



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:13 AM UTC

PDB ID : 6H2V / pdb_00006h2v
Title : Crystal structure of human METTL5-TRMT112 complex, the 18S rRNA
m6A1832 methyltransferase at 2.5Å resolution
Authors : van Tran, N.; Graille, M.
Deposited on : 2018-07-16
Resolution : 2.49 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)	:	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

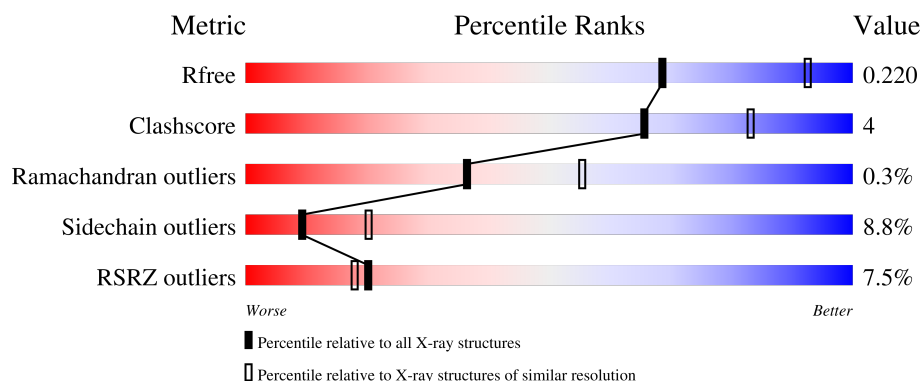
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	215	11% 74% 20% • •
1	C	215	7% 73% 15% • 10%
2	B	125	2% 73% 15% • 11%
2	D	125	6% 73% 19% 8%

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
2	CME	D	33[A]	-	-	-	X
2	CME	D	33[B]	-	-	-	X
5	PEG	B	201	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5209 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 Methyltransferase-like protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	1	0
			1677	1064	286	313	14			
1	C	194	Total	C	N	O	S	0	0	0
			1536	975	258	290	13			

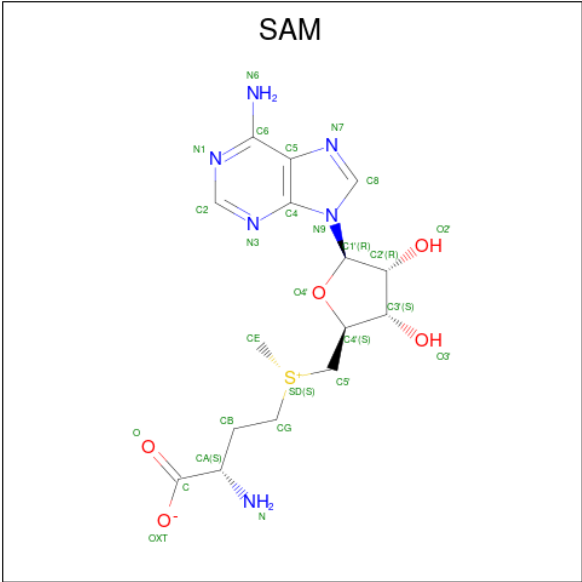
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	210	HIS	-	expression tag	UNP Q9NRN9
A	211	HIS	-	expression tag	UNP Q9NRN9
A	212	HIS	-	expression tag	UNP Q9NRN9
A	213	HIS	-	expression tag	UNP Q9NRN9
A	214	HIS	-	expression tag	UNP Q9NRN9
A	215	HIS	-	expression tag	UNP Q9NRN9
C	210	HIS	-	expression tag	UNP Q9NRN9
C	211	HIS	-	expression tag	UNP Q9NRN9
C	212	HIS	-	expression tag	UNP Q9NRN9
C	213	HIS	-	expression tag	UNP Q9NRN9
C	214	HIS	-	expression tag	UNP Q9NRN9
C	215	HIS	-	expression tag	UNP Q9NRN9

- Molecule 2 is a protein called Multifunctional methyltransferase subunit TRM112-like protein.

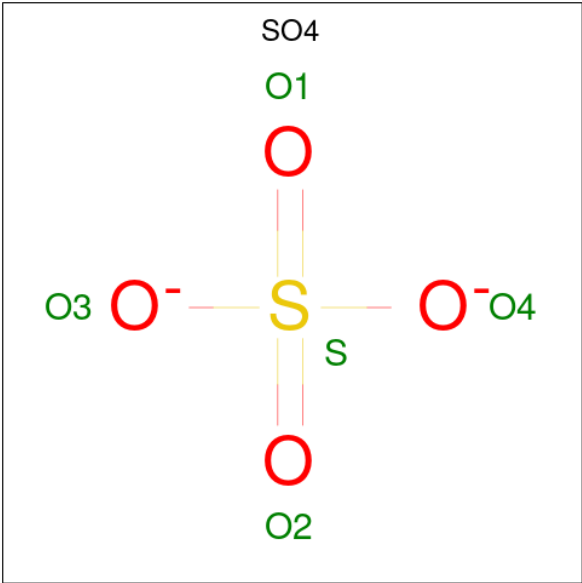
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	111	Total	C	N	O	S	0	0	0
			894	574	153	159	8			
2	D	115	Total	C	N	O	S	0	2	0
			954	610	160	174	10			

- Molecule 3 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: C₁₅H₂₂N₆O₅S).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



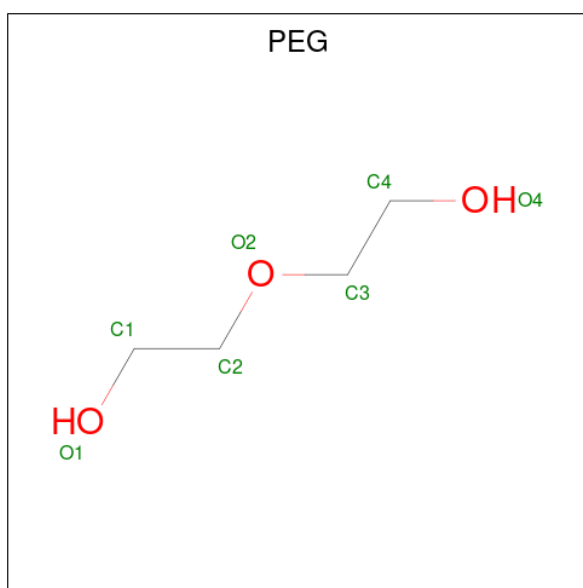
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



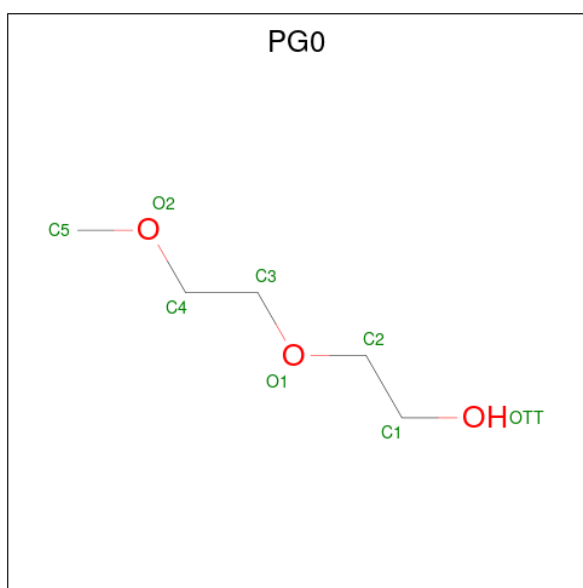
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 7 is 2-(2-METHOXYETHOXY)ETHANOL (CCD ID: PG0) (formula: $C_5H_{12}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			8	5	3		
7	D	1	Total	C	O	0	0
			8	5	3		

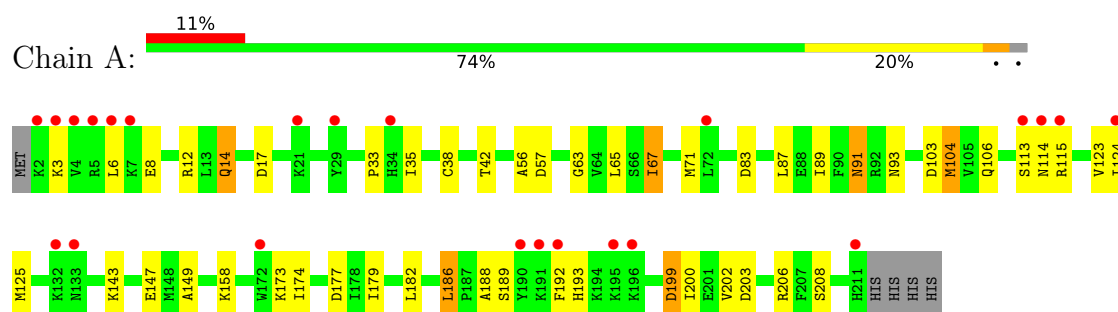
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	7	Total 7	O 7	0	0
8	B	5	Total 5	O 5	0	0
8	C	7	Total 7	O 7	0	0
8	D	9	Total 9	O 9	0	0

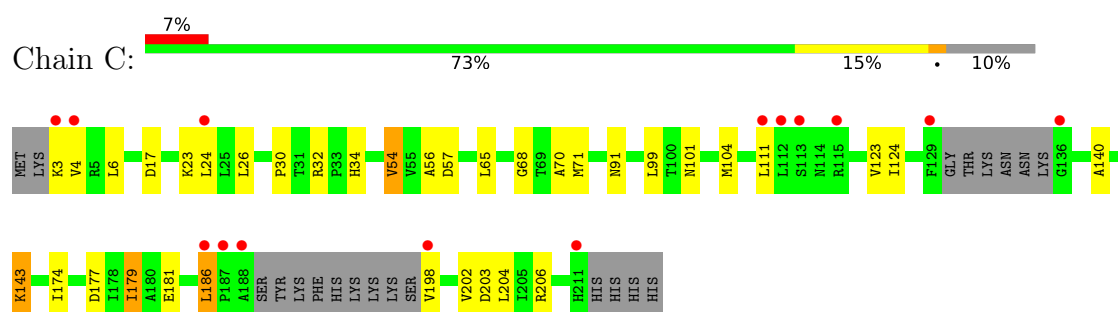
3 Residue-property plots [i](#)

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.

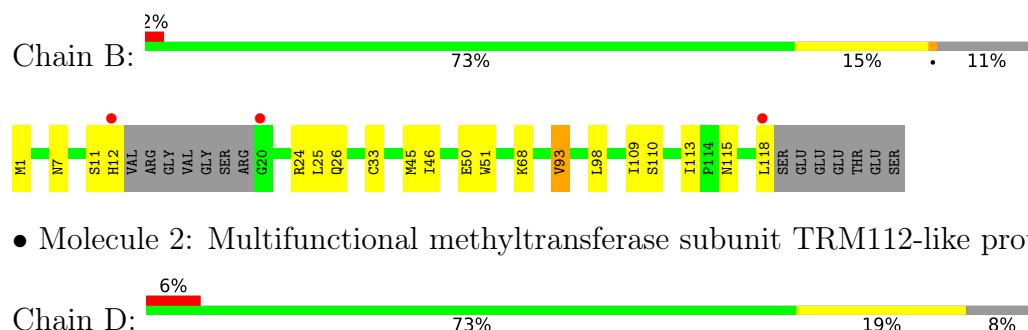
- Molecule 1: Methyltransferase-like protein 5



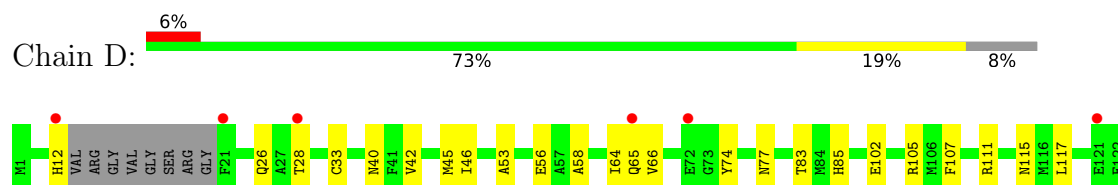
- Molecule 1: Methyltransferase-like protein 5



- Molecule 2: Multifunctional methyltransferase subunit TRM112-like protein



- Molecule 2: Multifunctional methyltransferase subunit TRM112-like protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.38Å 105.89Å 169.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.77 – 2.49 49.77 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.77-2.49) 99.8 (49.77-2.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 2.48Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.213 , 0.249 (Not available) , 0.220	Depositor DCC
R_{free} test set	1803 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	62.4	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5209	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, CME, PG0, SAM, EDO, SO4

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	0.86	0/1707	1.45	14/2298 (0.6%)
1	C	0.86	0/1561	1.46	14/2105 (0.7%)
2	B	0.94	1/903 (0.1%)	1.46	7/1220 (0.6%)
2	D	0.91	1/955 (0.1%)	1.44	8/1292 (0.6%)
All	All	0.89	2/5126 (0.0%)	1.46	43/6915 (0.6%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	46	ILE	CA-CB	7.74	1.57	1.54
2	D	46	ILE	CA-CB	5.83	1.57	1.54

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	203	ASP	CA-CB-CG	7.59	120.19	112.60
2	B	45	MET	CA-C-N	7.13	127.27	120.43
2	B	45	MET	C-N-CA	7.13	127.27	120.43
1	C	23	LYS	CA-C-N	7.10	129.79	120.28
1	C	23	LYS	C-N-CA	7.10	129.79	120.28
2	D	74	TYR	CA-C-N	6.64	129.18	120.28
2	D	74	TYR	C-N-CA	6.64	129.18	120.28
1	A	203	ASP	CA-CB-CG	6.49	119.09	112.60
2	D	45	MET	CA-C-N	6.49	126.66	120.43
2	D	45	MET	C-N-CA	6.49	126.66	120.43
1	C	3	LYS	CA-C-N	6.18	128.78	120.50
1	C	3	LYS	C-N-CA	6.18	128.78	120.50
2	B	93	VAL	N-CA-CB	6.13	117.81	110.95
1	C	57	ASP	CA-CB-CG	5.96	118.56	112.60
1	C	140	ALA	CA-C-N	5.74	128.44	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	140	ALA	C-N-CA	5.74	128.44	120.29
1	C	17	ASP	CA-CB-CG	5.72	118.32	112.60
2	D	77	ASN	CA-C-N	5.71	127.94	120.28
2	D	77	ASN	C-N-CA	5.71	127.94	120.28
2	D	53	ALA	CA-C-N	5.70	127.86	120.44
2	D	53	ALA	C-N-CA	5.70	127.86	120.44
1	A	188	ALA	CA-C-N	5.66	128.42	120.28
1	A	188	ALA	C-N-CA	5.66	128.42	120.28
1	A	91	ASN	CA-C-N	5.55	128.17	120.29
1	A	91	ASN	C-N-CA	5.55	128.17	120.29
1	A	83	ASP	CA-C-N	5.35	127.88	120.29
1	A	83	ASP	C-N-CA	5.35	127.88	120.29
1	C	186	LEU	N-CA-C	-5.33	102.95	110.31
1	C	143	LYS	CA-C-N	5.32	127.35	120.44
1	C	143	LYS	C-N-CA	5.32	127.35	120.44
1	A	63	GLY	N-CA-C	5.28	123.35	115.64
1	C	54	VAL	N-CA-CB	5.25	117.35	111.21
2	B	50	GLU	CA-C-N	5.20	127.77	120.28
2	B	50	GLU	C-N-CA	5.20	127.77	120.28
1	A	125	MET	N-CA-C	5.18	116.39	108.52
1	A	57	ASP	CA-CB-CG	5.16	117.76	112.60
2	B	51	TRP	N-CA-C	5.16	117.64	111.71
1	C	177	ASP	CA-CB-CG	5.12	117.72	112.60
2	B	93	VAL	CB-CA-C	5.10	117.05	111.08
1	A	177	ASP	CA-CB-CG	5.05	117.65	112.60
1	A	199	ASP	CA-CB-CG	5.04	117.64	112.60
1	A	38	CYS	CA-C-N	5.03	126.97	120.44
1	A	38	CYS	C-N-CA	5.03	126.97	120.44

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	1677	0	1688	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1536	0	1534	15	0
2	B	894	0	905	5	0
2	D	954	0	949	4	0
3	A	27	0	22	0	0
3	C	27	0	22	1	0
4	A	15	0	0	0	0
4	B	5	0	0	0	0
4	C	10	0	0	0	0
4	D	5	0	0	0	0
5	B	7	0	10	4	0
6	B	4	0	6	0	0
6	D	4	0	6	0	0
7	C	8	0	12	3	0
7	D	8	0	12	1	0
8	A	7	0	0	0	0
8	B	5	0	0	0	0
8	C	7	0	0	0	0
8	D	9	0	0	0	0
All	All	5209	0	5166	39	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 4.

All (39) 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:C:34:HIS:HB3	7:C:302:PG0:H52	1.56	0.87
2:B:115:ASN:HB2	5:B:201:PEG:H22	1.57	0.86
1:A:179:ILE:HD11	1:A:206:ARG:HB2	1.65	0.77
1:A:186:LEU:HG	1:A:200:ILE:HD11	1.67	0.74
1:C:179:ILE:HD11	1:C:206:ARG:HB2	1.71	0.73
1:C:24:LEU:H	1:C:24:LEU:HD12	1.63	0.62
1:A:87:LEU:HD22	1:A:104:MET:HG2	1.80	0.62
1:A:106:GLN:OE1	5:B:201:PEG:H41	2.00	0.61
1:A:14:GLN:HG3	1:A:33:PRO:HG2	1.85	0.59
1:C:68:GLY:HA2	1:C:71:MET:HE2	1.85	0.58
1:A:193:HIS:HD2	1:A:199:ASP:OD2	1.87	0.57
1:C:65:LEU:HB3	1:C:124:ILE:HD12	1.89	0.54
1:A:67:ILE:O	1:A:71:MET:HG3	2.08	0.54
1:A:113:SER:C	1:A:115:ARG:H	2.15	0.53
1:C:30:PRO:HD2	1:C:32:ARG:HH12	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:ASN:HA	1:C:104:MET:HE1	1.91	0.51
1:A:17:ASP:H	1:A:93:ASN:HD21	1.61	0.48
1:A:56:ALA:HB3	1:A:123:VAL:HG22	1.95	0.47
1:C:30:PRO:HD2	1:C:32:ARG:NH1	2.29	0.47
1:A:42:THR:HG21	1:A:179:ILE:HG21	1.98	0.46
2:D:111:ARG:HB3	7:D:202:PG0:H32	1.96	0.46
2:B:110:SER:HB3	5:B:201:PEG:H11	1.97	0.46
1:C:70:ALA:HB3	1:C:99:LEU:HD13	1.98	0.46
1:C:32:ARG:HB3	7:C:302:PG0:H53	1.96	0.45
1:C:56:ALA:HB3	1:C:123:VAL:HG22	2.00	0.44
2:B:98:LEU:HG	2:B:109:ILE:HD11	2.00	0.44
2:B:113:ILE:O	5:B:201:PEG:H21	2.19	0.43
2:B:1:MET:HE1	2:B:25:LEU:HD13	2.00	0.43
1:C:32:ARG:CB	7:C:302:PG0:H53	2.49	0.42
1:A:123:VAL:HG23	1:A:149:ALA:HB2	2.02	0.42
1:C:70:ALA:HB1	1:C:101:ASN:OD1	2.20	0.41
1:C:26:LEU:HB3	3:C:301:SAM:H2'	2.03	0.41
2:D:58:ALA:HB1	2:D:66:VAL:HG21	2.03	0.41
2:D:107:PHE:HB3	2:D:115:ASN:O	2.20	0.41
1:A:65:LEU:HB3	1:A:124:ILE:HD12	2.03	0.40
1:C:179:ILE:HD12	1:C:204:LEU:HG	2.04	0.40
1:A:35:ILE:HG23	1:A:182:LEU:HD13	2.03	0.40
2:D:42:VAL:HG21	2:D:85:HIS:HB2	2.04	0.40
1:A:193:HIS:CD2	1:A:199:ASP:OD2	2.72	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	209/215 (97%)	205 (98%)	3 (1%)	1 (0%)	24 43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	188/215 (87%)	184 (98%)	4 (2%)	0	100	100
2	B	106/125 (85%)	105 (99%)	0	1 (1%)	14	27
2	D	111/125 (89%)	109 (98%)	2 (2%)	0	100	100
All	All	614/680 (90%)	603 (98%)	9 (2%)	2 (0%)	36	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	11	SER
1	A	114	ASN

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	186/190 (98%)	166 (89%)	20 (11%)	6	13
1	C	170/190 (90%)	159 (94%)	11 (6%)	15	32
2	B	99/111 (89%)	92 (93%)	7 (7%)	13	29
2	D	105/111 (95%)	94 (90%)	11 (10%)	6	14
All	All	560/602 (93%)	511 (91%)	49 (9%)	9	20

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	6	LEU
1	A	8	GLU
1	A	12	ARG
1	A	14	GLN
1	A	67	ILE
1	A	89	ILE
1	A	91	ASN
1	A	103	ASP

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Mol	Chain	Res	Type
1	A	104	MET
1	A	143	LYS
1	A	147	GLU
1	A	158	LYS
1	A	173	LYS
1	A	174	ILE
1	A	186	LEU
1	A	189	SER
1	A	192	PHE
1	A	202	VAL
1	A	208	SER
2	B	7	ASN
2	B	12	HIS
2	B	24	ARG
2	B	26	GLN
2	B	68	LYS
2	B	93	VAL
2	B	118	LEU
1	C	4	VAL
1	C	6	LEU
1	C	54	VAL
1	C	111	LEU
1	C	143	LYS
1	C	174	ILE
1	C	179	ILE
1	C	181	GLU
1	C	186	LEU
1	C	198	VAL
1	C	202	VAL
2	D	12	HIS
2	D	26	GLN
2	D	28	THR
2	D	40	ASN
2	D	56	GLU
2	D	64	ILE
2	D	65	GLN
2	D	83	THR
2	D	102	GLU
2	D	105	ARG
2	D	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	91	ASN
1	A	93	ASN
1	A	166	GLN
1	A	193	HIS
2	B	26	GLN
2	B	38	ASN
2	B	60	ASN
1	C	14	GLN
1	C	15	GLN
1	C	45	ASN
1	C	93	ASN
2	D	38	ASN
2	D	40	ASN
2	D	99	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
2	CME	D	33[B]	2	8,9,10	0.75	0	6,9,11	1.91	2 (33%)
2	CME	B	33	2	8,9,10	1.01	0	6,9,11	1.42	2 (33%)
2	CME	D	33[A]	2	8,9,10	0.86	0	6,9,11	0.99	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
2	CME	D	33[B]	2	-	2/5/8/10	-
2	CME	B	33	2	-	2/5/8/10	-
2	CME	D	33[A]	2	-	1/5/8/10	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	33[B]	CME	CB-SG-SD	2.58	110.54	103.86
2	D	33[B]	CME	CB-CA-C	2.25	116.91	110.80
2	B	33	CME	CE-SD-SG	-2.25	93.59	103.46
2	B	33	CME	CB-SG-SD	-2.01	98.65	103.86

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	33	CME	SD-CE-CZ-OH
2	D	33[B]	CME	SD-CE-CZ-OH
2	B	33	CME	CZ-CE-SD-SG
2	D	33[B]	CME	N-CA-CB-SG
2	D	33[A]	CME	CZ-CE-SD-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 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	$\# Z > 2$
6	EDO	B	202	-	3,3,3	0.78	0	2,2,2	0.07	0
7	PG0	C	302	-	7,7,7	0.23	0	6,6,6	0.25	0
3	SAM	A	301	-	27,29,29	0.48	0	34,42,42	0.63	1 (2%)
4	SO4	A	302	-	4,4,4	0.29	0	6,6,6	0.16	0
4	SO4	D	203	-	4,4,4	0.23	0	6,6,6	0.21	0
5	PEG	B	201	-	6,6,6	0.24	0	5,5,5	0.28	0
4	SO4	C	304	-	4,4,4	0.21	0	6,6,6	0.16	0
4	SO4	B	203	-	4,4,4	0.26	0	6,6,6	0.04	0
7	PG0	D	202	-	7,7,7	0.15	0	6,6,6	0.29	0
4	SO4	A	303	-	4,4,4	0.26	0	6,6,6	0.10	0
4	SO4	A	304	-	4,4,4	0.24	0	6,6,6	0.18	0
6	EDO	D	201	-	3,3,3	0.47	0	2,2,2	0.46	0
3	SAM	C	301	-	27,29,29	0.47	0	34,42,42	0.71	2 (5%)
4	SO4	C	303	-	4,4,4	0.33	0	6,6,6	0.24	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
6	EDO	B	202	-	-	1/1/1/1	-
7	PG0	C	302	-	-	2/5/5/5	-
3	SAM	A	301	-	-	2/17/33/33	0/3/3/3
5	PEG	B	201	-	-	3/4/4/4	-
7	PG0	D	202	-	-	1/5/5/5	-
6	EDO	D	201	-	-	0/1/1/1	-
3	SAM	C	301	-	-	3/17/33/33	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	301	SAM	CB-CA-C	-2.58	103.60	110.45
3	A	301	SAM	CB-CA-C	-2.36	104.19	110.45
3	C	301	SAM	CG-SD-C5'	-2.16	98.15	103.43

There are no chirality outliers.

All (12) torsion outliers are listed below:

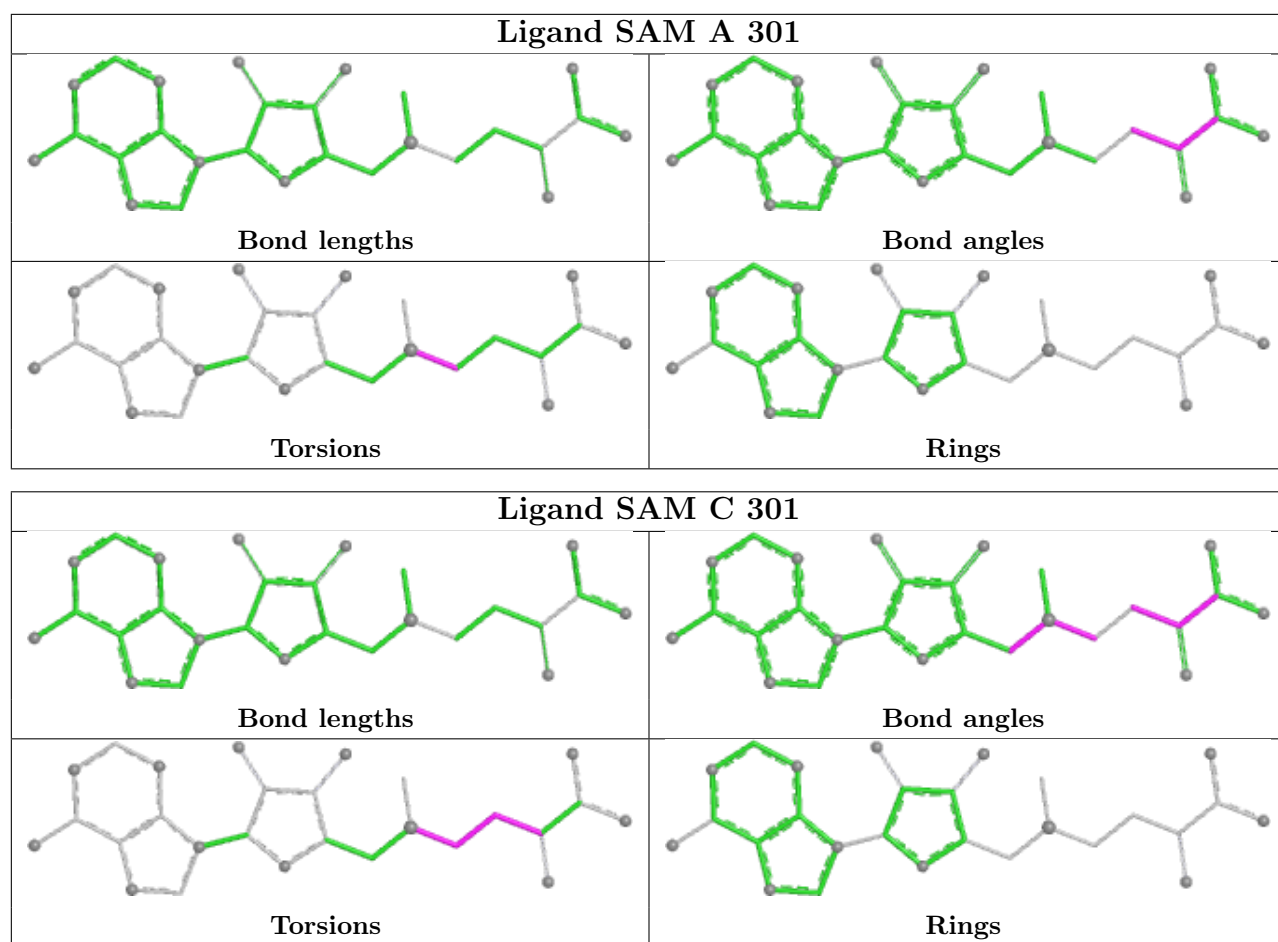
Mol	Chain	Res	Type	Atoms
3	A	301	SAM	CB-CG-SD-CE
3	C	301	SAM	CA-CB-CG-SD
5	B	201	PEG	O2-C3-C4-O4
7	C	302	PG0	C1-C2-O1-C3
5	B	201	PEG	C4-C3-O2-C2
3	A	301	SAM	CB-CG-SD-C5'
5	B	201	PEG	C1-C2-O2-C3
6	B	202	EDO	O1-C1-C2-O2
3	C	301	SAM	CB-CG-SD-CE
7	D	202	PG0	C4-C3-O1-C2
7	C	302	PG0	C4-C3-O1-C2
3	C	301	SAM	C-CA-CB-CG

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	302	PG0	3	0
5	B	201	PEG	4	0
7	D	202	PG0	1	0
3	C	301	SAM	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](#)

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	210/215 (97%)	0.57	23 (10%) 10 8	32, 74, 111, 143	1 (0%)
1	C	194/215 (90%)	0.46	14 (7%) 21 19	51, 73, 118, 132	0
2	B	110/125 (88%)	0.19	3 (2%) 56 51	48, 62, 86, 126	0
2	D	114/125 (91%)	0.31	7 (6%) 27 23	30, 66, 107, 144	1 (0%)
All	All	628/680 (92%)	0.42	47 (7%) 20 18	30, 70, 113, 144	2 (0%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	188	ALA	6.1
2	D	123	THR	5.5
1	C	187	PRO	4.7
2	D	12	HIS	4.3
2	B	12	HIS	4.0
1	C	24	LEU	3.7
1	C	211	HIS	3.6
2	D	21	PHE	3.6
1	C	198	VAL	3.5
1	C	3	LYS	3.3
1	A	190	TYR	3.2
1	C	4	VAL	3.1
1	C	112	LEU	3.0
1	C	111	LEU	2.9
1	A	29	TYR	2.9
1	A	4	VAL	2.9
1	A	115	ARG	2.9
1	A	3	LYS	2.8
1	A	195	LYS	2.8
1	A	2	LYS	2.8
1	C	113	SER	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	118	LEU	2.7
1	A	113	SER	2.7
1	A	211	HIS	2.7
1	A	6	LEU	2.6
1	C	186	LEU	2.5
1	A	132	LYS	2.4
1	A	72	LEU	2.4
1	C	115	ARG	2.4
1	A	114	ASN	2.4
1	C	129	PHE	2.3
1	A	192	PHE	2.3
2	B	20	GLY	2.2
1	A	7	LYS	2.2
1	A	133	ASN	2.1
1	A	124	ILE	2.1
1	C	136	GLY	2.1
2	D	28	THR	2.1
2	D	121	GLU	2.1
1	A	21	LYS	2.1
1	A	191	LYS	2.1
2	D	65	GLN	2.0
1	A	196	LYS	2.0
1	A	5	ARG	2.0
2	D	72	GLU	2.0
1	A	172	TRP	2.0
1	A	34	HIS	2.0

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

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
2	CME	D	33[A]	10/11	0.69	0.40	59,60,65,66	10
2	CME	D	33[B]	10/11	0.69	0.40	64,67,69,71	10
2	CME	B	33	10/11	0.82	0.18	71,82,97,97	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

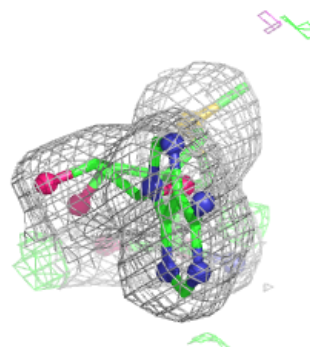
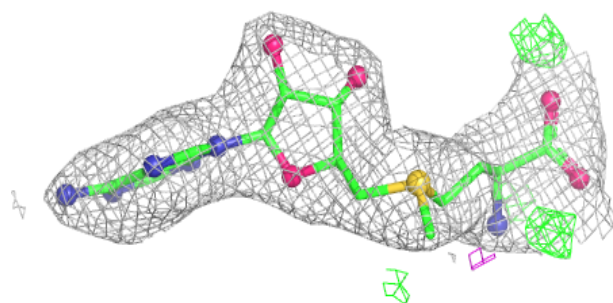
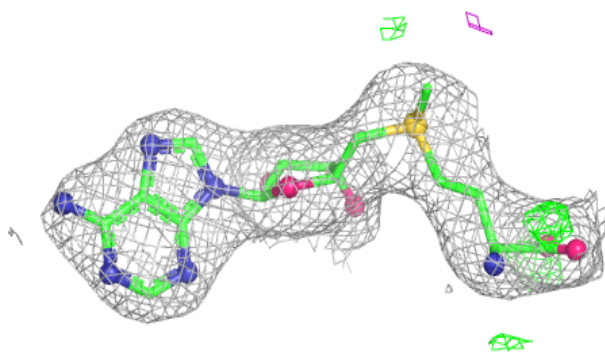
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SO4	A	303	5/5	0.69	0.11	144,144,145,145	0
4	SO4	A	304	5/5	0.69	0.12	131,133,133,134	0
4	SO4	B	203	5/5	0.72	0.12	150,151,151,151	0
4	SO4	A	302	5/5	0.74	0.17	156,157,157,158	0
4	SO4	C	304	5/5	0.75	0.12	149,149,150,150	0
7	PG0	C	302	8/8	0.78	0.25	106,107,108,109	0
5	PEG	B	201	7/7	0.81	0.20	74,75,80,83	0
7	PG0	D	202	8/8	0.81	0.21	86,91,94,95	0
6	EDO	B	202	4/4	0.82	0.18	76,81,83,84	0
4	SO4	D	203	5/5	0.84	0.10	115,115,116,116	0
4	SO4	C	303	5/5	0.88	0.10	105,105,107,108	0
6	EDO	D	201	4/4	0.91	0.23	92,92,92,93	0
3	SAM	A	301	27/27	0.95	0.10	56,65,82,86	0
3	SAM	C	301	27/27	0.97	0.07	60,65,72,75	0

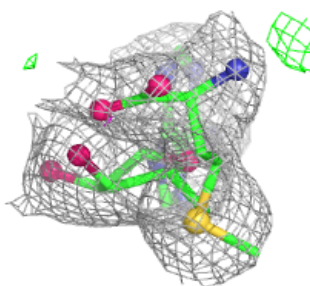
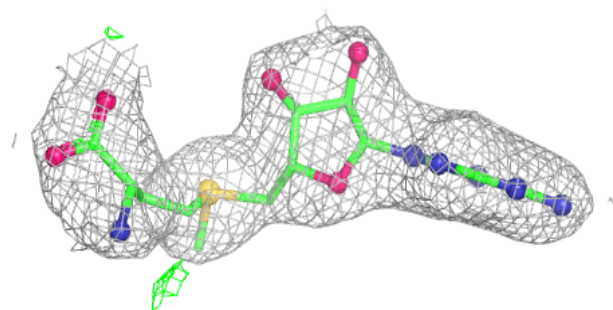
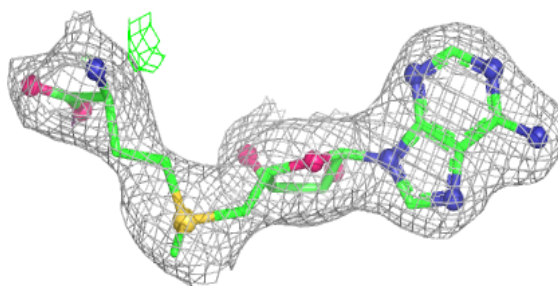
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SAM A 301:

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

**Electron density around SAM C 301:**

$2mF_o-DF_c$ (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.