



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 22, 2023 – 07:34 AM EDT

PDB ID : 2ZIF  
Title : Crystal Structure of TTHA0409, Putative DNA Modification Methylase from *Thermus thermophilus* HB8- Complexed with S-Adenosyl-L-Methionine  
Authors : Morita, R.; Ishikawa, H.; Nakagawa, N.; Masui, R.; Yokoyama, S.; Kuramitsu, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2008-02-15  
Resolution : 2.40 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](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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

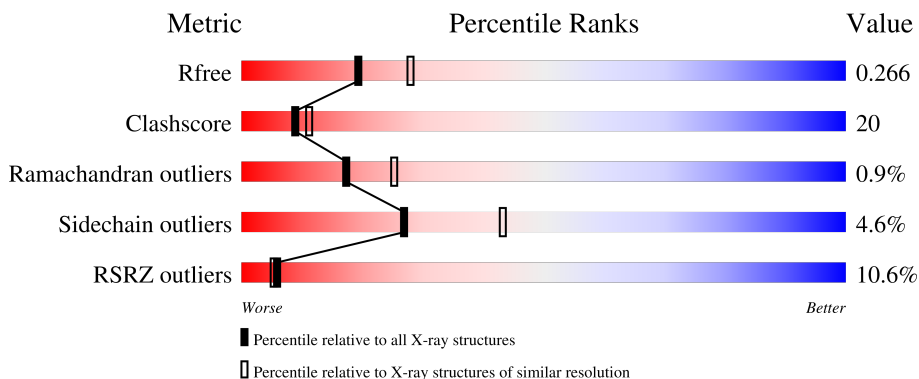
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	297	 10% 51% 28% • 20%
1	B	297	 7% 52% 26% • 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
2	SAM	B	298	-	-	X	-

## 2 Entry composition [i](#)

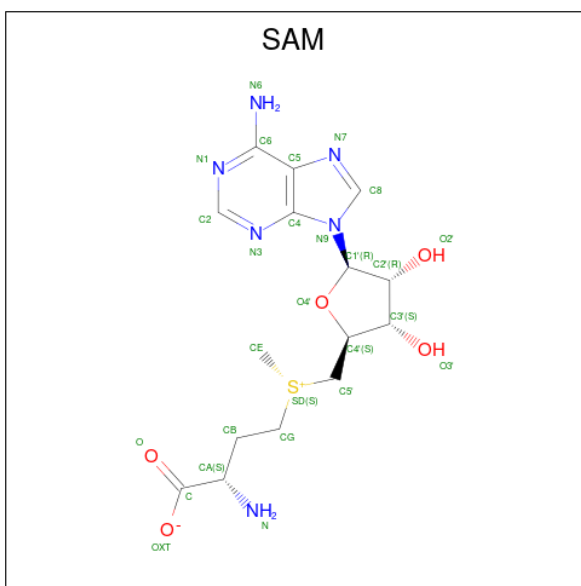
There are 3 unique types of molecules in this entry. The entry contains 4047 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Putative modification methylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	239	Total	C	N	O	S	0	0	0
			1951	1265	352	331	3			
1	B	243	Total	C	N	O	S	0	0	0
			1981	1280	362	336	3			

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: 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		

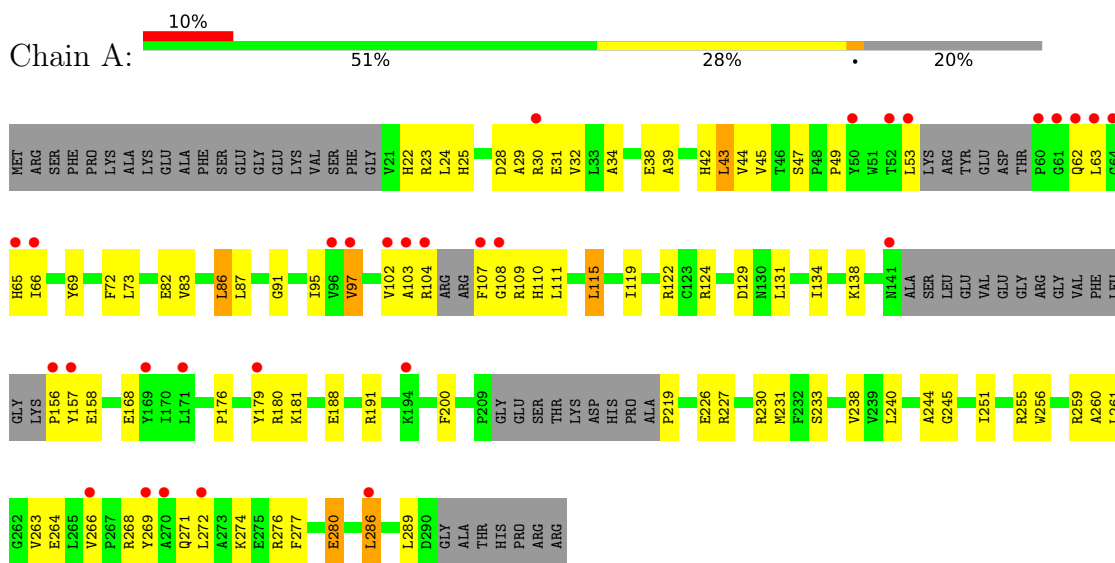
- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	35	Total 35	O 35	0	0
3	B	26	Total 26	O 26	0	0

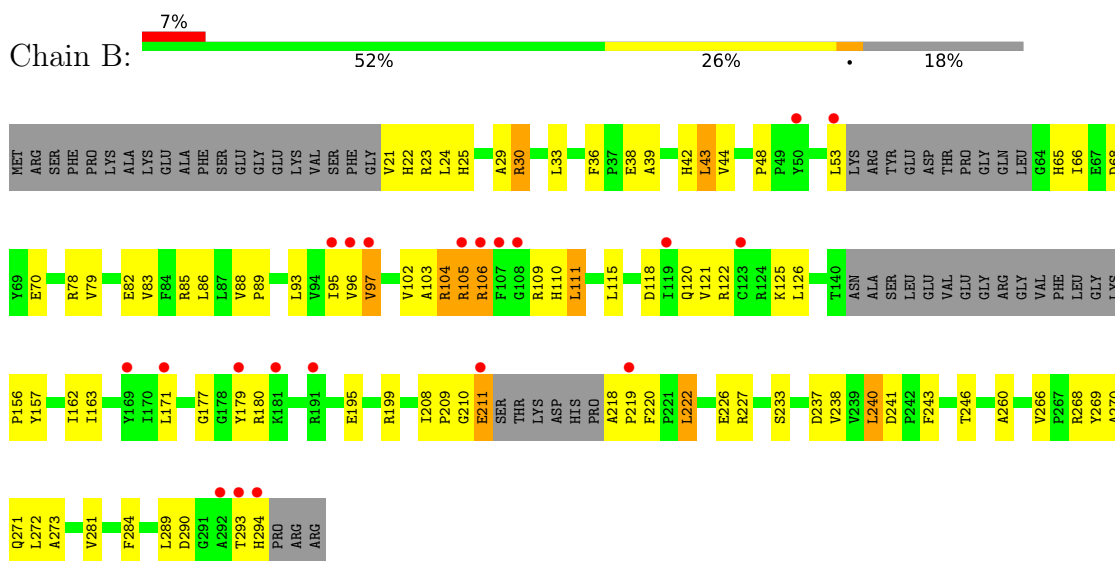
### 3 Residue-property plots [i](#)

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: Putative modification methylase



- Molecule 1: Putative modification methylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.90Å 58.64Å 81.22Å 90.00° 106.06° 90.00°	Depositor
Resolution (Å)	40.67 – 2.40 40.66 – 2.40	Depositor EDS
% Data completeness (in resolution range)	93.5 (40.67-2.40) 93.3 (40.66-2.40)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.03	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.10 (at 2.39Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.217 , 0.273 0.208 , 0.266	Depositor DCC
$R_{free}$ test set	2247 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.0	Xtrriage
Anisotropy	0.341	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4047	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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: SAM

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	0.38	0/2004	0.63	0/2714
1	B	0.36	0/2035	0.63	0/2757
All	All	0.37	0/4039	0.63	0/5471

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1951	0	1955	78	0
1	B	1981	0	1981	84	0
2	A	27	0	22	3	0
2	B	27	0	22	11	0
3	A	35	0	0	2	0
3	B	26	0	0	2	0
All	All	4047	0	3980	162	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 20.

All (162) 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)
2:B:298:SAM:CB	2:B:298:SAM:CG	1.78	1.56
1:B:219:PRO:HD2	2:B:298:SAM:HB2	1.49	0.91
1:B:42:HIS:HD2	1:B:238:VAL:H	1.08	0.89
1:A:42:HIS:HD2	1:A:238:VAL:H	1.18	0.86
1:B:22:HIS:HD2	1:B:260:ALA:H	1.24	0.86
1:B:44:VAL:HG22	1:B:240:LEU:HB3	1.59	0.83
1:B:103:ALA:HB2	1:B:110:HIS:ND1	1.95	0.81
1:B:96:VAL:HG21	1:B:220:PHE:HD2	1.49	0.75
1:B:243:PHE:O	2:B:298:SAM:HG2	1.86	0.74
1:A:62:GLN:HG2	1:A:63:LEU:HD12	1.68	0.74
1:A:22:HIS:HD2	1:A:260:ALA:H	1.35	0.74
1:B:293:THR:HG22	1:B:294:HIS:H	1.53	0.73
1:A:95:ILE:HG22	1:A:97:VAL:HG22	1.69	0.73
1:B:96:VAL:HG21	1:B:220:PHE:CD2	2.24	0.71
1:A:34:ALA:HA	1:A:82:GLU:OE2	1.90	0.71
1:B:219:PRO:CD	2:B:298:SAM:HB2	2.19	0.71
1:B:42:HIS:CD2	1:B:238:VAL:H	2.00	0.70
1:B:30:ARG:NH1	1:B:78:ARG:HH21	1.91	0.69
1:A:83:VAL:HA	1:A:86:LEU:HD11	1.74	0.68
1:A:43:LEU:HD23	1:A:44:VAL:N	2.08	0.68
1:A:271:GLN:HE22	1:A:274:LYS:HE3	1.60	0.67
1:A:30:ARG:HH11	1:A:30:ARG:HG3	1.60	0.67
1:B:21:VAL:HG11	1:B:23:ARG:HH21	1.59	0.67
1:B:43:LEU:HD12	1:B:233:SER:HB3	1.77	0.66
1:A:42:HIS:CD2	1:A:238:VAL:H	2.08	0.65
1:A:179:TYR:HE1	1:A:181:LYS:HZ2	1.45	0.65
1:A:49:PRO:HA	2:A:298:SAM:H5'1	1.79	0.64
1:B:180:ARG:HH22	1:B:237:ASP:CG	2.00	0.64
1:B:42:HIS:HB3	1:B:180:ARG:HH21	1.63	0.64
1:A:268:ARG:O	1:A:272:LEU:HG	1.98	0.63
1:B:96:VAL:O	1:B:96:VAL:HG23	1.99	0.62
1:B:66:ILE:O	1:B:70:GLU:HG2	1.99	0.62
1:A:188:GLU:HA	1:A:191:ARG:HH11	1.64	0.62
1:A:111:LEU:HD11	3:A:324:HOH:O	1.99	0.62
1:A:219:PRO:HA	3:A:323:HOH:O	2.00	0.61
1:A:43:LEU:HD12	1:A:233:SER:HB3	1.83	0.60
1:A:240:LEU:HA	1:A:261:LEU:O	2.01	0.60
1:A:62:GLN:HG2	1:A:63:LEU:CD1	2.32	0.60
1:B:42:HIS:HB3	1:B:180:ARG:NH2	2.16	0.60
2:B:298:SAM:CG	2:B:298:SAM:CA	2.77	0.59
1:B:243:PHE:HB3	2:B:298:SAM:H5'2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ALA:HA	1:A:110:HIS:HA	1.85	0.59
1:A:179:TYR:HE1	1:A:181:LYS:NZ	2.00	0.59
2:B:298:SAM:CB	2:B:298:SAM:SD	2.91	0.58
1:B:268:ARG:O	1:B:272:LEU:HG	2.03	0.58
1:B:30:ARG:HH11	1:B:30:ARG:HG3	1.69	0.58
1:B:240:LEU:HD23	1:B:241:ASP:N	2.18	0.58
1:A:23:ARG:HH11	1:A:25:HIS:CE1	2.21	0.58
1:B:22:HIS:CD2	1:B:260:ALA:H	2.15	0.58
1:B:38:GLU:HG2	1:B:39:ALA:N	2.19	0.58
1:B:25:HIS:CE1	1:B:289:LEU:HD12	2.40	0.57
1:A:226:GLU:OE1	1:A:255:ARG:HD2	2.04	0.57
1:B:195:GLU:HG2	1:B:199:ARG:HH22	1.69	0.57
1:A:43:LEU:HD23	1:A:44:VAL:H	1.70	0.57
1:B:156:PRO:HG2	1:B:157:TYR:H	1.70	0.56
1:B:82:GLU:O	1:B:86:LEU:HD13	2.05	0.56
1:B:103:ALA:HB1	1:B:110:HIS:HB2	1.88	0.56
1:A:227:ARG:O	1:A:231:MET:HG3	2.06	0.56
1:B:79:VAL:O	1:B:83:VAL:HG23	2.05	0.56
1:A:83:VAL:HA	1:A:86:LEU:CD1	2.36	0.56
1:B:122:ARG:O	1:B:126:LEU:HG	2.07	0.55
1:B:53:LEU:HD21	1:B:102:VAL:HG11	1.88	0.54
1:A:276:ARG:NH2	1:A:280:GLU:OE2	2.40	0.54
1:A:124:ARG:NH2	1:B:118:ASP:OD2	2.41	0.54
1:A:29:ALA:HA	1:A:263:VAL:HG11	1.89	0.54
1:A:43:LEU:CD2	1:A:44:VAL:N	2.69	0.54
1:B:30:ARG:HH12	1:B:78:ARG:HH21	1.56	0.54
1:B:156:PRO:O	1:B:157:TYR:HB2	2.08	0.54
1:A:30:ARG:HD2	1:A:30:ARG:O	2.07	0.54
1:A:109:ARG:O	1:A:109:ARG:HG3	2.08	0.54
1:A:134:ILE:HD11	1:B:163:ILE:CD1	2.38	0.54
1:A:25:HIS:CE1	1:A:289:LEU:HD11	2.43	0.54
1:A:73:LEU:HB3	1:A:122:ARG:NE	2.23	0.54
1:A:24:LEU:HB2	1:A:286:LEU:HD21	1.89	0.53
1:A:82:GLU:O	1:A:86:LEU:HG	2.07	0.53
1:A:188:GLU:HA	1:A:191:ARG:NH1	2.23	0.53
1:A:104:ARG:HA	1:A:108:GLY:O	2.08	0.53
1:B:65:HIS:NE2	1:B:106:ARG:HG2	2.25	0.52
1:A:43:LEU:HD22	1:A:45:VAL:HG23	1.91	0.52
1:B:102:VAL:HG13	1:B:102:VAL:O	2.09	0.52
1:A:102:VAL:O	1:A:102:VAL:HG23	2.09	0.52
1:A:138:LYS:HD2	1:A:168:GLU:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:HIS:HD2	1:B:238:VAL:N	1.92	0.51
1:B:222:LEU:O	1:B:226:GLU:HG3	2.09	0.51
1:B:290:ASP:HB2	3:B:324:HOH:O	2.09	0.51
1:A:97:VAL:HG11	1:A:115:LEU:HD13	1.93	0.51
1:A:251:ILE:HD11	1:A:276:ARG:HG2	1.93	0.51
1:A:28:ASP:OD2	1:A:30:ARG:HB3	2.09	0.51
1:A:191:ARG:HH11	1:A:191:ARG:HG3	1.77	0.50
1:A:240:LEU:HD12	1:A:261:LEU:O	2.12	0.50
1:A:180:ARG:HG2	1:A:180:ARG:HH21	1.76	0.49
1:B:29:ALA:O	1:B:33:LEU:HG	2.11	0.49
1:B:89:PRO:HB3	1:B:177:GLY:HA3	1.94	0.49
1:A:277:PHE:CG	1:A:286:LEU:HB2	2.46	0.49
1:B:48:PRO:CG	1:B:97:VAL:HG13	2.41	0.49
1:A:97:VAL:CG1	1:A:115:LEU:HD13	2.42	0.49
1:A:53:LEU:HD12	1:A:53:LEU:N	2.28	0.49
1:B:83:VAL:HG11	1:B:93:LEU:HD13	1.96	0.48
2:B:298:SAM:HG1	3:B:311:HOH:O	2.12	0.48
1:B:39:ALA:O	1:B:88:VAL:HG12	2.13	0.48
1:B:22:HIS:HB3	1:B:260:ALA:HB3	1.96	0.47
1:B:210:GLY:O	1:B:211:GLU:HB2	2.15	0.47
1:B:95:ILE:HG22	1:B:97:VAL:HG22	1.97	0.47
1:A:115:LEU:HD22	1:A:119:ILE:HD11	1.96	0.47
1:B:44:VAL:HG21	1:B:83:VAL:HG13	1.97	0.47
1:A:129:ASP:OD2	1:A:176:PRO:HB3	2.15	0.47
1:A:30:ARG:HG3	1:A:30:ARG:NH1	2.24	0.47
1:B:240:LEU:HD23	1:B:241:ASP:H	1.77	0.47
1:B:102:VAL:HG22	1:B:105:ARG:HB2	1.97	0.46
1:B:120:GLN:HG3	1:B:171:LEU:HD22	1.98	0.46
1:A:65:HIS:ND1	1:A:66:ILE:N	2.64	0.46
1:B:53:LEU:HD12	1:B:53:LEU:O	2.16	0.45
1:B:104:ARG:HH11	1:B:104:ARG:HG3	1.81	0.45
1:B:281:VAL:HG12	1:B:284:PHE:HB2	1.99	0.45
1:B:23:ARG:NH1	1:B:289:LEU:HD11	2.31	0.45
1:A:277:PHE:CD2	1:A:286:LEU:HB2	2.52	0.45
1:A:53:LEU:HD23	1:A:107:PHE:HZ	1.82	0.45
1:A:28:ASP:O	1:A:32:VAL:HG23	2.16	0.44
1:B:111:LEU:O	1:B:111:LEU:HD23	2.18	0.44
1:A:87:LEU:HG	1:A:91:GLY:HA3	1.98	0.44
1:A:65:HIS:ND1	1:A:66:ILE:HG23	2.32	0.44
1:A:230:ARG:HD2	1:A:256:TRP:CE2	2.52	0.44
1:A:271:GLN:NE2	1:A:274:LYS:HE3	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:ARG:NH1	1:B:30:ARG:HG3	2.32	0.44
1:B:36:PHE:O	1:B:85:ARG:NH1	2.47	0.43
1:A:69:TYR:O	1:A:72:PHE:HB3	2.17	0.43
1:A:138:LYS:HD2	1:A:168:GLU:CG	2.48	0.43
1:B:110:HIS:CD2	1:B:162:ILE:HD12	2.53	0.43
1:A:156:PRO:O	1:A:158:GLU:N	2.49	0.43
1:B:208:ILE:HD11	1:B:227:ARG:CZ	2.49	0.43
1:A:245:GLY:HA3	2:A:298:SAM:O	2.19	0.43
1:B:246:THR:N	2:B:298:SAM:O	2.44	0.42
1:B:38:GLU:HG3	1:B:85:ARG:O	2.19	0.42
1:A:129:ASP:OD2	1:B:109:ARG:HD2	2.19	0.42
1:A:31:GLU:O	1:A:34:ALA:HB3	2.20	0.42
1:B:121:VAL:HG12	1:B:125:LYS:HZ3	1.84	0.42
1:B:121:VAL:HG12	1:B:125:LYS:NZ	2.35	0.42
1:A:180:ARG:HG2	1:A:180:ARG:NH2	2.33	0.42
1:B:65:HIS:HA	1:B:68:ASP:OD2	2.19	0.42
1:B:109:ARG:NH1	1:B:111:LEU:HD13	2.35	0.42
1:B:30:ARG:O	1:B:30:ARG:HD2	2.19	0.42
1:A:28:ASP:OD1	2:A:298:SAM:N6	2.48	0.42
1:B:23:ARG:HH11	1:B:289:LEU:HD11	1.84	0.41
1:B:96:VAL:O	1:B:96:VAL:CG2	2.67	0.41
1:B:270:ALA:O	1:B:273:ALA:HB3	2.19	0.41
1:A:38:GLU:HG2	1:A:39:ALA:N	2.36	0.41
1:B:48:PRO:HD3	1:B:95:ILE:HG23	2.02	0.41
1:B:82:GLU:OE1	1:B:82:GLU:HA	2.20	0.41
1:A:131:LEU:HD22	1:B:110:HIS:CD2	2.56	0.41
1:A:244:ALA:HB3	1:A:264:GLU:HB2	2.03	0.41
1:B:243:PHE:HB3	2:B:298:SAM:C4'	2.50	0.41
1:A:24:LEU:CB	1:A:286:LEU:HD21	2.50	0.41
1:B:65:HIS:CD2	1:B:106:ARG:HG2	2.56	0.41
1:B:218:ALA:HA	1:B:219:PRO:HD2	1.83	0.40
1:B:103:ALA:C	1:B:105:ARG:H	2.23	0.40
1:B:208:ILE:HA	1:B:209:PRO:HD2	1.94	0.40
1:B:243:PHE:HB3	2:B:298:SAM:C5'	2.52	0.40
1:A:102:VAL:HG22	1:A:111:LEU:O	2.20	0.40
1:A:200:PHE:N	1:A:200:PHE:CD1	2.89	0.40
1:A:266:VAL:HB	1:A:269:TYR:CD2	2.56	0.40
1:B:266:VAL:HB	1:B:269:TYR:CD1	2.56	0.40
1:A:63:LEU:HG	1:A:66:ILE:HD11	2.03	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	229/297 (77%)	217 (95%)	11 (5%)	1 (0%)	34	48
1	B	235/297 (79%)	220 (94%)	12 (5%)	3 (1%)	12	17
All	All	464/594 (78%)	437 (94%)	23 (5%)	4 (1%)	17	25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	105	ARG
1	A	157	TYR
1	B	106	ARG
1	B	179	TYR

### 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	205/251 (82%)	197 (96%)	8 (4%)	32	50
1	B	206/251 (82%)	195 (95%)	11 (5%)	22	37
All	All	411/502 (82%)	392 (95%)	19 (5%)	27	43

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LEU
1	A	47	SER

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Mol	Chain	Res	Type
1	A	86	LEU
1	A	97	VAL
1	A	115	LEU
1	A	259	ARG
1	A	280	GLU
1	A	286	LEU
1	B	24	LEU
1	B	30	ARG
1	B	43	LEU
1	B	97	VAL
1	B	104	ARG
1	B	111	LEU
1	B	115	LEU
1	B	211	GLU
1	B	222	LEU
1	B	240	LEU
1	B	271	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	42	HIS
1	A	271	GLN
1	B	22	HIS
1	B	25	HIS
1	B	42	HIS
1	B	184	GLN
1	B	271	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 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
2	SAM	A	298	-	24,29,29	1.29	1 (4%)	23,42,42	1.62	4 (17%)
2	SAM	B	298	-	24,29,29	1.96	1 (4%)	23,42,42	1.42	4 (17%)

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	SAM	A	298	-	-	3/12/33/33	0/3/3/3
2	SAM	B	298	-	-	4/12/33/33	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	298	SAM	CG-CB	8.75	1.78	1.51
2	A	298	SAM	CG-CB	5.00	1.67	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	298	SAM	C1'-N9-C4	-4.71	118.37	126.64
2	B	298	SAM	N3-C2-N1	-3.58	123.08	128.68
2	A	298	SAM	N3-C2-N1	-3.57	123.10	128.68
2	B	298	SAM	C1'-N9-C4	-2.69	121.91	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	298	SAM	C4-C5-N7	-2.36	106.94	109.40
2	A	298	SAM	C4-C5-N7	-2.35	106.95	109.40
2	A	298	SAM	O4'-C1'-C2'	-2.13	103.82	106.93
2	B	298	SAM	O4'-C1'-C2'	-2.10	103.85	106.93

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	298	SAM	N-CA-CB-CG
2	A	298	SAM	C-CA-CB-CG
2	B	298	SAM	OXT-C-CA-CB
2	B	298	SAM	O-C-CA-CB
2	B	298	SAM	C-CA-CB-CG
2	A	298	SAM	O-C-CA-N
2	B	298	SAM	OXT-C-CA-N

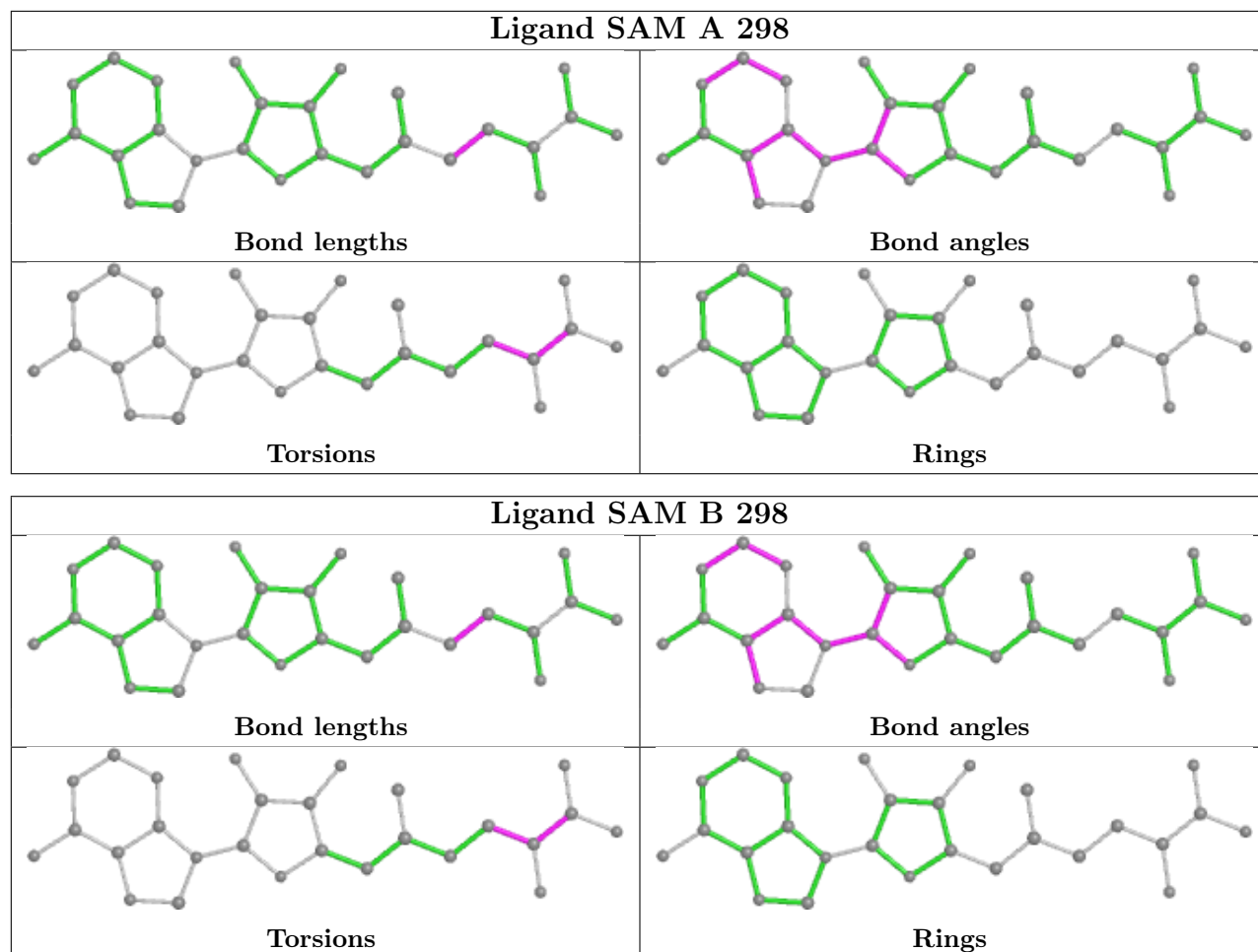
There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	298	SAM	3	0
2	B	298	SAM	11	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, 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	239/297 (80%)	0.65	30 (12%) <b>3</b> <b>3</b>	19, 40, 74, 104	0
1	B	243/297 (81%)	0.48	21 (8%) <b>10</b> <b>9</b>	22, 43, 75, 96	0
All	All	482/594 (81%)	0.57	51 (10%) <b>6</b> <b>5</b>	19, 42, 75, 104	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	61	GLY	7.4
1	A	60	PRO	6.5
1	B	107	PHE	5.5
1	A	63	LEU	5.1
1	A	62	GLN	4.9
1	A	107	PHE	4.9
1	B	294	HIS	4.8
1	A	53	LEU	4.5
1	B	106	ARG	4.3
1	B	179	TYR	4.0
1	A	179	TYR	3.8
1	A	65	HIS	3.6
1	B	50	TYR	3.5
1	A	102	VAL	3.4
1	A	66	ILE	3.3
1	A	50	TYR	3.2
1	B	96	VAL	3.2
1	A	270	ALA	3.2
1	A	269	TYR	3.0
1	A	103	ALA	2.9
1	B	169	TYR	2.9
1	A	64	GLY	2.8
1	B	171	LEU	2.8
1	A	104	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	95	ILE	2.7
1	B	108	GLY	2.7
1	A	97	VAL	2.6
1	A	156	PRO	2.5
1	A	141	ASN	2.5
1	B	53	LEU	2.5
1	B	292	ALA	2.5
1	B	293	THR	2.5
1	A	52	THR	2.4
1	B	119	ILE	2.4
1	A	194	LYS	2.4
1	B	219	PRO	2.3
1	A	169	TYR	2.3
1	A	157	TYR	2.3
1	A	286	LEU	2.3
1	B	123	CYS	2.3
1	B	191	ARG	2.3
1	B	181	LYS	2.3
1	A	30	ARG	2.2
1	B	211	GLU	2.2
1	B	105	ARG	2.2
1	B	97	VAL	2.1
1	A	266	VAL	2.1
1	A	108	GLY	2.1
1	A	171	LEU	2.1
1	A	96	VAL	2.0
1	A	272	LEU	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.

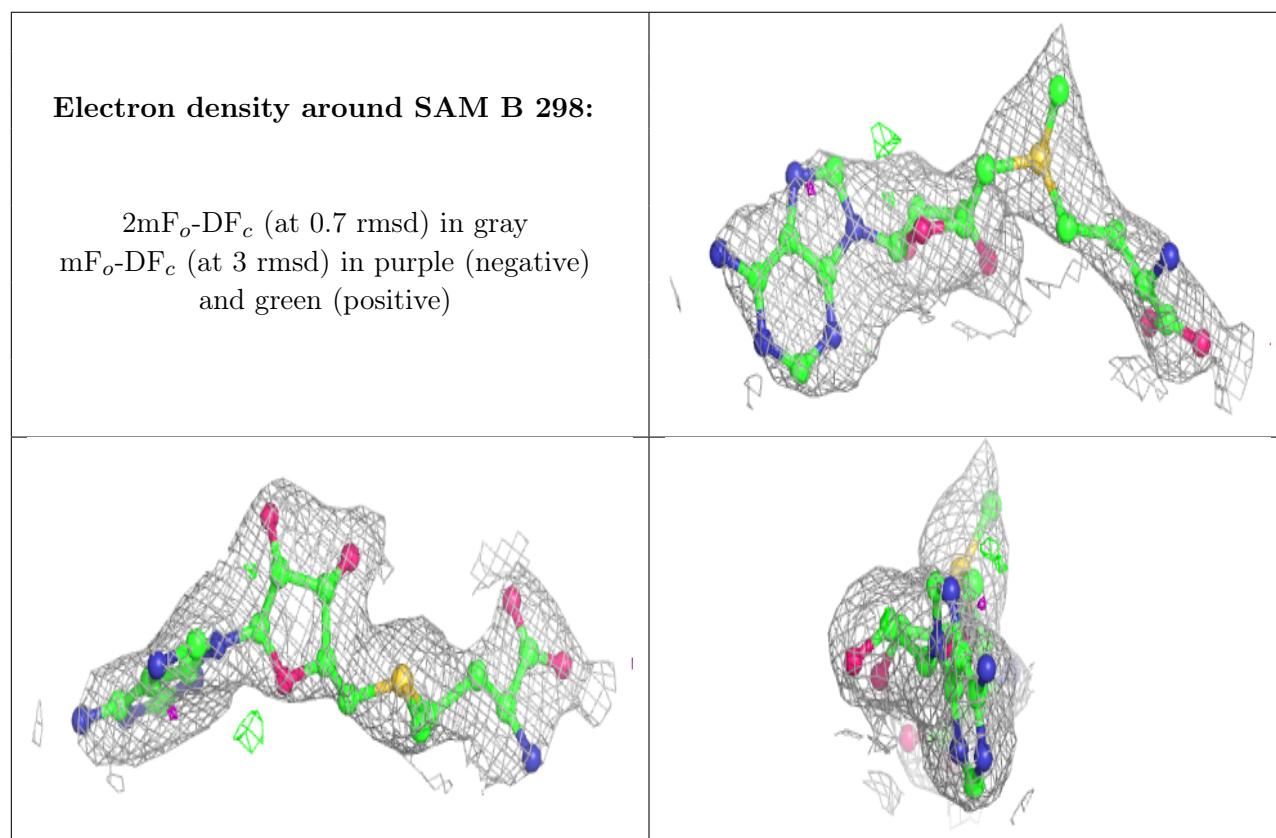
## 6.4 Ligands [i](#)

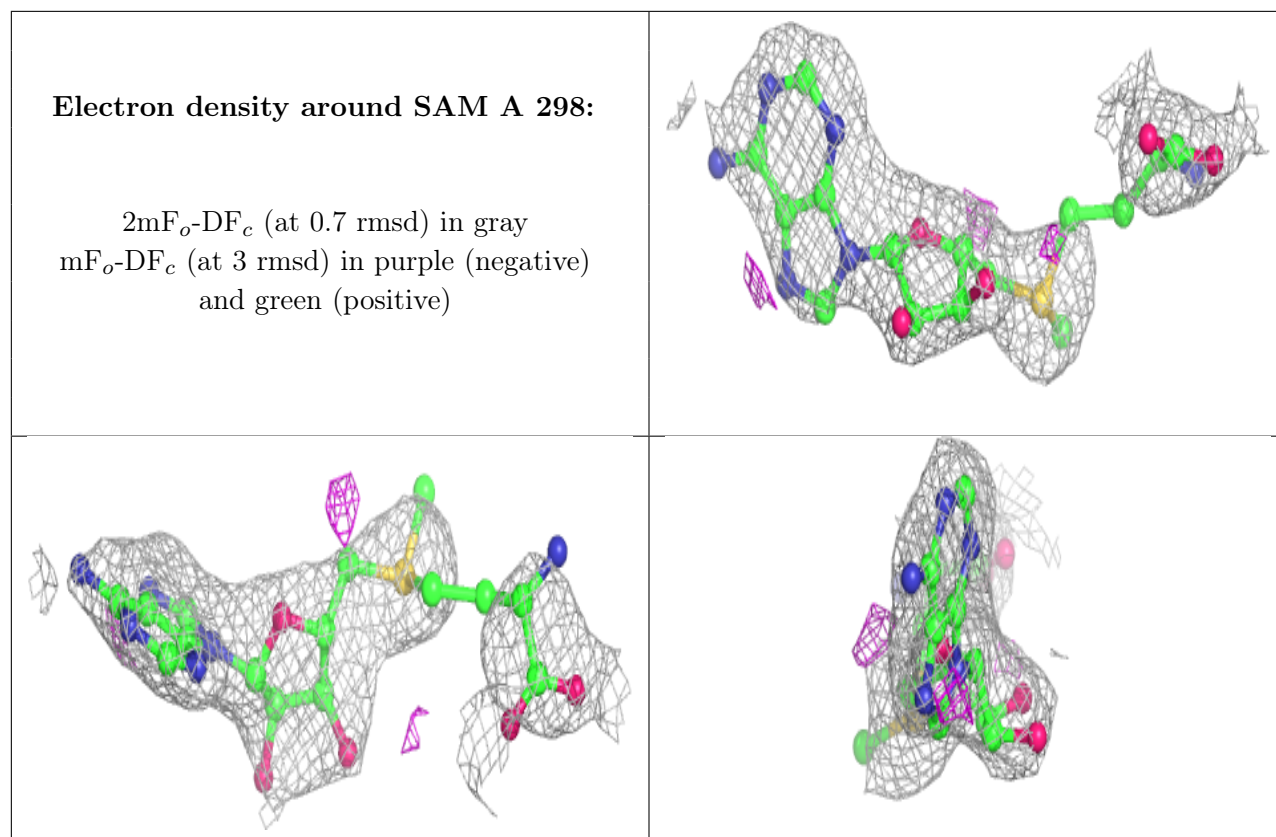
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 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(Å <sup>2</sup> )	Q<0.9
2	SAM	B	298	27/27	0.85	0.24	62,66,69,70	0
2	SAM	A	298	27/27	0.87	0.24	64,65,76,77	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.