



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 9, 2023 – 04:23 PM EDT

PDB ID : 4INE
Title : Crystal structure of N-methyl transferase (PMT-2) from *Caenorhabditis elegans* complexed with S-adenosyl homocysteine and phosphoethanolamine
Authors : Lukk, T.; Nair, S.K.
Deposited on : 2013-01-04
Resolution : 1.45 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

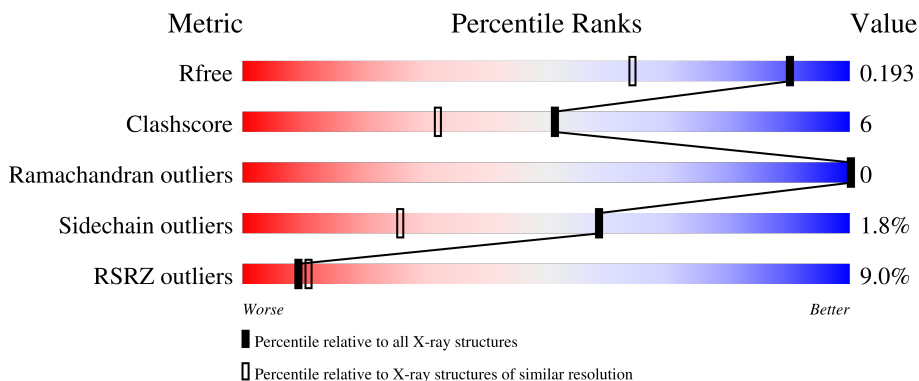
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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))
R_{free}	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	454	 5% 86% 9% • 5%
1	B	454	 12% 85% 9% 6%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 8171 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 Protein PMT-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	431	Total	C	N	O	S	0	8	0
			3535	2250	596	680	9			
1	B	428	Total	C	N	O	S	0	4	0
			3474	2210	583	672	9			

There are 46 discrepancies between the modelled and reference sequences:

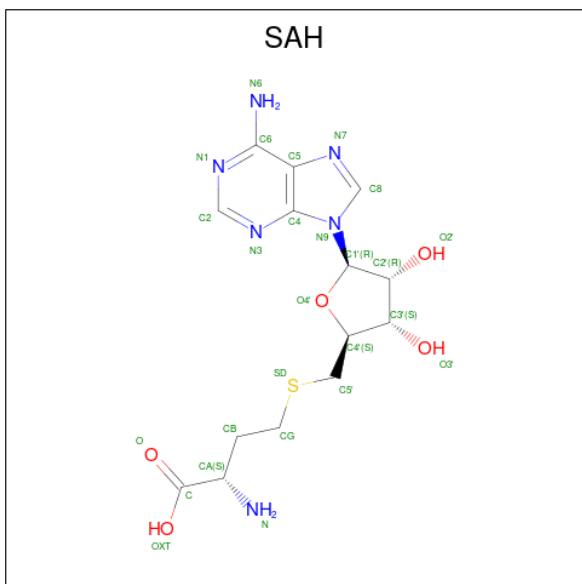
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q22993
A	-18	GLY	-	expression tag	UNP Q22993
A	-17	SER	-	expression tag	UNP Q22993
A	-16	SER	-	expression tag	UNP Q22993
A	-15	HIS	-	expression tag	UNP Q22993
A	-14	HIS	-	expression tag	UNP Q22993
A	-13	HIS	-	expression tag	UNP Q22993
A	-12	HIS	-	expression tag	UNP Q22993
A	-11	HIS	-	expression tag	UNP Q22993
A	-10	HIS	-	expression tag	UNP Q22993
A	-9	SER	-	expression tag	UNP Q22993
A	-8	SER	-	expression tag	UNP Q22993
A	-7	GLY	-	expression tag	UNP Q22993
A	-6	LEU	-	expression tag	UNP Q22993
A	-5	VAL	-	expression tag	UNP Q22993
A	-4	PRO	-	expression tag	UNP Q22993
A	-3	ARG	-	expression tag	UNP Q22993
A	-2	GLY	-	expression tag	UNP Q22993
A	-1	SER	-	expression tag	UNP Q22993
A	0	HIS	-	expression tag	UNP Q22993
A	?	-	ASN	SEE REMARK 999	UNP Q22993
A	?	-	ALA	SEE REMARK 999	UNP Q22993
A	?	-	THR	SEE REMARK 999	UNP Q22993
B	-19	MET	-	initiating methionine	UNP Q22993
B	-18	GLY	-	expression tag	UNP Q22993

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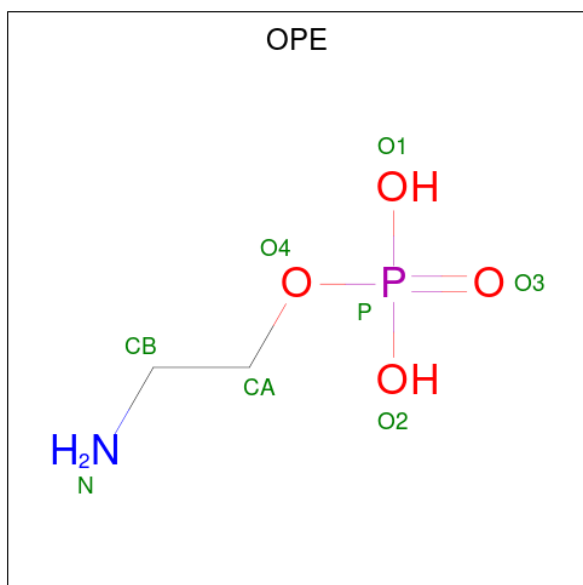
Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	SER	-	expression tag	UNP Q22993
B	-16	SER	-	expression tag	UNP Q22993
B	-15	HIS	-	expression tag	UNP Q22993
B	-14	HIS	-	expression tag	UNP Q22993
B	-13	HIS	-	expression tag	UNP Q22993
B	-12	HIS	-	expression tag	UNP Q22993
B	-11	HIS	-	expression tag	UNP Q22993
B	-10	HIS	-	expression tag	UNP Q22993
B	-9	SER	-	expression tag	UNP Q22993
B	-8	SER	-	expression tag	UNP Q22993
B	-7	GLY	-	expression tag	UNP Q22993
B	-6	LEU	-	expression tag	UNP Q22993
B	-5	VAL	-	expression tag	UNP Q22993
B	-4	PRO	-	expression tag	UNP Q22993
B	-3	ARG	-	expression tag	UNP Q22993
B	-2	GLY	-	expression tag	UNP Q22993
B	-1	SER	-	expression tag	UNP Q22993
B	0	HIS	-	expression tag	UNP Q22993
B	?	-	ASN	SEE REMARK 999	UNP Q22993
B	?	-	ALA	SEE REMARK 999	UNP Q22993
B	?	-	THR	SEE REMARK 999	UNP Q22993

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is PHOSPHORIC ACID MONO-(2-AMINO-ETHYL) ESTER (three-letter code: OPE) (formula: C₂H₈NO₄P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	B	1	Total	C	N	O	P	0	0
			8	2	1	4	1		

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	600	Total	O	0	0
			600	600		
5	B	486	Total	O	0	0
			486	486		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.13Å 68.01Å 74.74Å 107.18° 96.30° 106.51°	Depositor
Resolution (Å)	29.63 – 1.45 29.63 – 1.45	Depositor EDS
% Data completeness (in resolution range)	85.7 (29.63-1.45) 85.7 (29.63-1.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.74 (at 1.45Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.170 , 0.194 0.169 , 0.193	Depositor DCC
R_{free} test set	7671 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtrriage
Anisotropy	0.096	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8171	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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.

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: OPE, SAH, BME

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	0.54	0/3607	0.67	0/4878
1	B	0.49	2/3544 (0.1%)	0.62	0/4792
All	All	0.51	2/7151 (0.0%)	0.65	0/9670

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	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	80	ASN	C-N	6.62	1.49	1.34
1	B	412	TRP	CD2-CE2	5.07	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	18	THR	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	3535	0	3454	47	0
1	B	3474	0	3388	32	0
2	A	26	0	19	0	0
2	B	26	0	19	0	0
3	A	8	0	6	0	0
3	B	8	0	6	0	0
4	A	4	0	5	0	0
4	B	4	0	5	0	0
5	A	600	0	0	10	0
5	B	486	0	0	5	0
All	All	8171	0	6902	79	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 6.

All (79) 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:405:ARG:CZ	1:A:409[B]:ILE:HD12	1.69	1.22
1:A:374:MET:HG2	5:A:1064:HOH:O	1.42	1.13
1:B:393:GLU:HG2	1:B:405:ARG:NH1	1.68	1.08
1:A:325[A]:LEU:HD11	1:A:428:PHE:CE1	2.00	0.95
1:A:242[A]:VAL:CG1	1:A:250:VAL:HG21	2.00	0.92
1:B:360:ILE:O	1:B:364[B]:THR:HG22	1.70	0.90
1:B:129:THR:CG2	1:B:133:GLY:HA2	2.03	0.88
1:A:242[A]:VAL:HG11	1:A:250:VAL:HG21	1.55	0.88
1:B:393:GLU:HG2	1:B:405:ARG:HH12	1.33	0.87
1:A:218[A]:ARG:HD3	1:A:428:PHE:CZ	2.10	0.87
1:A:405:ARG:CZ	1:A:409[B]:ILE:CD1	2.53	0.86
1:B:393:GLU:OE2	1:B:405:ARG:CZ	2.27	0.82
1:B:129:THR:HG23	1:B:133:GLY:HA2	1.61	0.80
1:A:316:LYS:HE2	5:A:735:HOH:O	1.79	0.80
1:B:164:ARG:HD2	5:B:1014:HOH:O	1.82	0.79
1:A:218[A]:ARG:CD	1:A:428:PHE:CE1	2.66	0.78
1:A:421:LYS:HE2	5:A:920:HOH:O	1.81	0.78
1:A:405:ARG:NH2	1:A:409[B]:ILE:CD1	2.46	0.77
1:B:393:GLU:CG	1:B:405:ARG:NH1	2.49	0.76
1:A:405:ARG:NH2	1:A:409[B]:ILE:HD12	2.04	0.72
1:B:242[A]:VAL:CG2	1:B:250:VAL:HG21	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218[A]:ARG:HD2	1:A:428:PHE:CE1	2.25	0.71
1:B:380:GLU:O	1:B:384:GLU:HG3	1.92	0.70
1:B:316:LYS:HE2	5:B:705:HOH:O	1.96	0.66
1:A:355:LYS:HE3	5:A:1147:HOH:O	1.96	0.65
1:B:201:VAL:HG13	5:B:904:HOH:O	1.98	0.64
1:A:242[A]:VAL:HG22	1:A:248:VAL:HB	1.80	0.63
1:A:242[A]:VAL:HG11	1:A:250:VAL:CG2	2.29	0.63
1:A:218[A]:ARG:HD3	1:A:428:PHE:CE1	2.30	0.62
1:A:218[A]:ARG:HD2	1:A:428:PHE:HE1	1.64	0.61
1:A:355:LYS:NZ	1:A:359:ASP:OD1	2.25	0.61
1:A:405:ARG:NH1	1:A:409[B]:ILE:HD12	2.14	0.61
1:A:242[A]:VAL:CG1	1:A:250:VAL:CG2	2.80	0.59
1:A:20:GLY:H	1:A:21:ARG:NH1	2.01	0.59
1:B:393:GLU:CG	1:B:405:ARG:HH12	2.13	0.58
1:A:113:LYS:HB2	5:A:860:HOH:O	2.03	0.57
1:A:19:GLU:HA	5:A:1012:HOH:O	2.04	0.57
1:A:242[A]:VAL:HG13	1:A:250:VAL:HG21	1.84	0.57
1:B:53:HIS:HB3	1:B:58:GLN:OE1	2.05	0.57
1:A:16:LYS:O	1:A:19:GLU:HB3	2.04	0.57
1:A:204:ILE:HG13	1:A:259:MET:HE1	1.87	0.56
1:A:325[A]:LEU:CD1	1:A:428:PHE:CE1	2.84	0.55
1:B:242[A]:VAL:CG2	1:B:250:VAL:CG2	2.84	0.54
1:A:60:SER:O	1:A:63:ARG:NH1	2.38	0.53
1:B:55:SER:OG	1:B:57:GLU:HG2	2.10	0.51
1:A:218[A]:ARG:CD	1:A:428:PHE:CZ	2.88	0.51
1:A:270:GLU:OE1	5:A:895:HOH:O	2.19	0.51
1:B:390:GLU:HG3	1:B:409:ILE:HD12	1.94	0.50
1:B:364[B]:THR:HB	5:B:784:HOH:O	2.12	0.49
1:A:388:HIS:HE1	5:A:1083:HOH:O	1.96	0.49
1:B:129:THR:HG23	1:B:133:GLY:CA	2.35	0.49
1:B:81:ALA:HB1	1:B:122:TYR:OH	2.14	0.48
1:A:218[B]:ARG:HD2	5:A:1040:HOH:O	2.14	0.47
1:A:154:GLN:HB3	1:A:271:LYS:HD3	1.96	0.47
1:B:147[B]:GLU:HG3	5:B:773:HOH:O	2.15	0.46
1:A:20:GLY:H	1:A:21:ARG:HH11	1.62	0.46
1:A:201[B]:VAL:HG13	5:A:912:HOH:O	2.15	0.46
1:A:325[B]:LEU:HD23	1:A:326:ILE:N	2.31	0.45
1:A:239:ALA:O	1:A:242[A]:VAL:HG12	2.17	0.45
1:B:311:PHE:HB3	1:B:364[B]:THR:HG21	1.99	0.44
1:B:393:GLU:OE2	1:B:405:ARG:NH1	2.50	0.44
1:B:179:ARG:HG2	1:B:255:LEU:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ILE:HG22	1:A:278:SER:HB2	2.00	0.44
1:B:242[B]:VAL:HG12	1:B:248:VAL:HB	2.00	0.44
1:B:129:THR:HG22	1:B:130:ASP:O	2.18	0.43
1:A:60:SER:O	1:A:63:ARG:NH2	2.48	0.43
1:B:113:LYS:HA	1:B:113:LYS:HD2	1.86	0.43
1:A:219:PHE:CZ	1:A:325[A]:LEU:HB3	2.53	0.43
1:A:62:ILE:O	1:A:63:ARG:NH1	2.52	0.43
1:B:253:ILE:HG22	1:B:278:SER:HB2	2.01	0.42
1:B:354:LEU:HG	1:B:371:THR:HB	2.01	0.42
1:A:405:ARG:NH2	1:A:409[B]:ILE:HD13	2.28	0.42
1:A:242[A]:VAL:HG13	1:A:250:VAL:CG2	2.48	0.41
1:B:32:CYS:SG	1:B:35:GLN:HG3	2.59	0.41
1:A:179:ARG:HG2	1:A:255:LEU:O	2.20	0.41
1:A:405:ARG:NE	1:A:409[B]:ILE:HD12	2.28	0.41
1:B:393:GLU:CD	1:B:405:ARG:NH1	2.74	0.41
1:B:393:GLU:CD	1:B:405:ARG:CZ	2.88	0.40
1:A:380:GLU:O	1:A:384:GLU:HG3	2.22	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	437/454 (96%)	428 (98%)	9 (2%)	0	100	100
1	B	428/454 (94%)	421 (98%)	7 (2%)	0	100	100
All	All	865/908 (95%)	849 (98%)	16 (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 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	389/401 (97%)	382 (98%)	7 (2%)	59	26
1	B	383/401 (96%)	376 (98%)	7 (2%)	59	26
All	All	772/802 (96%)	758 (98%)	14 (2%)	59	26

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	21	ARG
1	A	22	SER
1	A	104	ARG
1	A	164	ARG
1	A	224	PRO
1	A	405	ARG
1	B	54	THR
1	B	63	ARG
1	B	104	ARG
1	B	164	ARG
1	B	308	GLU
1	B	354	LEU
1	B	403	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	388	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	OPE	A	502	-	7,7,7	0.88	0	9,9,9	0.87	1 (11%)
4	BME	A	503	1	3,3,3	0.33	0	1,2,2	0.53	0
4	BME	B	503	1	3,3,3	0.32	0	1,2,2	0.38	0
2	SAH	A	501	-	24,28,28	1.12	2 (8%)	25,40,40	1.77	6 (24%)
2	SAH	B	501	-	24,28,28	1.14	3 (12%)	25,40,40	1.42	3 (12%)
3	OPE	B	502	-	7,7,7	0.73	0	9,9,9	0.86	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	OPE	A	502	-	-	0/5/5/5	-
4	BME	A	503	1	-	0/1/1/1	-
4	BME	B	503	1	-	0/1/1/1	-
2	SAH	A	501	-	-	0/11/31/31	0/3/3/3
2	SAH	B	501	-	-	0/11/31/31	0/3/3/3
3	OPE	B	502	-	-	0/5/5/5	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	SAH	O4'-C1'	2.89	1.45	1.41
2	B	501	SAH	C5-C4	2.43	1.47	1.40
2	B	501	SAH	OXT-C	-2.07	1.23	1.30
2	A	501	SAH	OXT-C	-2.02	1.23	1.30
2	A	501	SAH	C2-N3	2.00	1.35	1.32

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	SAH	O4'-C1'-C2'	-5.14	99.42	106.93
2	B	501	SAH	C4-C5-N7	-3.26	106.00	109.40
2	A	501	SAH	N3-C2-N1	-3.25	123.59	128.68
2	A	501	SAH	C1'-N9-C4	-2.95	121.45	126.64
2	B	501	SAH	O4'-C1'-C2'	-2.89	102.70	106.93
2	B	501	SAH	N3-C2-N1	-2.60	124.61	128.68
2	A	501	SAH	C2-N1-C6	2.51	123.06	118.75
2	A	501	SAH	OXT-C-O	-2.48	118.46	124.09
2	A	501	SAH	N6-C6-N1	2.38	123.50	118.57
3	A	502	OPE	O2-P-O1	2.23	116.15	107.64

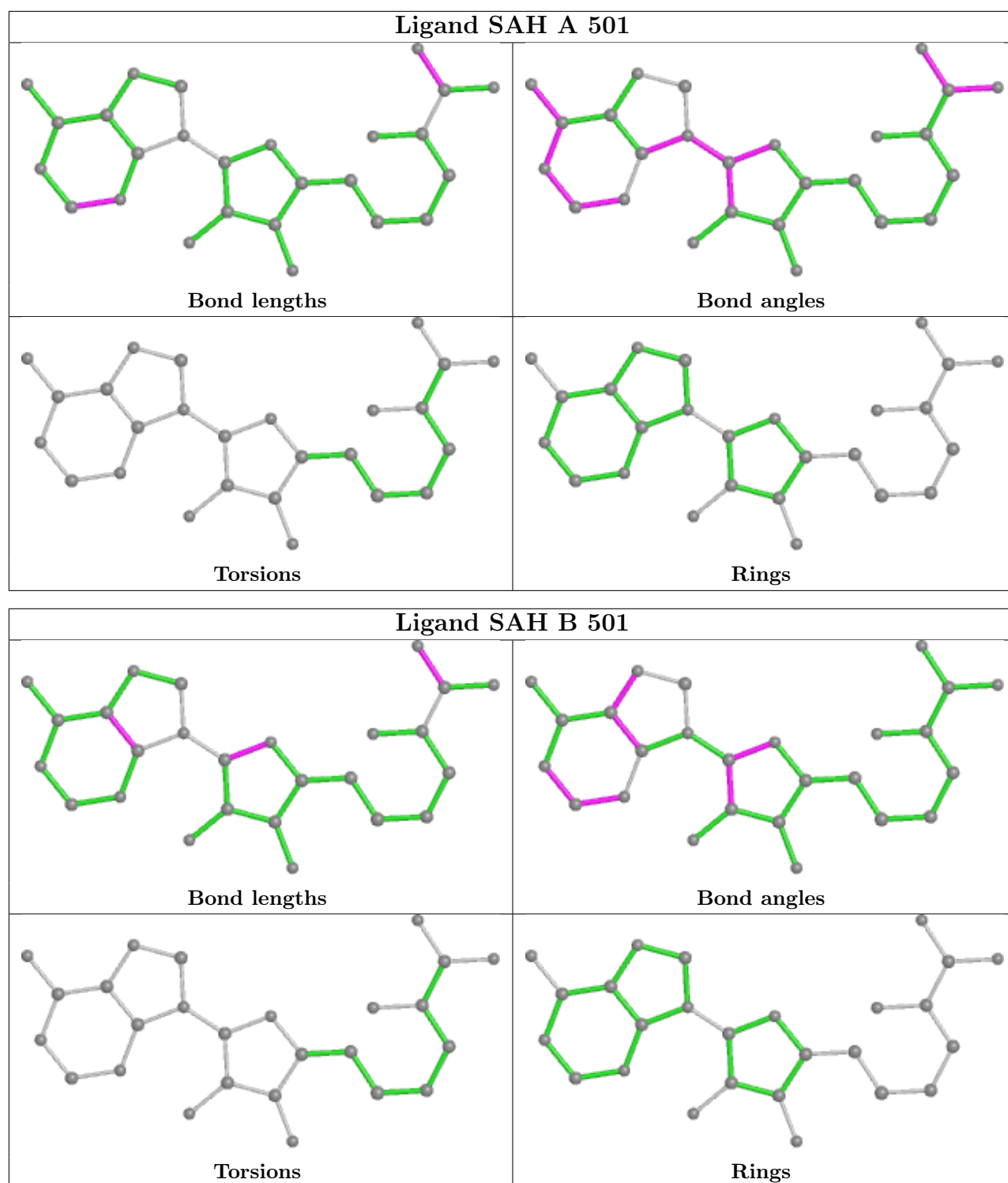
There are no chirality outliers.

There are no torsion outliers.

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	431/454 (94%)	0.19	22 (5%) 28 30	8, 14, 30, 46	0
1	B	428/454 (94%)	0.57	55 (12%) 3 4	11, 18, 40, 66	0
All	All	859/908 (94%)	0.38	77 (8%) 9 11	8, 16, 36, 66	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	SER	7.2
1	A	20	GLY	6.5
1	B	171	THR	6.3
1	B	60	SER	6.2
1	B	63	ARG	6.0
1	A	21	ARG	5.8
1	B	131	SER	5.8
1	B	61	THR	5.4
1	A	63	ARG	5.2
1	A	19	GLU	5.0
1	A	435	PHE	4.9
1	B	394	ALA	4.3
1	B	57	GLU	4.3
1	B	167	VAL	4.2
1	B	169	ALA	4.2
1	B	22	SER	4.1
1	B	56	LEU	4.0
1	A	172	THR	3.9
1	B	172	THR	3.8
1	B	132	ASP	3.8
1	B	82	ASP	3.5
1	B	435	PHE	3.5
1	B	76	GLN	3.4
1	B	174	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	122	TYR	3.3
1	B	399	LYS	3.3
1	A	61	THR	3.2
1	B	391	GLN	3.2
1	A	57	GLU	3.1
1	B	59	LEU	3.1
1	B	81	ALA	3.1
1	A	173	ASP	3.1
1	B	393	GLU	3.0
1	B	133	GLY	3.0
1	B	403	ARG	3.0
1	B	170	PRO	3.0
1	A	59	LEU	2.9
1	B	79	THR	2.9
1	A	62	ILE	2.9
1	A	56	LEU	2.9
1	A	22	SER	2.8
1	B	111	SER	2.8
1	B	279	ILE	2.7
1	A	170	PRO	2.7
1	A	428	PHE	2.7
1	B	398	SER	2.6
1	B	159	PHE	2.6
1	B	69	ILE	2.6
1	B	103	ILE	2.6
1	B	176	ILE	2.5
1	B	64	ASN	2.4
1	B	83	LEU	2.4
1	B	161	PHE	2.4
1	A	270	GLU	2.4
1	B	33	GLN	2.4
1	B	396	PHE	2.4
1	B	2	SER	2.3
1	B	130	ASP	2.3
1	A	143	VAL	2.3
1	B	143	VAL	2.3
1	A	269	GLU	2.3
1	B	270	GLU	2.3
1	B	34	LYS	2.3
1	B	335	GLU	2.2
1	A	64	ASN	2.2
1	B	397	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	329	TYR	2.2
1	B	62	ILE	2.2
1	B	160	ILE	2.2
1	A	161	PHE	2.1
1	A	2	SER	2.1
1	B	58	GLN	2.1
1	B	54	THR	2.1
1	B	175	THR	2.1
1	B	97	ILE	2.0
1	B	96	ALA	2.0
1	B	102	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

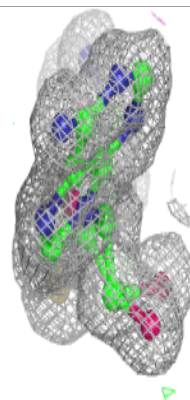
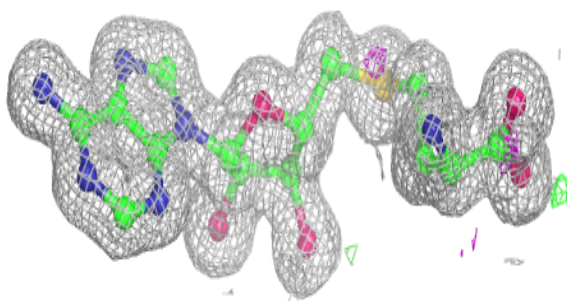
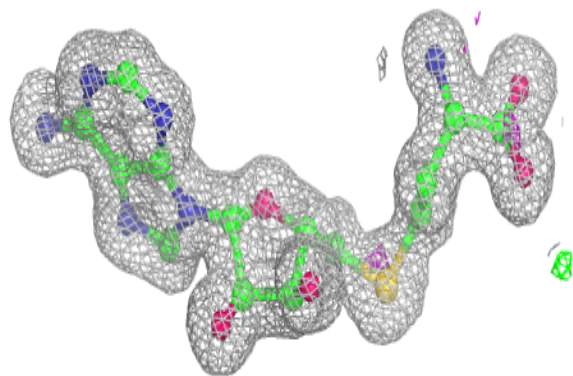
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BME	B	503	4/4	0.89	0.22	39,42,43,47	0
4	BME	A	503	4/4	0.95	0.17	30,33,34,37	0
3	OPE	B	502	8/8	0.98	0.09	13,14,15,16	0
2	SAH	A	501	26/26	0.98	0.09	9,10,12,12	0
2	SAH	B	501	26/26	0.98	0.08	12,14,14,15	0
3	OPE	A	502	8/8	0.99	0.09	10,10,11,11	0

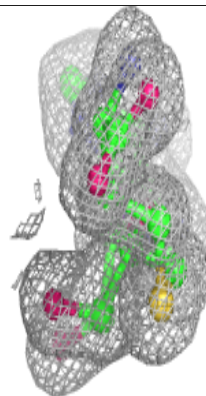
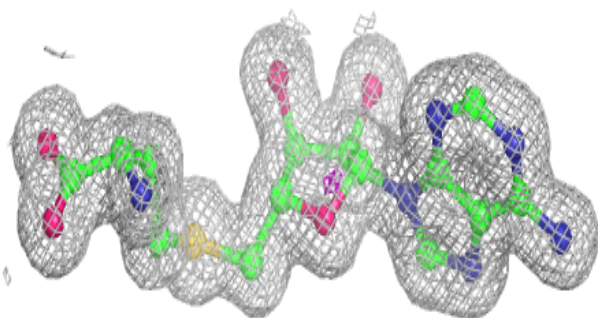
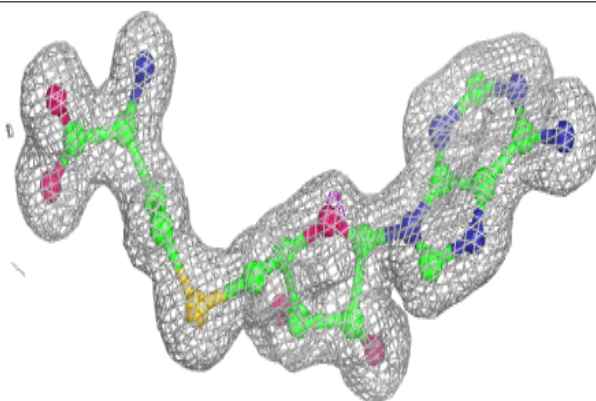
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around SAH A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around SAH B 501:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.