 (0.2%)
All	All	0.41	0/10770	0.90	32/14588 (0.2%)

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	GLY	N-CA-C	7.45	120.64	112.29
1	D	65	GLY	N-CA-C	7.20	120.35	112.29
1	F	65	GLY	N-CA-C	6.86	119.97	112.29
1	C	65	GLY	N-CA-C	6.75	119.85	112.29
1	B	65	GLY	N-CA-C	6.67	119.76	112.29

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	1743	0	1758	22	0
1	B	1743	0	1758	29	0
1	C	1806	0	1823	37	0
1	D	1743	0	1758	30	0
1	E	1743	0	1758	40	0
1	F	1806	0	1823	39	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	19	0	13	1	0
3	B	19	0	13	1	0
3	D	19	0	13	1	0
3	E	19	0	13	1	0
4	A	52	0	0	1	0
4	B	48	0	0	0	0
4	C	49	0	0	1	0
4	D	55	0	0	1	0
4	E	51	0	0	0	0
4	F	49	0	0	0	0
All	All	10994	0	10730	186	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.

The worst 5 of 186 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:E:113:GLY:HA2	1:F:113:GLY:HA2	1.51	0.90
1:F:112:GLN:NE2	1:F:123:ASN:HB3	1.90	0.87
1:C:53:ASN:HB2	1:C:235:THR:HG21	1.64	0.78
1:D:6:ILE:HD11	1:D:72:VAL:HG13	1.66	0.78
1:E:218:GLU:HG3	1:E:221:LYS:HB3	1.65	0.78

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	223/236 (94%)	217 (97%)	5 (2%)	1 (0%)	30	27
1	B	223/236 (94%)	217 (97%)	5 (2%)	1 (0%)	30	27
1	C	233/236 (99%)	222 (95%)	8 (3%)	3 (1%)	9	5
1	D	223/236 (94%)	217 (97%)	5 (2%)	1 (0%)	30	27
1	E	223/236 (94%)	215 (96%)	7 (3%)	1 (0%)	30	27
1	F	233/236 (99%)	227 (97%)	6 (3%)	0	100	100
All	All	1358/1416 (96%)	1315 (97%)	36 (3%)	7 (0%)	24	21

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	114	GLY
1	B	164	ASP
1	C	114	GLY
1	E	164	ASP
1	C	209	LYS

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	188/195 (96%)	186 (99%)	2 (1%)	65	73
1	B	188/195 (96%)	188 (100%)	0	100	100
1	C	194/195 (100%)	191 (98%)	3 (2%)	57	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	188/195 (96%)	188 (100%)	0	100	100
1	E	188/195 (96%)	187 (100%)	1 (0%)	81	87
1	F	194/195 (100%)	194 (100%)	0	100	100
All	All	1140/1170 (97%)	1134 (100%)	6 (0%)	81	87

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	134	LEU
1	C	196	LYS
1	E	35	ASN
1	A	207	LEU
1	A	9	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	35	ASN
1	E	153	ASN
1	F	112	GLN
1	F	111	ASN
1	D	35	ASN

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

10 ligands are 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
3	ADN	E	4260	-	21,21,21	1.52	4 (19%)	31,31,31	1.09	2 (6%)
2	SO4	A	1250	-	4,4,4	0.41	0	6,6,6	0.10	0
3	ADN	B	2260	-	21,21,21	1.53	4 (19%)	31,31,31	1.11	2 (6%)
3	ADN	D	3260	-	21,21,21	1.53	2 (9%)	31,31,31	1.09	2 (6%)
2	SO4	F	6250	-	4,4,4	0.41	0	6,6,6	0.12	0
2	SO4	E	5250	-	4,4,4	0.44	0	6,6,6	0.09	0
3	ADN	A	1260	-	21,21,21	1.51	2 (9%)	31,31,31	1.11	2 (6%)
2	SO4	D	4250	-	4,4,4	0.40	0	6,6,6	0.09	0
2	SO4	B	2250	-	4,4,4	0.44	0	6,6,6	0.13	0
2	SO4	C	3250	-	4,4,4	0.44	0	6,6,6	0.10	0

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	ADN	E	4260	-	-	2/6/22/22	0/3/3/3
3	ADN	D	3260	-	-	2/6/22/22	0/3/3/3
3	ADN	B	2260	-	-	2/6/22/22	0/3/3/3
3	ADN	A	1260	-	-	2/6/22/22	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	3260	ADN	C1'-N9	4.62	1.59	1.46
3	A	1260	ADN	C1'-N9	4.49	1.58	1.46
3	B	2260	ADN	C1'-N9	4.49	1.58	1.46
3	E	4260	ADN	C1'-N9	4.32	1.58	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	3260	ADN	O3'-C3'	2.47	1.49	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1260	ADN	C3'-C2'-C1'	3.59	108.25	101.46
3	D	3260	ADN	C3'-C2'-C1'	3.58	108.23	101.46
3	B	2260	ADN	C3'-C2'-C1'	3.51	108.10	101.46
3	E	4260	ADN	C3'-C2'-C1'	3.44	107.97	101.46
3	B	2260	ADN	C4-N9-C1'	2.33	132.07	126.63

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1260	ADN	C2'-C1'-N9-C4
3	B	2260	ADN	C2'-C1'-N9-C8
3	B	2260	ADN	C2'-C1'-N9-C4
3	D	3260	ADN	C2'-C1'-N9-C4
3	E	4260	ADN	C2'-C1'-N9-C8

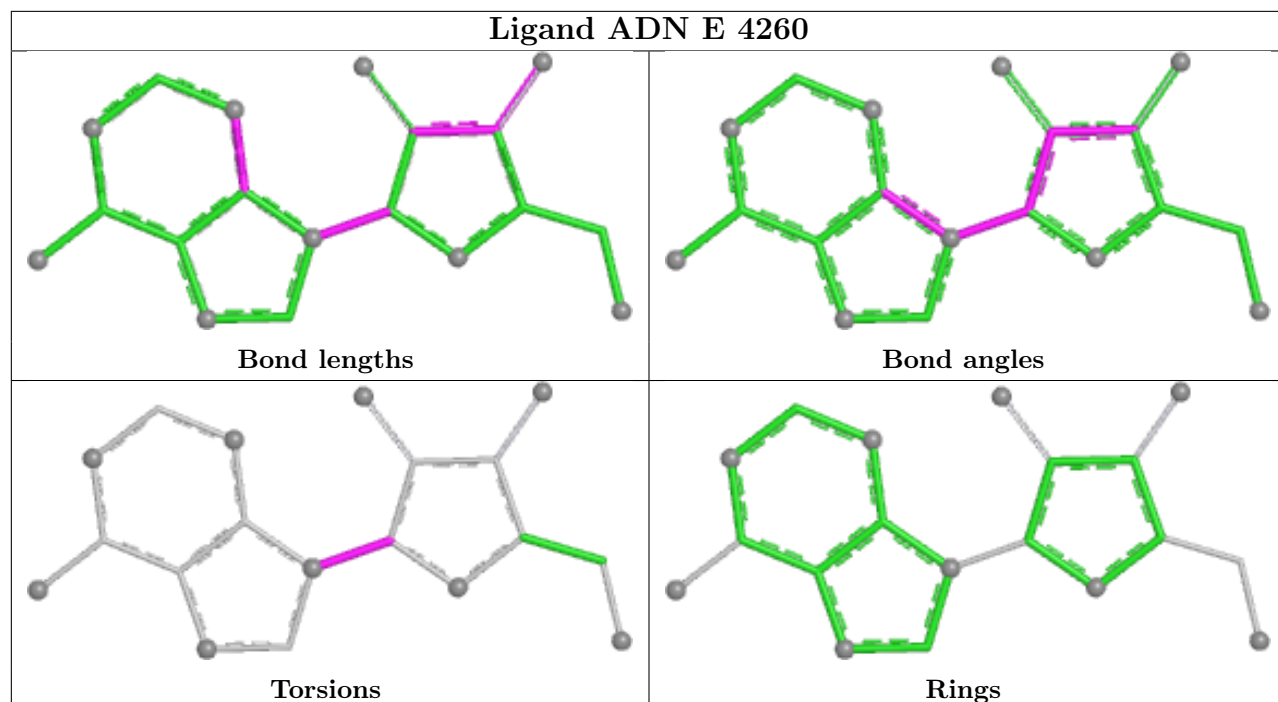
There are no ring outliers.

4 monomers are involved in 4 short contacts:

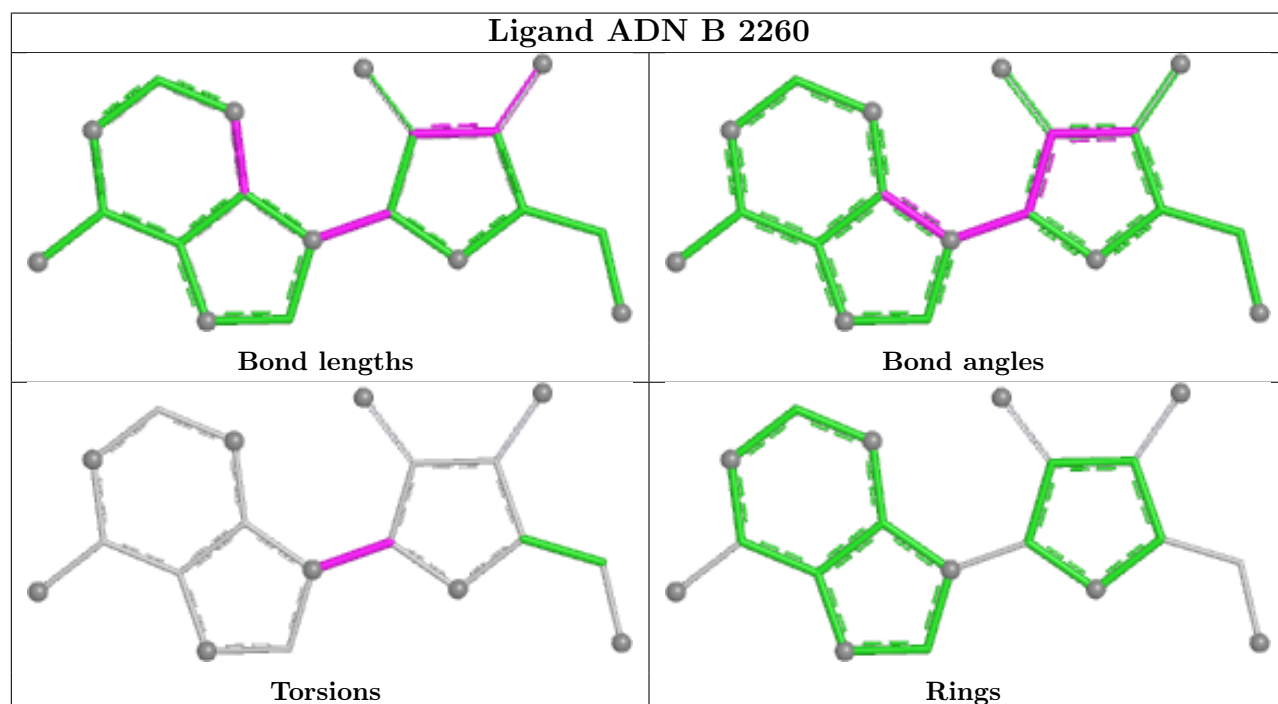
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	4260	ADN	1	0
3	B	2260	ADN	1	0
3	D	3260	ADN	1	0
3	A	1260	ADN	1	0

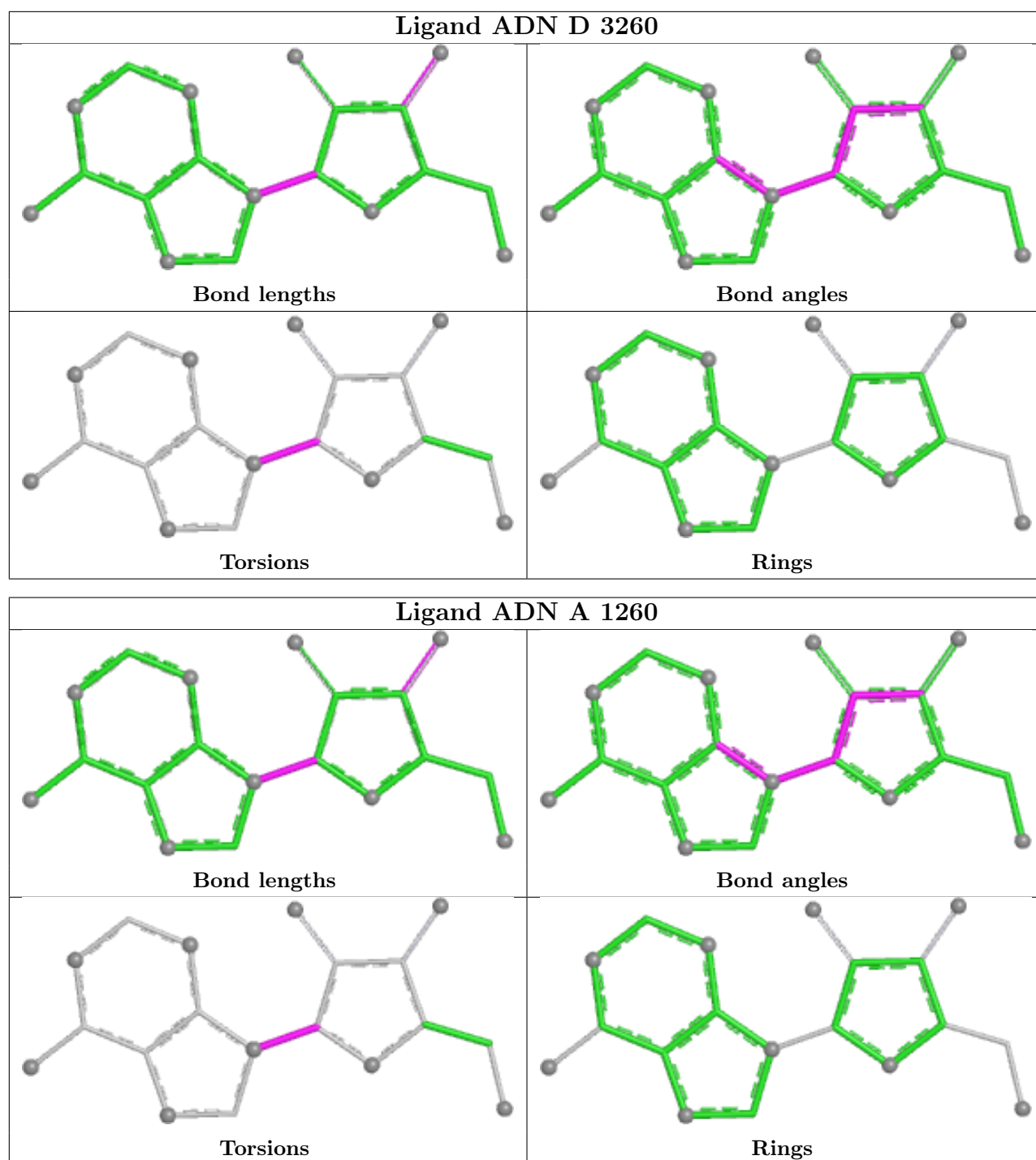
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand ADN E 4260



Ligand ADN B 2260





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

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.