



# wwPDB X-ray Structure Validation Summary Report

Mar 5, 2026 – 01:04 PM UTC

PDB ID : 4BLV / pdb\_00004blv  
Title : Crystal structure of Escherichia coli 23S rRNA (A2030-N6)- methyltransferase RlmJ in complex with S-adenosylmethionine (AdoMet)  
Authors : Punekar, A.S.; Liljeruhm, J.; Shepherd, T.R.; Forster, A.C.; Selmer, M.  
Deposited on : 2013-05-04  
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](mailto: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>.

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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)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

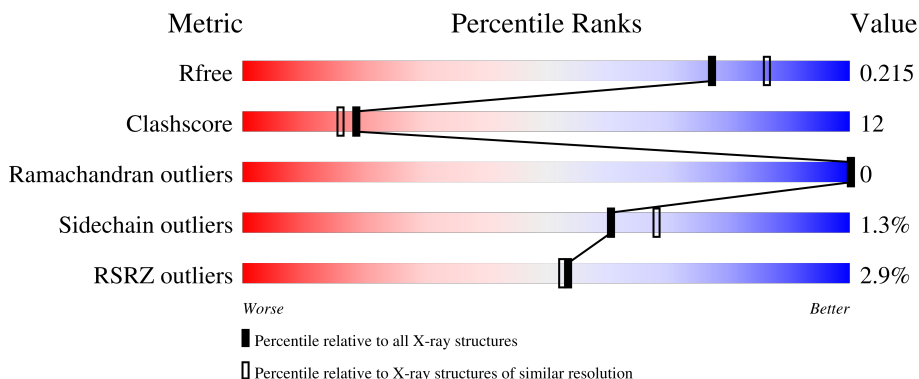
# 1 Overall quality at a glance

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))
$R_{free}$	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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  $\geq 3$ , 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	289	 4% 78% 18% ..
1	B	289	 2% 76% 18% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	A	1284	-	-	X	-
5	EDO	A	1285	-	-	X	-
5	EDO	A	1287	-	-	X	-
5	EDO	A	1289	-	-	X	-
5	EDO	A	1291	-	-	X	-
5	EDO	B	1284	-	-	X	-
5	EDO	B	1285	-	-	X	-
5	EDO	B	1286	-	-	X	-
5	EDO	B	1288	-	-	X	-
5	EDO	B	1289	-	-	X	-
5	EDO	B	1291	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5199 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.

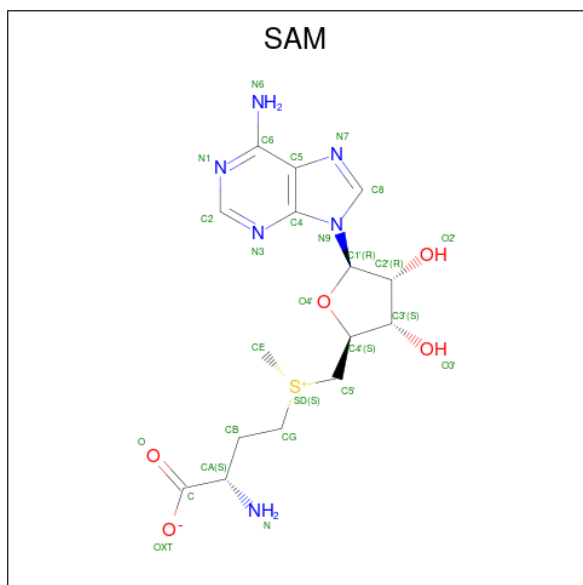
- Molecule 1 is a protein called RIBOSOMAL RNA LARGE SUBUNIT METHYLTRANSFERASE J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	280	2303	1477	405	415	6	0	10	0
1	B	276	2265	1453	399	408	5	0	9	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	SER	-	expression tag	UNP P37634
A	282	LYS	-	expression tag	UNP P37634
A	283	GLY	-	expression tag	UNP P37634
A	284	HIS	-	expression tag	UNP P37634
A	285	HIS	-	expression tag	UNP P37634
A	286	HIS	-	expression tag	UNP P37634
A	287	HIS	-	expression tag	UNP P37634
A	288	HIS	-	expression tag	UNP P37634
A	289	HIS	-	expression tag	UNP P37634
B	281	SER	-	expression tag	UNP P37634
B	282	LYS	-	expression tag	UNP P37634
B	283	GLY	-	expression tag	UNP P37634
B	284	HIS	-	expression tag	UNP P37634
B	285	HIS	-	expression tag	UNP P37634
B	286	HIS	-	expression tag	UNP P37634
B	287	HIS	-	expression tag	UNP P37634
B	288	HIS	-	expression tag	UNP P37634
B	289	HIS	-	expression tag	UNP P37634

- Molecule 2 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: C<sub>15</sub>H<sub>22</sub>N<sub>6</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



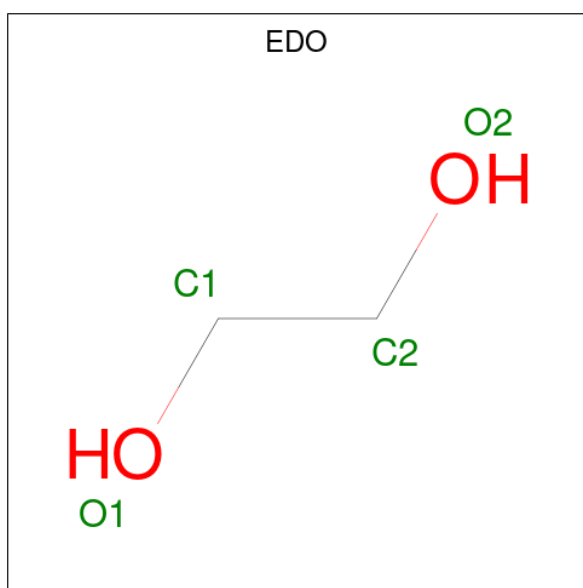
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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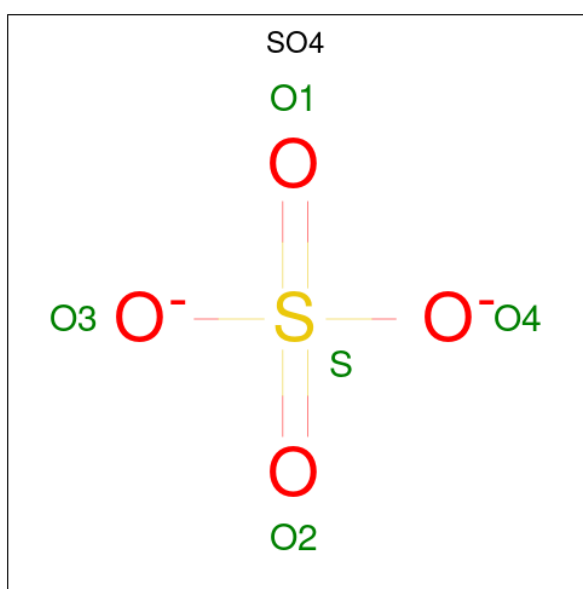
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total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

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

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0

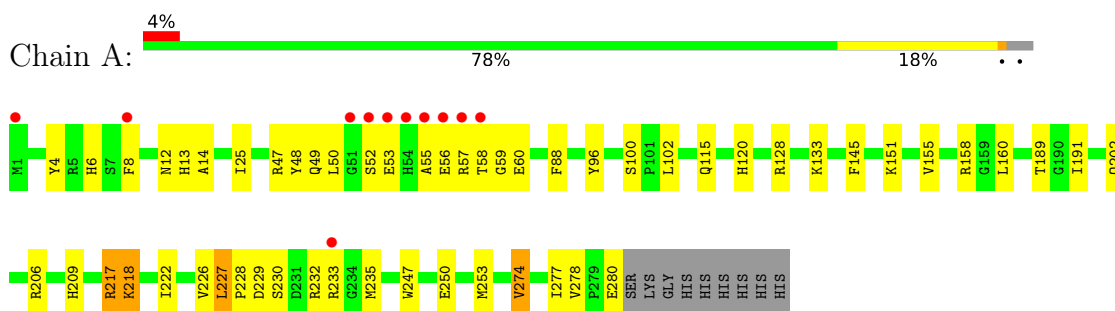
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	244	Total O 244 244	0	0
7	B	195	Total O 195 195	0	0

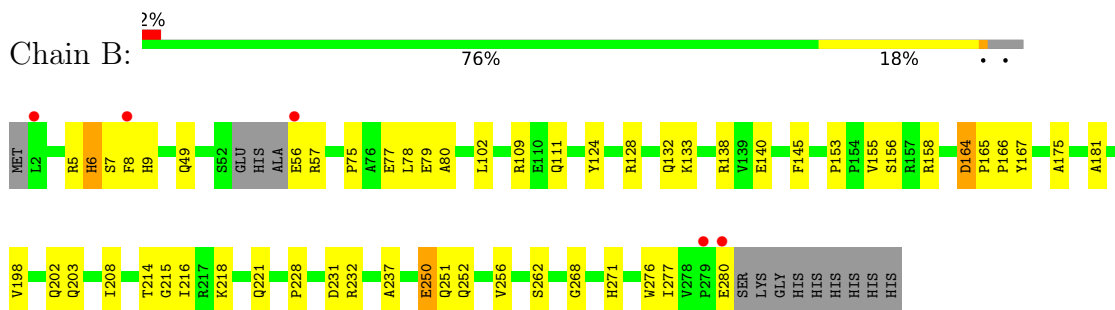
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

- Molecule 1: RIBOSOMAL RNA LARGE SUBUNIT METHYLTRANSFERASE J



- Molecule 1: RIBOSOMAL RNA LARGE SUBUNIT METHYLTRANSFERASE J



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.68Å 77.57Å 82.70Å 90.00° 103.50° 90.00°	Depositor
Resolution (Å)	45.39 – 2.00 45.39 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.39-2.00) 99.8 (45.39-2.00)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.56 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.170 , 0.213 0.178 , 0.215	Depositor DCC
$R_{free}$ test set	2009 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtrriage
Anisotropy	0.338	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 39.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5199	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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.

## 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, PEG, GOL, SAM, EDO

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	0.63	3/2386 (0.1%)	0.87	6/3235 (0.2%)
1	B	0.91	10/2346 (0.4%)	1.02	18/3180 (0.6%)
All	All	0.78	13/4732 (0.3%)	0.95	24/6415 (0.4%)

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	B	0	1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	7	SER	C-N	-22.02	1.02	1.33
1	B	215	GLY	C-N	-13.86	1.16	1.33
1	B	214	THR	C-N	-13.69	1.12	1.33
1	B	6	HIS	C-N	-9.71	1.21	1.33
1	B	156	SER	C-O	-7.26	1.14	1.24

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	164	ASP	CA-C-N	12.57	133.33	120.38
1	B	164	ASP	C-N-CA	12.57	133.33	120.38
1	B	216	ILE	O-C-N	10.10	132.59	122.79
1	B	5	ARG	O-C-N	-8.73	111.40	123.01
1	B	215	GLY	CA-C-N	8.42	132.98	120.69

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	6	HIS	Mainchain

## 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	2303	0	2345	57	0
1	B	2265	0	2303	49	0
2	A	27	0	21	4	0
2	B	27	0	22	0	0
3	A	6	0	8	0	0
4	A	7	0	10	1	0
4	B	7	0	10	0	0
5	A	52	0	78	29	0
5	B	56	0	84	33	0
6	A	10	0	0	0	0
7	A	244	0	0	9	0
7	B	195	0	0	6	0
All	All	5199	0	4881	115	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 12.

The worst 5 of 115 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:228:PRO:HA	5:A:1289:EDO:H12	1.31	1.12
5:B:1285:EDO:H12	5:B:1289:EDO:H21	1.18	1.09
1:A:12:ASN:HD21	5:A:1287:EDO:H12	1.22	1.02
5:B:1285:EDO:C1	5:B:1289:EDO:H21	1.92	0.98
1:B:268:GLY:HA2	5:B:1292:EDO:H21	1.53	0.90

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	288/289 (100%)	282 (98%)	6 (2%)	0	100	100
1	B	281/289 (97%)	272 (97%)	9 (3%)	0	100	100
All	All	569/578 (98%)	554 (97%)	15 (3%)	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	251/249 (101%)	245 (98%)	6 (2%)	43	47
1	B	247/249 (99%)	246 (100%)	1 (0%)	84	89
All	All	498/498 (100%)	491 (99%)	7 (1%)	61	66

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	227	LEU
1	A	274[A]	VAL
1	B	56	GLU
1	A	274[B]	VAL
1	A	218	LYS

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	146	GLN
1	B	9	HIS
1	B	146	GLN
1	B	203	GLN
1	B	221	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](#)

34 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$
5	EDO	B	1290	-	3,3,3	0.42	0	2,2,2	0.38	0
2	SAM	A	1281	-	27,29,29	2.12	8 (29%)	34,42,42	2.39	15 (44%)
2	SAM	B	1281	-	27,29,29	2.11	7 (25%)	34,42,42	2.36	14 (41%)
5	EDO	B	1291	-	3,3,3	0.13	0	2,2,2	0.55	0
5	EDO	B	1293	-	3,3,3	0.42	0	2,2,2	0.38	0
4	PEG	A	1283	-	6,6,6	0.62	0	5,5,5	1.39	0
5	EDO	B	1286	-	3,3,3	0.42	0	2,2,2	0.24	0
5	EDO	B	1294	-	3,3,3	0.50	0	2,2,2	0.15	0
5	EDO	B	1296	-	3,3,3	0.45	0	2,2,2	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	EDO	B	1284	-	3,3,3	0.43	0	2,2,2	0.39	0
5	EDO	A	1289	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	A	1285	-	3,3,3	0.44	0	2,2,2	0.25	0
3	GOL	A	1282	-	5,5,5	0.52	0	5,5,5	0.22	0
5	EDO	A	1293	-	3,3,3	0.49	0	2,2,2	0.27	0
5	EDO	A	1290	-	3,3,3	0.44	0	2,2,2	0.37	0
5	EDO	A	1287	-	3,3,3	0.69	0	2,2,2	0.66	0
5	EDO	A	1284	-	3,3,3	0.33	0	2,2,2	0.38	0
5	EDO	B	1289	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	B	1285	-	3,3,3	0.43	0	2,2,2	0.38	0
6	SO4	A	1298	-	4,4,4	0.32	0	6,6,6	0.25	0
5	EDO	A	1288	-	3,3,3	0.43	0	2,2,2	0.38	0
5	EDO	A	1291	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	A	1286	-	3,3,3	0.42	0	2,2,2	0.47	0
5	EDO	B	1288	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	B	1292	-	3,3,3	0.43	0	2,2,2	0.38	0
5	EDO	B	1287	-	3,3,3	0.44	0	2,2,2	0.35	0
5	EDO	B	1283	-	3,3,3	0.48	0	2,2,2	0.11	0
6	SO4	A	1297	-	4,4,4	0.22	0	6,6,6	0.19	0
5	EDO	A	1295	-	3,3,3	0.43	0	2,2,2	0.41	0
5	EDO	A	1294	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	A	1292	-	3,3,3	0.60	0	2,2,2	0.44	0
5	EDO	A	1296	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EDO	B	1295	-	3,3,3	0.41	0	2,2,2	0.39	0
4	PEG	B	1282	-	6,6,6	0.44	0	5,5,5	0.31	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	1290	-	-	0/1/1/1	-
2	SAM	A	1281	-	-	7/17/33/33	0/3/3/3
2	SAM	B	1281	-	-	6/17/33/33	0/3/3/3
5	EDO	B	1291	-	-	0/1/1/1	-
5	EDO	B	1293	-	-	1/1/1/1	-
4	PEG	A	1283	-	-	4/4/4/4	-
5	EDO	B	1286	-	-	0/1/1/1	-
5	EDO	B	1294	-	-	0/1/1/1	-
5	EDO	B	1296	-	-	0/1/1/1	-
5	EDO	B	1284	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	1289	-	-	1/1/1/1	-
5	EDO	A	1285	-	-	1/1/1/1	-
3	GOL	A	1282	-	-	4/4/4/4	-
5	EDO	A	1293	-	-	1/1/1/1	-
5	EDO	A	1290	-	-	1/1/1/1	-
5	EDO	A	1287	-	-	0/1/1/1	-
5	EDO	A	1284	-	-	0/1/1/1	-
5	EDO	B	1289	-	-	1/1/1/1	-
5	EDO	B	1285	-	-	1/1/1/1	-
5	EDO	A	1288	-	-	1/1/1/1	-
5	EDO	A	1291	-	-	1/1/1/1	-
5	EDO	A	1286	-	-	1/1/1/1	-
5	EDO	B	1288	-	-	1/1/1/1	-
5	EDO	B	1292	-	-	1/1/1/1	-
5	EDO	B	1287	-	-	0/1/1/1	-
5	EDO	B	1283	-	-	1/1/1/1	-
5	EDO	A	1295	-	-	1/1/1/1	-
5	EDO	A	1294	-	-	1/1/1/1	-
5	EDO	A	1292	-	-	0/1/1/1	-
5	EDO	A	1296	-	-	1/1/1/1	-
5	EDO	B	1295	-	-	0/1/1/1	-
4	PEG	B	1282	-	-	3/4/4/4	-

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1281	SAM	C5-N7	-4.74	1.30	1.39
2	A	1281	SAM	C5-N7	-4.65	1.30	1.39
2	B	1281	SAM	OXT-C	-4.55	1.16	1.30
2	A	1281	SAM	CE-SD	-4.48	1.50	1.78
2	B	1281	SAM	C5-C4	3.95	1.46	1.39

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1281	SAM	C5-C4-N3	-5.52	119.11	126.72
2	B	1281	SAM	C4-C5-N7	-5.29	104.53	110.58
2	B	1281	SAM	C5-C4-N3	-4.82	120.08	126.72
2	B	1281	SAM	O4'-C4'-C5'	4.81	121.03	108.88
2	B	1281	SAM	C5-N7-C8	4.47	110.48	103.45

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1281	SAM	N-CA-CB-CG
2	A	1281	SAM	C4'-C5'-SD-CE
2	B	1281	SAM	N-CA-CB-CG
2	B	1281	SAM	C4'-C5'-SD-CE
4	B	1282	PEG	O2-C3-C4-O4

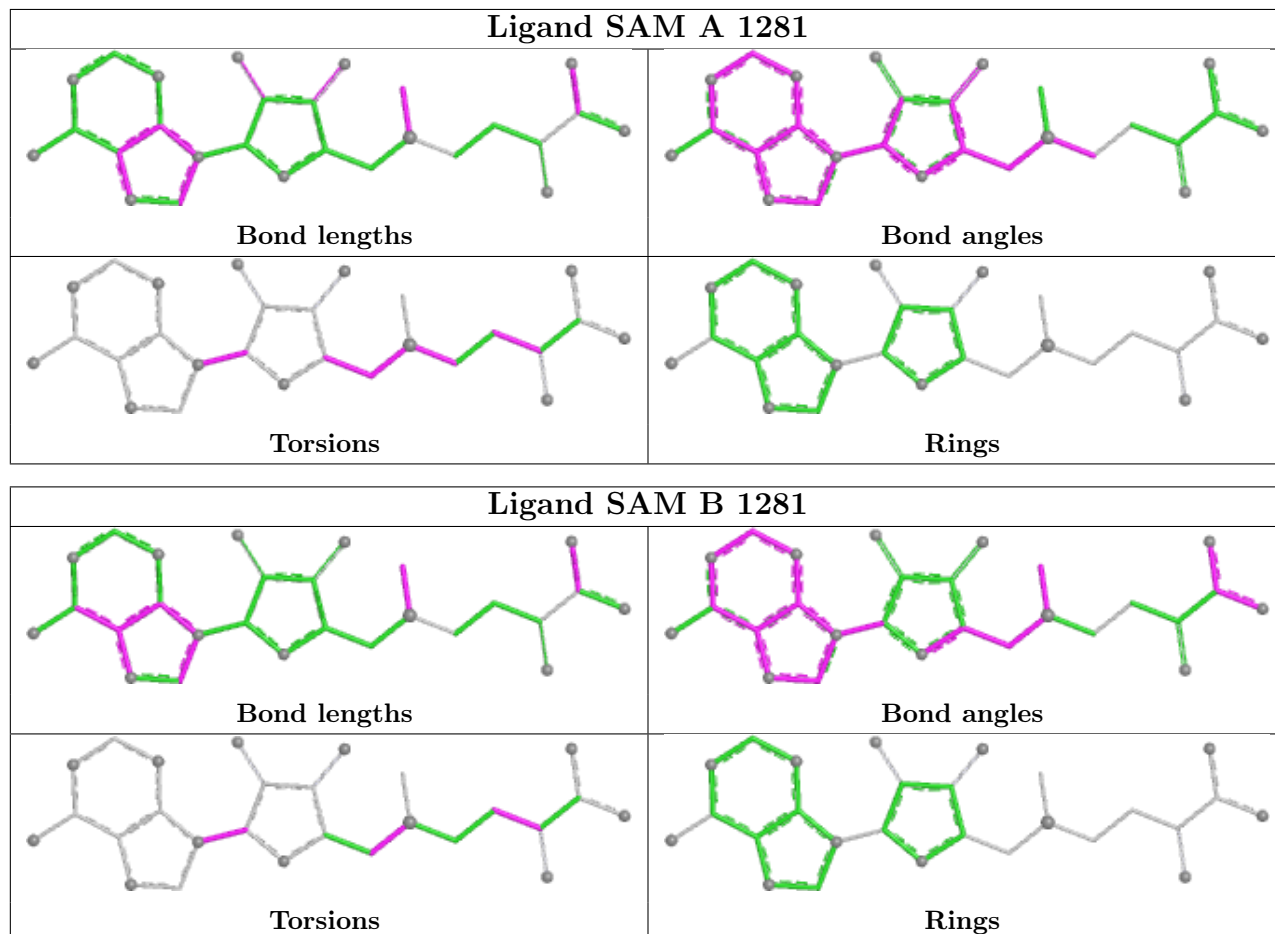
There are no ring outliers.

24 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1290	EDO	2	0
2	A	1281	SAM	4	0
5	B	1291	EDO	4	0
5	B	1293	EDO	1	0
4	A	1283	PEG	1	0
5	B	1286	EDO	5	0
5	B	1294	EDO	1	0
5	B	1296	EDO	2	0
5	B	1284	EDO	4	0
5	A	1289	EDO	6	0
5	A	1285	EDO	4	0
5	A	1290	EDO	1	0
5	A	1287	EDO	5	0
5	A	1284	EDO	4	0
5	B	1289	EDO	4	0
5	B	1285	EDO	4	0
5	A	1291	EDO	4	0
5	B	1288	EDO	4	0
5	B	1292	EDO	3	0
5	B	1287	EDO	1	0
5	B	1283	EDO	2	0
5	A	1295	EDO	3	0
5	A	1294	EDO	1	0
5	A	1292	EDO	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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	215:GLY	C	216:ILE	N	1.16
1	B	214:THR	C	215:GLY	N	1.12
1	B	7:SER	C	8:PHE	N	1.02

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	280/289 (96%)	-0.50	11 (3%) 43 42	2, 10, 36, 78	10 (3%)
1	B	276/289 (95%)	-0.53	5 (1%) 67 67	4, 12, 33, 59	9 (3%)
All	All	556/578 (96%)	-0.51	16 (2%) 53 52	2, 11, 34, 78	19 (3%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	52	SER	4.3
1	A	51	GLY	4.0
1	A	55	ALA	3.6
1	A	54	HIS	3.6
1	A	58	THR	3.4

### 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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

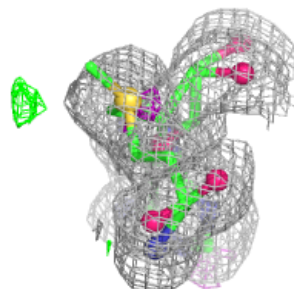
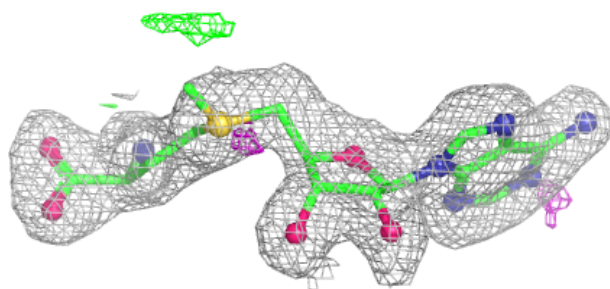
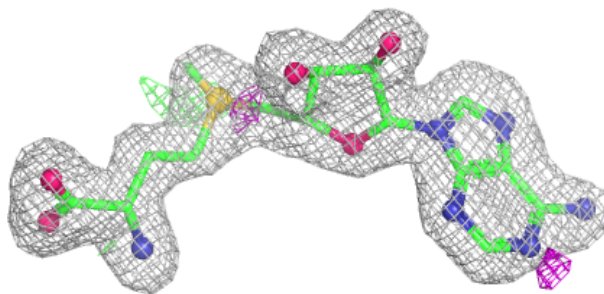
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	EDO	B	1292	4/4	0.70	0.20	22,27,33,34	0
4	PEG	B	1282	7/7	0.72	0.18	30,39,50,54	0
5	EDO	A	1286	4/4	0.74	0.21	29,33,37,38	0
5	EDO	B	1288	4/4	0.77	0.14	29,35,36,37	0
5	EDO	A	1296	4/4	0.77	0.14	30,31,38,41	0
3	GOL	A	1282	6/6	0.80	0.22	24,31,34,42	0
5	EDO	B	1287	4/4	0.80	0.14	36,36,36,43	0
5	EDO	B	1289	4/4	0.81	0.25	13,17,17,27	0
5	EDO	B	1295	4/4	0.81	0.14	38,39,43,45	0
5	EDO	B	1290	4/4	0.82	0.18	15,21,33,34	0
5	EDO	B	1291	4/4	0.83	0.22	16,26,37,38	0
5	EDO	A	1294	4/4	0.83	0.20	22,24,25,33	0
5	EDO	B	1294	4/4	0.83	0.18	27,37,38,42	0
5	EDO	A	1285	4/4	0.83	0.23	26,29,30,33	0
5	EDO	A	1287	4/4	0.84	0.20	12,17,23,29	0
5	EDO	A	1292	4/4	0.84	0.17	21,23,28,28	0
5	EDO	B	1284	4/4	0.85	0.18	17,20,25,26	0
5	EDO	B	1293	4/4	0.85	0.21	25,28,32,40	0
5	EDO	A	1291	4/4	0.86	0.18	14,19,20,24	0
5	EDO	A	1284	4/4	0.87	0.17	18,29,37,41	0
5	EDO	A	1290	4/4	0.88	0.25	20,22,32,42	0
4	PEG	A	1283	7/7	0.88	0.16	23,27,39,46	0
5	EDO	B	1286	4/4	0.88	0.16	21,29,29,37	0
5	EDO	B	1283	4/4	0.89	0.22	14,26,29,35	0
5	EDO	A	1289	4/4	0.89	0.19	17,28,28,32	0
5	EDO	B	1296	4/4	0.89	0.14	24,27,28,43	0
5	EDO	B	1285	4/4	0.90	0.21	16,21,22,24	0
5	EDO	A	1288	4/4	0.90	0.13	23,27,27,32	0
5	EDO	A	1293	4/4	0.90	0.16	25,30,33,43	0
2	SAM	B	1281	27/27	0.94	0.07	9,15,22,44	0
5	EDO	A	1295	4/4	0.95	0.12	11,18,20,30	0
2	SAM	A	1281	27/27	0.95	0.06	6,12,14,21	0
6	SO4	A	1298	5/5	0.95	0.08	15,16,25,27	0
6	SO4	A	1297	5/5	0.96	0.09	22,23,34,40	0

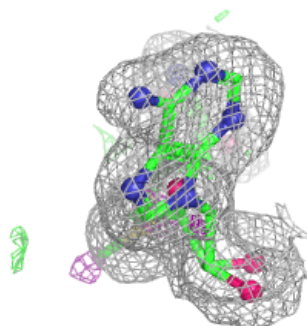
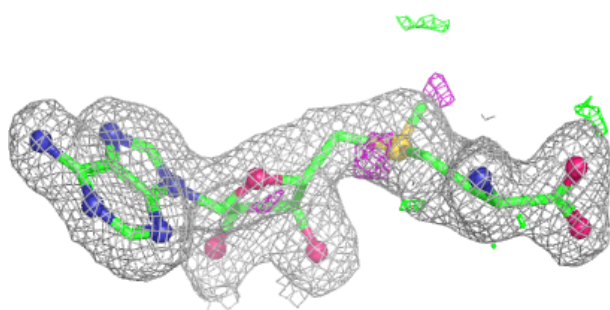
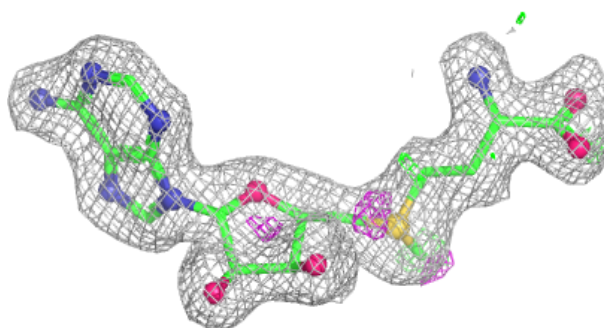
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around SAM B 1281:**

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

**Electron density around SAM A 1281:**

$2mF_o-DF_c$  (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.