



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:04 PM UTC

PDB ID : 1MXB / pdb_00001mxb
Title : S-ADENOSYLMETHIONINE SYNTHETASE WITH ADP
Authors : Takusagawa, F.; Kamitori, S.; Markham, G.D.
Deposited on : 1996-01-10
Resolution : 2.80 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

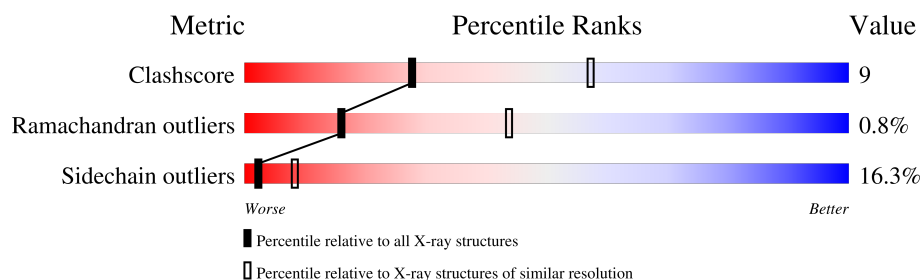
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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	383	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3539 atoms, of which 604 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 S-ADENOSYLMETHIONINE SYNTHETASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	378	Total	C	H	N	O	S	600	0	1
			3499	1830	600	496	560	13			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		

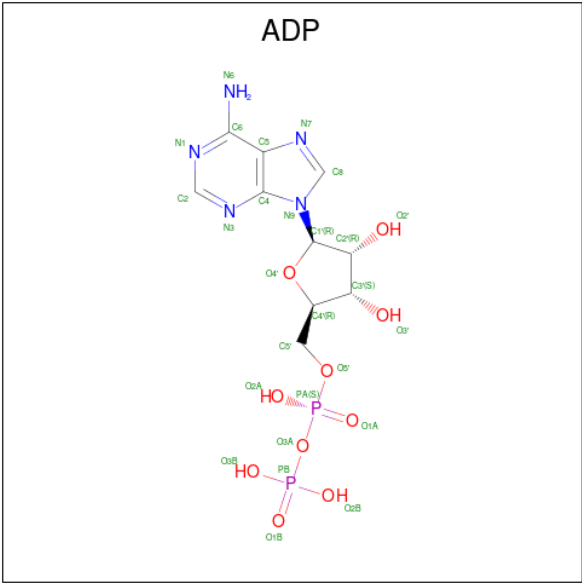
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	K	0	0
			2	2		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



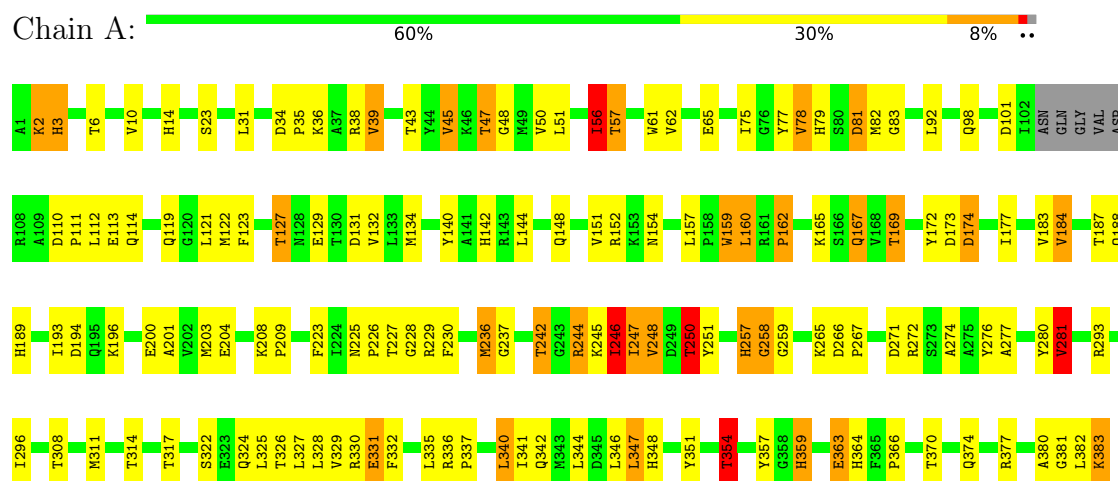
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	P	4	0
			31	10	4	5	10	2		

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: S-ADENOSYLMETHIONINE SYNTHETASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	128.90Å 128.90Å 139.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.80	Depositor
% Data completeness (in resolution range)	94.4 (10.00-2.80)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.194 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3539	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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: MG, K, PO4, ADP

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	0.91	11/2957 (0.4%)	1.70	41/4007 (1.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	11

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	257	HIS	CD2-NE2	-7.41	1.29	1.37
1	A	364	HIS	CD2-NE2	-7.30	1.29	1.37
1	A	348	HIS	CD2-NE2	-6.97	1.30	1.37
1	A	189	HIS	CD2-NE2	-6.89	1.30	1.37
1	A	101	ASP	C-N	-6.79	1.23	1.33
1	A	79	HIS	CD2-NE2	-6.44	1.30	1.37
1	A	3	HIS	CD2-NE2	-6.29	1.30	1.37
1	A	359	HIS	CD2-NE2	-6.26	1.30	1.37
1	A	142	HIS	CD2-NE2	-6.23	1.30	1.37
1	A	14	HIS	CD2-NE2	-6.07	1.31	1.37
1	A	257	HIS	CG-ND1	-5.75	1.31	1.38

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	271	ASP	CA-CB-CG	10.07	122.67	112.60
1	A	250	THR	N-CA-CB	-8.74	95.71	110.49

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	THR	CA-CB-CG2	7.78	123.73	110.50
1	A	119	GLN	N-CA-CB	-7.70	99.83	110.38
1	A	359	HIS	CB-CG-CD2	-7.60	121.32	131.20
1	A	247	ILE	N-CA-C	7.55	117.67	110.42
1	A	162	PRO	N-CA-C	7.34	123.73	113.53
1	A	348	HIS	CB-CG-CD2	-7.07	122.02	131.20
1	A	174	ASP	CA-CB-CG	-6.92	105.68	112.60
1	A	246	ILE	N-CA-CB	-6.77	103.00	110.51
1	A	314	THR	N-CA-C	-6.69	97.83	108.73
1	A	14	HIS	CB-CG-CD2	-6.62	122.59	131.20
1	A	3	HIS	CB-CG-CD2	-6.33	122.97	131.20
1	A	174	ASP	N-CA-C	6.27	119.31	109.96
1	A	119	GLN	OE1-CD-NE2	-6.21	116.39	122.60
1	A	359	HIS	CB-CG-ND1	6.20	132.00	122.70
1	A	281	VAL	N-CA-CB	6.18	117.78	110.55
1	A	248	VAL	N-CA-CB	6.18	118.94	110.54
1	A	79	HIS	CB-CG-CD2	-6.11	123.26	131.20
1	A	258	GLY	O-C-N	-5.83	115.37	122.71
1	A	250	THR	N-CA-C	5.82	123.19	110.80
1	A	266	ASP	CA-C-N	5.78	125.45	119.56
1	A	266	ASP	C-N-CA	5.78	125.45	119.56
1	A	364	HIS	CB-CG-CD2	-5.71	123.78	131.20
1	A	34	ASP	O-C-N	-5.70	117.24	121.23
1	A	230	PHE	N-CA-CB	-5.61	101.99	110.35
1	A	57	THR	CB-CA-C	5.57	119.88	110.79
1	A	56	ILE	CA-CB-CG2	5.57	119.97	110.50
1	A	78	VAL	N-CA-CB	-5.52	102.13	111.23
1	A	267	PRO	N-CA-C	5.44	120.91	113.84
1	A	114	GLN	OE1-CD-NE2	-5.28	117.32	122.60
1	A	61	TRP	N-CA-C	-5.28	100.42	109.24
1	A	81	ASP	CA-CB-CG	5.26	117.86	112.60
1	A	382	LEU	N-CA-C	5.24	117.68	110.35
1	A	167	GLN	OE1-CD-NE2	-5.22	117.38	122.60
1	A	225	ASN	OD1-CG-ND2	-5.17	117.43	122.60
1	A	354	THR	N-CA-CB	-5.17	102.27	110.22
1	A	230	PHE	CA-CB-CG	5.14	118.94	113.80
1	A	363	GLU	N-CA-C	5.12	121.72	110.80
1	A	57	THR	CA-CB-CG2	5.12	119.20	110.50
1	A	159	TRP	CE2-CD2-CG	-5.06	101.12	107.20

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	140	TYR	Sidechain
1	A	173	ASP	Peptide
1	A	227	THR	Peptide
1	A	228	GLY	Peptide
1	A	244	ARG	Sidechain
1	A	259	GLY	Peptide
1	A	276	TYR	Sidechain
1	A	280	TYR	Sidechain
1	A	336	ARG	Sidechain
1	A	357	TYR	Sidechain
1	A	48	GLY	Peptide

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	2899	600	2866	52	0
2	A	5	0	0	0	0
3	A	2	0	0	0	0
4	A	2	0	0	0	0
5	A	27	4	12	1	0
All	All	2935	604	2878	52	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 (52) 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:257:HIS:HD2	1:A:258:GLY:O	1.74	0.71
1:A:127:THR:HG22	1:A:293:ARG:HG2	1.73	0.71
1:A:47:THR:HG22	1:A:237:GLY:H	1.58	0.68
1:A:167:GLN:HB3	1:A:184:VAL:HG13	1.79	0.63
1:A:23:SER:OG	1:A:242:THR:HG21	1.99	0.62
1:A:272:ARG:HH21	1:A:354:THR:HG21	1.64	0.62
1:A:10:VAL:HG12	1:A:165:LYS:HG2	1.82	0.60
1:A:157:LEU:HB3	1:A:160:LEU:HD22	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:354:THR:HG23	1:A:359:HIS:NE2	2.17	0.60
1:A:272:ARG:NH2	1:A:354:THR:HG21	2.17	0.60
1:A:324:GLN:O	1:A:328:LEU:HD12	2.02	0.60
1:A:281:VAL:HG21	1:A:329:VAL:HG13	1.86	0.57
1:A:43:THR:H	1:A:242:THR:HG23	1.70	0.55
1:A:132:VAL:HG23	1:A:134:MET:HB2	1.88	0.54
1:A:265:LYS:HE2	5:A:385:ADP:H5'2	1.90	0.54
1:A:203:MET:HE3	1:A:208:LYS:HG3	1.90	0.53
1:A:281:VAL:HG22	1:A:296:ILE:CD1	2.40	0.52
1:A:151:VAL:HA	1:A:154:ASN:OD1	2.10	0.52
1:A:223:PHE:HB3	1:A:226:PRO:HG3	1.93	0.51
1:A:337:PRO:O	1:A:340:LEU:HD22	2.10	0.51
1:A:122:MET:HG2	1:A:274:ALA:HB3	1.92	0.50
1:A:45:VAL:HG12	1:A:50:VAL:HG22	1.94	0.50
1:A:127:THR:HB	1:A:129:GLU:HG2	1.94	0.49
1:A:57:THR:HA	1:A:98:GLN:O	2.13	0.48
1:A:110:ASP:HB3	1:A:113:GLU:HG3	1.94	0.48
1:A:380:ALA:O	1:A:383:LYS:NZ	2.47	0.48
1:A:322:SER:HA	1:A:325:LEU:HB2	1.97	0.47
1:A:77:TYR:CZ	1:A:162:PRO:HB2	2.49	0.47
1:A:341:ILE:HA	1:A:346:LEU:HD12	1.97	0.46
1:A:157:LEU:HD11	1:A:201:ALA:HB1	1.98	0.46
1:A:6:THR:OG1	1:A:169:THR:HB	2.17	0.45
1:A:38:ARG:HB2	1:A:57:THR:HG23	1.98	0.45
1:A:83:GLY:O	1:A:236:MET:HG2	2.16	0.45
1:A:244:ARG:O	1:A:246:ILE:HG22	2.17	0.44
1:A:35:PRO:HB2	1:A:347:LEU:HB3	1.99	0.44
1:A:257:HIS:CD2	1:A:258:GLY:O	2.64	0.44
1:A:159:TRP:CE3	1:A:193:ILE:HG21	2.52	0.44
1:A:123:PHE:HA	1:A:296:ILE:O	2.17	0.43
1:A:326:THR:HG22	1:A:330:ARG:HE	1.84	0.43
1:A:351:TYR:O	1:A:354:THR:HG22	2.19	0.43
1:A:331:GLU:HG3	1:A:332:PHE:N	2.33	0.42
1:A:250:THR:HG22	1:A:251:TYR:N	2.34	0.42
1:A:277:ALA:HA	1:A:344:LEU:HD11	2.01	0.42
1:A:374:GLN:O	1:A:377:ARG:HB3	2.20	0.42
1:A:75:ILE:O	1:A:152:ARG:NH2	2.53	0.41
1:A:78:VAL:HG12	1:A:82:MET:HE1	2.02	0.41
1:A:2:LYS:HA	1:A:172:TYR:O	2.20	0.41
1:A:250:THR:HG23	1:A:251:TYR:CD2	2.55	0.41
1:A:246:ILE:HG12	1:A:257:HIS:CE1	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:VAL:HB	1:A:56:ILE:HG13	2.03	0.41
1:A:204:GLU:O	1:A:209:PRO:HD3	2.21	0.41
1:A:187:THR:HG22	1:A:188:GLN:O	2.21	0.40

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 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	374/383 (98%)	348 (93%)	23 (6%)	3 (1%)	16	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	363	GLU
1	A	250	THR
1	A	381	GLY

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 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	306/311 (98%)	256 (84%)	50 (16%)	2	8

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	3	HIS
1	A	31	LEU
1	A	36	LYS
1	A	39	VAL
1	A	45	VAL
1	A	47	THR
1	A	51	LEU
1	A	56	ILE
1	A	62	VAL
1	A	65	GLU
1	A	81	ASP
1	A	92	LEU
1	A	111	PRO
1	A	112	LEU
1	A	121	LEU
1	A	127	THR
1	A	131	ASP
1	A	144	LEU
1	A	148	GLN
1	A	160	LEU
1	A	169	THR
1	A	174	ASP
1	A	177	ILE
1	A	183	VAL
1	A	184	VAL
1	A	194	ASP
1	A	196	LYS
1	A	200	GLU
1	A	229	ARG
1	A	236	MET
1	A	242	THR
1	A	245	LYS
1	A	246	ILE
1	A	247	ILE
1	A	248	VAL
1	A	281	VAL
1	A	308	THR
1	A	311	MET
1	A	317	THR
1	A	327	LEU
1	A	331	GLU
1	A	335	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	340	LEU
1	A	342	GLN
1	A	347	LEU
1	A	354	THR
1	A	366	PRO
1	A	370	THR
1	A	383	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	33	GLN
1	A	114	GLN
1	A	142	HIS
1	A	167	GLN
1	A	189	HIS
1	A	257	HIS
1	A	359	HIS
1	A	374	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 6 ligands modelled in this entry, 4 are 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	PO4	A	384	3	4,4,4	2.09	3 (75%)	6,6,6	0.50	0
5	ADP	A	385	3	28,29,29	1.06	1 (3%)	43,45,45	0.91	1 (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
5	ADP	A	385	3	-	7/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	385	ADP	PA-O3A	4.14	1.64	1.59
2	A	384	PO4	P-O3	-2.46	1.47	1.54
2	A	384	PO4	P-O1	-2.43	1.45	1.50
2	A	384	PO4	P-O2	-2.08	1.48	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	385	ADP	C2'-C3'-C4'	2.05	106.58	102.61

There are no chirality outliers.

All (7) torsion outliers are listed below:

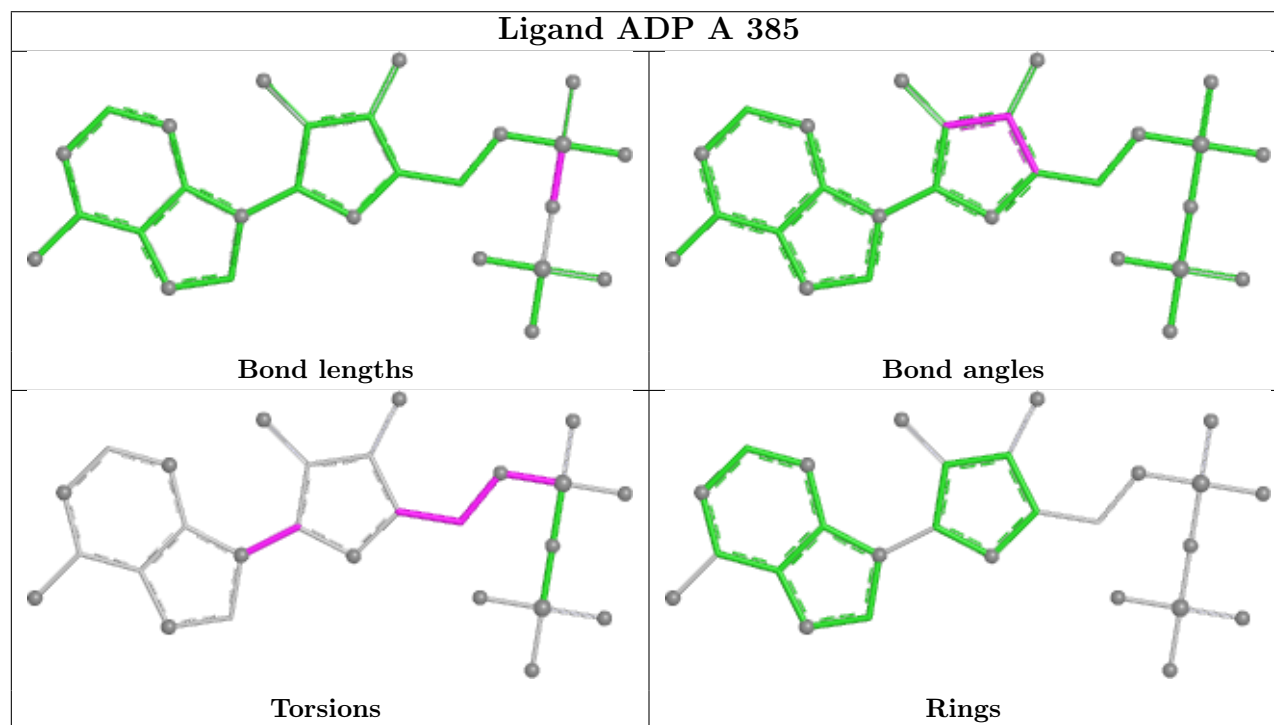
Mol	Chain	Res	Type	Atoms
5	A	385	ADP	C5'-O5'-PA-O1A
5	A	385	ADP	C5'-O5'-PA-O2A
5	A	385	ADP	C5'-O5'-PA-O3A
5	A	385	ADP	O4'-C4'-C5'-O5'
5	A	385	ADP	C3'-C4'-C5'-O5'
5	A	385	ADP	C2'-C1'-N9-C8
5	A	385	ADP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	385	ADP	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.



5.7 Other polymers ⓘ

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.