Full wwPDB X-ray Structure Validation Report (i)

Sep 25, 2023 – 09:42 PM EDT

PDB ID	:	6BRR
Title	:	Crystal structure of DNMT3A (R836A)-DNMT3L in complex with DNA containing two CpG sites
Authors	:	Zhang, Z.M.; Song, J.
Deposited on	:	2017-11-30
Resolution	:	2.97 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 (i) 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 (i)) were used in the production of this report:

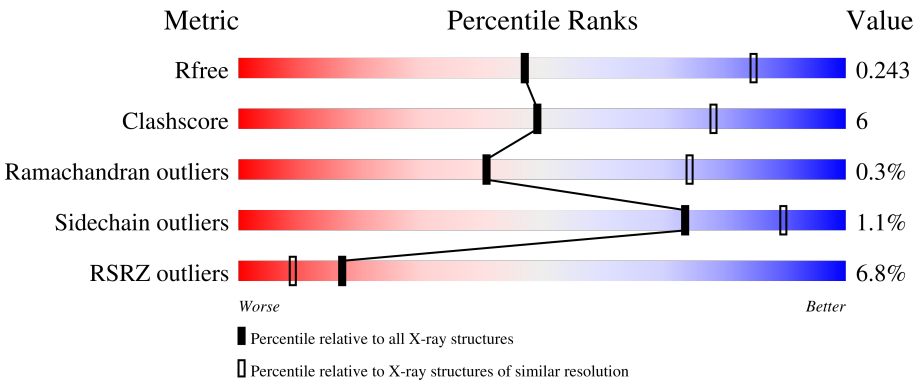
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.97 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	2754 (3.00-2.96)
Clashscore	141614	3103 (3.00-2.96)
Ramachandran outliers	138981	2993 (3.00-2.96)
Sidechain outliers	138945	2996 (3.00-2.96)
RSRZ outliers	127900	2644 (3.00-2.96)

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 <=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	285	2%, 88%, 12%
1	D	285	2%, 86%, 13%
2	B	209	10%, 76%, 12%, •, 11%
2	C	209	16%, 67%, 17%, 17%
3	E	25	60%, 36%, •

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Mol	Chain	Length	Quality of chain
3	F	25	4% 64% 32%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8254 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 DNA (cytosine-5)-methyltransferase 3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	285	2251	1439	399	400	13	0	0	0
1	D	285	2264	1448	400	403	13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	836	ALA	ARG	engineered mutation	UNP Q9Y6K1
D	836	ALA	ARG	engineered mutation	UNP Q9Y6K1

- Molecule 2 is a protein called DNA (cytosine-5)-methyltransferase 3-like.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	187	1398	918	233	244	3	0	0	0
2	C	174	1269	825	213	229	2	0	0	0

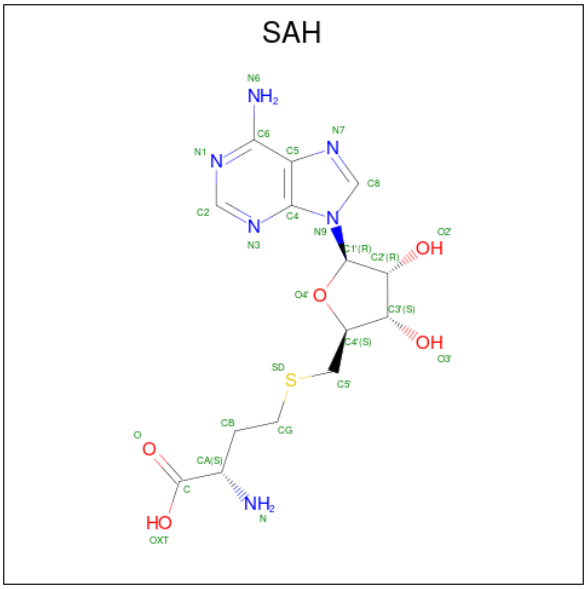
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	SER	see remark 999	UNP Q9UJW3
C	?	-	SER	see remark 999	UNP Q9UJW3

- Molecule 3 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	E	25	510	245	93	148	24	0	0	0
3	F	25	510	245	93	148	24	0	0	0

- Molecule 4 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



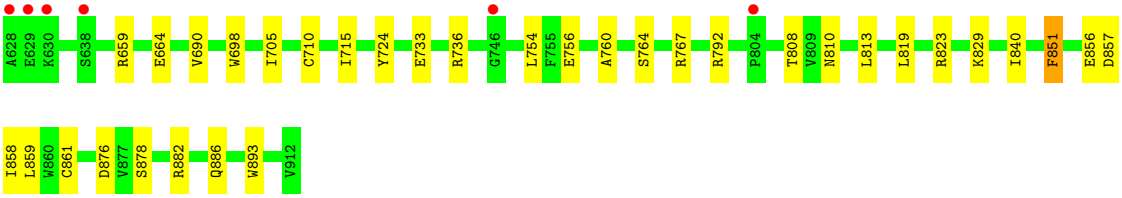
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	26	14	6	5	1	0	0
			Total	C	N	O	S		
4	D	1	26	14	6	5	1	0	0

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.

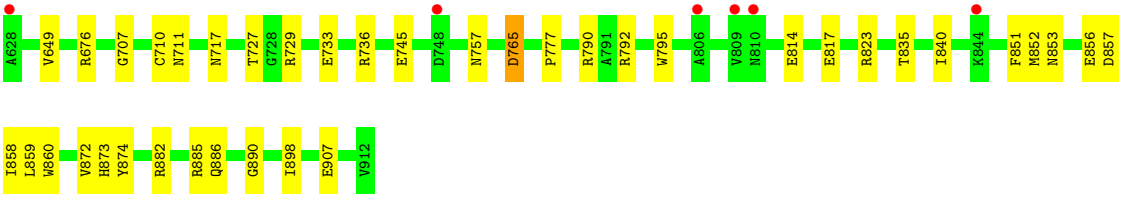
• Molecule 1: DNA (cytosine-5)-methyltransferase 3A

Chain A:



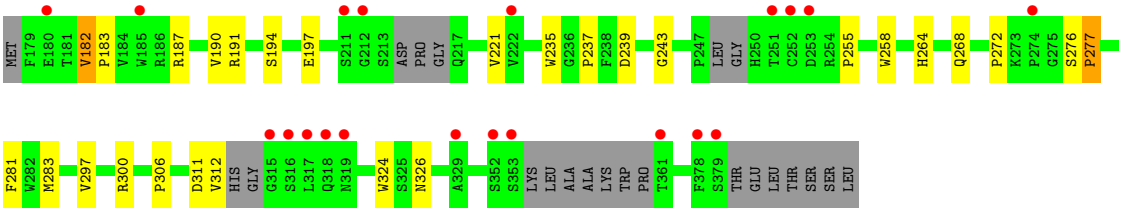
• Molecule 1: DNA (cytosine-5)-methyltransferase 3A

Chain D:



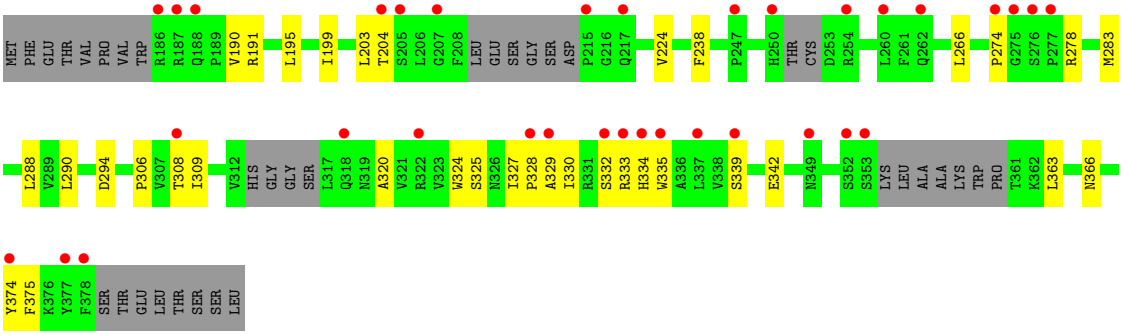
• Molecule 2: DNA (cytosine-5)-methyltransferase 3-like

Chain B:



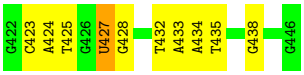
• Molecule 2: DNA (cytosine-5)-methyltransferase 3-like

Chain C:



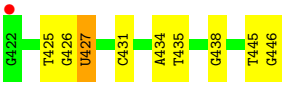
- Molecule 3: DNA (25-MER)

Chain E:



- Molecule 3: DNA (25-MER)

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	205.00Å 205.00Å 89.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.95 – 2.97 19.95 – 2.97	Depositor EDS
% Data completeness (in resolution range)	98.2 (19.95-2.97) 98.2 (19.95-2.97)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 2.98Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.199 , 0.242 0.201 , 0.243	Depositor DCC
R_{free} test set	1994 reflections (7.05%)	wwPDB-VP
Wilson B-factor (Å^2)	99.7	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 86.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.001 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8254	wwPDB-VP
Average B, all atoms (Å^2)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: SAH, PYO

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	0.22	0/2305	0.36	0/3120
1	D	0.22	0/2318	0.37	0/3134
2	B	0.23	0/1440	0.39	0/1975
2	C	0.28	0/1306	0.46	0/1789
3	E	0.50	0/550	0.91	0/846
3	F	0.52	0/550	0.91	0/846
All	All	0.28	0/8469	0.50	0/11710

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	2251	0	2188	23	0
1	D	2264	0	2218	24	0
2	B	1398	0	1247	16	0
2	C	1269	0	1099	23	0
3	E	510	0	279	10	0
3	F	510	0	279	7	0
4	A	26	0	19	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	26	0	19	1	0
All	All	8254	0	7348	91	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 (91) 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:C:327:ILE:HG22	2:C:329:ALA:H	1.52	0.74
2:C:288:LEU:HD11	2:C:320:ALA:HB3	1.74	0.69
1:D:710:CYS:N	3:E:427:PYO:HC5	2.12	0.64
1:A:808:THR:HG23	1:A:810:ASN:H	1.63	0.63
3:E:432:DT:H2"	3:E:433:DA:C8	2.34	0.63
2:C:325:SER:HB3	2:C:330:ILE:HG21	1.82	0.62
2:C:333:ARG:O	2:C:335:TRP:N	2.32	0.62
1:A:733:GLU:OE1	1:A:736:ARG:NH1	2.34	0.61
1:D:882:ARG:NH2	1:D:886:GLN:OE1	2.35	0.59
3:E:428:DG:OP2	3:E:428:DG:H8	1.85	0.58
1:D:733:GLU:OE1	1:D:736:ARG:NH1	2.32	0.58
1:A:851:PHE:HE1	1:A:856:GLU:HG2	1.69	0.57
1:A:792:ARG:NH1	3:F:427:PYO:O4'	2.38	0.57
2:C:190:VAL:HG21	2:C:375:PHE:CD1	2.40	0.57
2:C:327:ILE:O	2:C:330:ILE:HG22	2.04	0.56
2:C:195:LEU:HD11	2:C:266:LEU:HD12	1.88	0.55
2:B:297:VAL:HG22	2:B:300:ARG:HH12	1.72	0.55
1:A:710:CYS:N	3:F:427:PYO:HC5	2.21	0.54
2:C:306:PRO:HB3	2:C:324:TRP:CE2	2.41	0.54
2:C:309:ILE:HD12	2:C:335:TRP:CD2	2.43	0.54
1:A:876:ASP:OD1	1:D:885:ARG:NH2	2.40	0.54
1:D:840:ILE:HD11	1:D:859:LEU:HD12	1.90	0.54
2:B:182:VAL:HG22	2:B:183:PRO:HD2	1.90	0.54
1:A:659:ARG:NH1	1:A:698:TRP:O	2.40	0.54
1:A:882:ARG:NH2	1:A:886:GLN:OE1	2.42	0.53
1:D:882:ARG:NH1	3:F:438:DG:OP2	2.42	0.53
1:A:690:VAL:O	1:A:736:ARG:NH2	2.42	0.53
1:A:857:ASP:OD1	1:A:858:ILE:N	2.43	0.51
2:B:182:VAL:O	2:B:187:ARG:NH1	2.45	0.50
1:A:705:ILE:HG22	1:A:754:LEU:HB3	1.94	0.49
1:D:790:ARG:NH2	1:D:890:GLY:O	2.46	0.49
3:E:423:DC:H2"	3:E:424:DA:N7	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:840:ILE:HD11	1:A:859:LEU:HD12	1.94	0.49
1:A:882:ARG:NH1	3:E:438:DG:OP2	2.46	0.49
2:B:255:PRO:HG2	2:B:258:TRP:HB2	1.95	0.49
3:F:434:DA:H2"	3:F:435:DT:H5"	1.93	0.49
2:C:190:VAL:HG21	2:C:375:PHE:CE1	2.49	0.48
1:D:835:THR:OG1	3:E:428:DG:OP1	2.19	0.48
1:A:756:GLU:OE1	1:A:893:TRP:NE1	2.45	0.48
2:B:306:PRO:HB3	2:B:324:TRP:CE2	2.49	0.47
1:D:857:ASP:OD1	1:D:858:ILE:N	2.47	0.47
2:C:283:MET:HG3	2:C:325:SER:HB2	1.96	0.47
3:F:425:DT:H2"	3:F:426:DG:C8	2.50	0.47
2:B:191:ARG:HD2	2:B:237:PRO:O	2.15	0.47
2:B:243:GLY:N	2:B:283:MET:O	2.47	0.47
2:C:328:PRO:O	2:C:332:SER:OG	2.14	0.47
1:D:717:ASN:HB2	3:E:428:DG:O4'	2.15	0.47
1:D:823:ARG:HG2	1:D:852:MET:HB2	1.97	0.47
1:D:649:VAL:HG21	1:D:898:ILE:HB	1.97	0.46
1:D:814:GLU:HB2	1:D:817:GLU:HG3	1.98	0.46
1:D:676:ARG:HE	1:D:874:TYR:HA	1.81	0.46
3:F:431:DC:H5"	3:F:431:DC:H6	1.81	0.46
1:D:872:VAL:HG12	1:D:873:HIS:CD2	2.51	0.46
2:C:224:VAL:HB	2:C:266:LEU:HD11	1.98	0.46
3:F:445:DT:H2"	3:F:446:DG:C8	2.51	0.46
2:C:329:ALA:HA	2:C:332:SER:HB2	1.96	0.45
1:D:792:ARG:NH1	3:E:427:PYO:O4'	2.50	0.45
1:D:711:ASN:OD1	1:D:727:THR:OG1	2.29	0.45
4:A:1001:SAH:H4'	4:A:1001:SAH:HG2	1.45	0.45
1:A:664:GLU:OE1	4:A:1001:SAH:O2'	2.24	0.44
2:B:264:HIS:O	2:B:268:GLN:HG2	2.17	0.44
2:C:339:SER:HB3	2:C:342:GLU:HG3	1.99	0.44
2:B:194:SER:OG	2:B:197:GLU:O	2.35	0.44
1:A:715:ILE:HG12	1:A:760:ALA:HB1	2.00	0.44
2:B:311:ASP:HA	2:B:312:VAL:HA	1.66	0.44
2:C:363:LEU:HD12	2:C:366:ASN:CB	2.48	0.44
2:B:190:VAL:HG23	2:B:239:ASP:HB2	1.99	0.43
2:B:281:PHE:HA	2:B:326:ASN:HD21	1.82	0.43
1:D:851:PHE:CD2	1:D:856:GLU:HG2	2.53	0.43
1:D:777:PRO:HB3	1:D:795:TRP:CE2	2.54	0.43
2:B:221:VAL:HG21	2:B:235:TRP:CZ3	2.54	0.43
2:C:195:LEU:HD22	2:C:224:VAL:HG11	2.01	0.43
1:A:724:TYR:CZ	2:B:258:TRP:HD1	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:878:SER:HA	1:D:860:TRP:CE2	2.54	0.43
1:A:813:LEU:O	1:A:829:LYS:NZ	2.43	0.42
1:A:861:CYS:SG	1:A:882:ARG:HG2	2.58	0.42
2:B:272:PRO:HB2	2:B:276:SER:CB	2.50	0.42
2:C:191:ARG:HB2	2:C:238:PHE:HA	2.00	0.42
1:D:707:GLY:O	4:D:1001:SAH:H5'2	2.19	0.42
1:D:765:ASP:OD1	1:D:765:ASP:N	2.52	0.42
1:D:745:GLU:HB2	2:C:274:PRO:HG3	2.00	0.42
2:C:308:THR:C	2:C:309:ILE:HD13	2.39	0.41
2:C:199:ILE:HB	2:C:203:LEU:HD13	2.02	0.41
2:B:276:SER:HA	2:B:277:PRO:HD3	1.90	0.41
2:C:290:LEU:HB3	2:C:294:ASP:HB2	2.01	0.41
1:A:819:LEU:HB3	1:A:823:ARG:HB2	2.03	0.41
3:E:424:DA:H2"	3:E:425:DT:H71	2.03	0.41
2:C:374:TYR:C	2:C:375:PHE:CD1	2.94	0.41
1:A:764:SER:OG	1:A:767:ARG:NH2	2.53	0.40
1:A:876:ASP:OD2	1:D:873:HIS:ND1	2.48	0.40
3:E:434:DA:H1'	3:E:435:DT:H5"	2.04	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	283/285 (99%)	273 (96%)	10 (4%)	0	100	100
1	D	283/285 (99%)	273 (96%)	10 (4%)	0	100	100
2	B	177/209 (85%)	166 (94%)	10 (6%)	1 (1%)	25	61
2	C	164/209 (78%)	146 (89%)	16 (10%)	2 (1%)	13	45
All	All	907/988 (92%)	858 (95%)	46 (5%)	3 (0%)	41	74

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	334	HIS
2	B	277	PRO
2	C	278	ARG

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	233/249 (94%)	232 (100%)	1 (0%)	91	97
1	D	237/249 (95%)	232 (98%)	5 (2%)	53	80
2	B	131/191 (69%)	130 (99%)	1 (1%)	81	92
2	C	116/191 (61%)	115 (99%)	1 (1%)	78	91
All	All	717/880 (82%)	709 (99%)	8 (1%)	73	90

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	851	PHE
2	B	182	VAL
1	D	729	ARG
1	D	757	ASN
1	D	765	ASP
1	D	853	ASN
1	D	907	GLU
2	C	204	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	$\#\|Z\| > 2$
3	PYO	E	427	1,3	16,20,21	1.24	2 (12%)	22,28,31	1.23	2 (9%)
3	PYO	F	427	1,3	16,20,21	1.25	2 (12%)	22,28,31	1.21	2 (9%)

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	PYO	E	427	1,3	-	4/7/25/26	0/2/2/2
3	PYO	F	427	1,3	-	4/7/25/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	427	PYO	C2-N1	-3.53	1.32	1.40
3	E	427	PYO	C2-N1	-3.51	1.32	1.40
3	E	427	PYO	C6-C5	2.61	1.41	1.35
3	F	427	PYO	C6-C5	2.60	1.41	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	427	PYO	C5-C4-N3	-4.34	118.96	124.29
3	F	427	PYO	C5-C4-N3	-4.27	119.06	124.29
3	F	427	PYO	C5-C6-N1	-2.08	119.09	121.19
3	E	427	PYO	C5-C6-N1	-2.06	119.11	121.19

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	427	PYO	C2'-C1'-N1-C6
3	E	427	PYO	O4'-C1'-N1-C2
3	E	427	PYO	C2'-C1'-N1-C2
3	E	427	PYO	O4'-C1'-N1-C6
3	F	427	PYO	O4'-C1'-N1-C6
3	F	427	PYO	C2'-C1'-N1-C6
3	F	427	PYO	O4'-C1'-N1-C2
3	F	427	PYO	C2'-C1'-N1-C2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	427	PYO	2	0
3	F	427	PYO	2	0

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	$\#\|Z\| > 2$
4	SAH	D	1001	-	24,28,28	1.26	2 (8%)	25,40,40	1.60	4 (16%)
4	SAH	A	1001	-	24,28,28	1.25	3 (12%)	25,40,40	1.55	4 (16%)

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
4	SAH	D	1001	-	-	4/11/31/31	0/3/3/3
4	SAH	A	1001	-	-	1/11/31/31	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1001	SAH	C2-N3	4.23	1.38	1.32
4	A	1001	SAH	C2-N3	4.14	1.38	1.32
4	D	1001	SAH	C2-N1	2.44	1.38	1.33
4	A	1001	SAH	C2-N1	2.42	1.38	1.33
4	A	1001	SAH	OXT-C	-2.05	1.23	1.30

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1001	SAH	N3-C2-N1	-5.23	120.50	128.68
4	D	1001	SAH	N3-C2-N1	-5.16	120.62	128.68
4	D	1001	SAH	C5'-SD-CG	-3.41	92.05	102.27
4	A	1001	SAH	C5'-SD-CG	-2.79	93.89	102.27
4	A	1001	SAH	OXT-C-O	-2.78	117.77	124.09
4	D	1001	SAH	OXT-C-O	-2.76	117.83	124.09
4	D	1001	SAH	OXT-C-CA	2.31	121.26	113.38
4	A	1001	SAH	OXT-C-CA	2.01	120.22	113.38

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1001	SAH	N-CA-CB-CG
4	D	1001	SAH	CB-CG-SD-C5'
4	D	1001	SAH	O-C-CA-CB
4	D	1001	SAH	OXT-C-CA-CB
4	A	1001	SAH	C4'-C5'-SD-CG

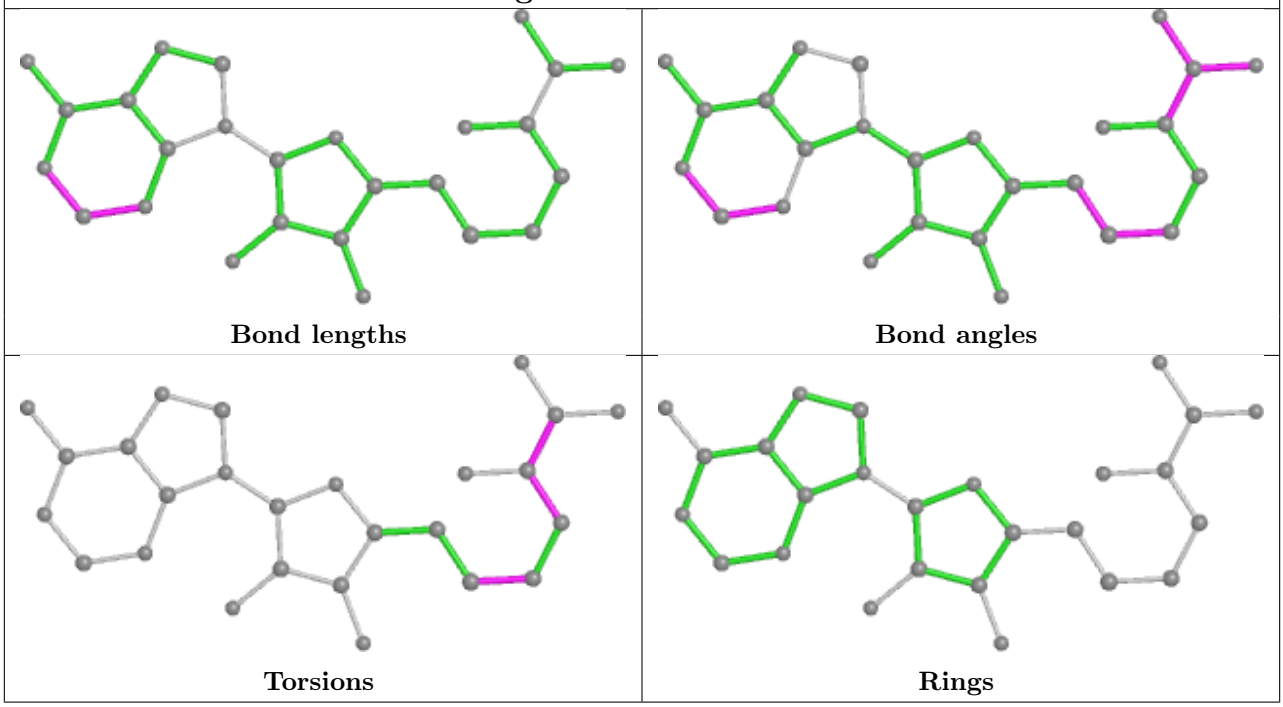
There are no ring outliers.

2 monomers are involved in 3 short contacts:

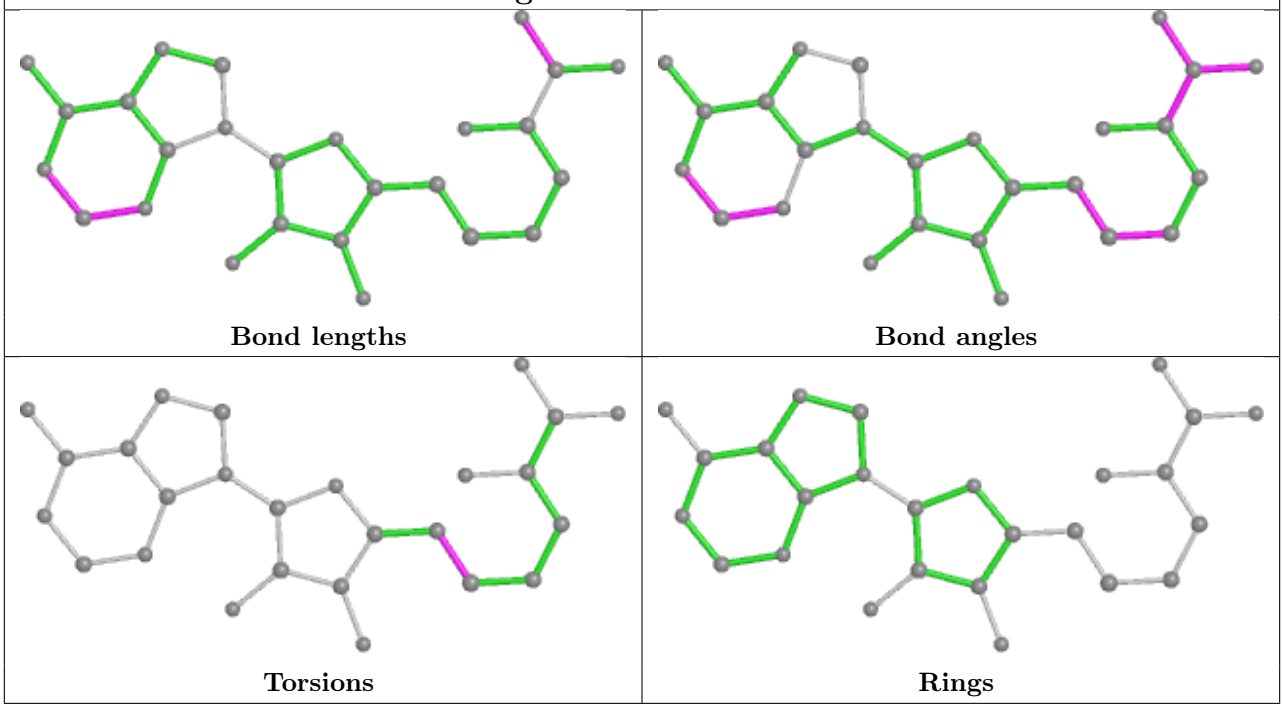
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1001	SAH	1	0
4	A	1001	SAH	2	0

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 then 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.

Ligand SAH D 1001



Ligand SAH A 1001



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 (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, 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	285/285 (100%)	-0.08	6 (2%) 63 43	69, 97, 132, 186	0
1	D	285/285 (100%)	-0.09	6 (2%) 63 43	64, 88, 118, 153	0
2	B	187/209 (89%)	0.51	20 (10%) 6 3	99, 137, 174, 198	0
2	C	174/209 (83%)	0.94	34 (19%) 1 0	108, 152, 190, 214	0
3	E	24/25 (96%)	0.02	0 100 100	104, 123, 146, 155	0
3	F	24/25 (96%)	0.04	1 (4%) 36 21	100, 125, 137, 139	0
All	All	979/1038 (94%)	0.22	67 (6%) 17 9	64, 110, 176, 214	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	328	PRO	6.6
2	C	275	GLY	5.9
2	C	335	TRP	5.7
2	C	274	PRO	5.5
2	C	247	PRO	5.4
2	B	353	SER	5.1
2	C	334	HIS	4.5
2	C	332	SER	4.5
2	B	316	SER	4.3
2	B	361	THR	4.2
2	C	352	SER	4.2
2	B	252	CYS	3.9
1	A	804	PRO	3.8
1	D	628	ALA	3.8
1	A	628	ALA	3.8
2	C	188	GLN	3.8
2	B	274	PRO	3.7
2	B	379	SER	3.6
2	C	333	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
2	B	222	VAL	3.5
1	A	629	GLU	3.4
2	C	215	PRO	3.4
2	B	180	GLU	3.4
2	C	204	THR	3.3
2	C	339	SER	3.3
2	B	352	SER	3.3
2	C	378	PHE	3.2
2	B	211	SER	3.2
1	A	746	GLY	3.1
2	B	378	PHE	3.1
2	B	251	THR	3.1
2	C	277	PRO	3.1
2	B	319	ASN	3.0
2	C	349	ASN	3.0
2	C	374	TYR	3.0
2	B	318	GLN	3.0
2	C	260	LEU	2.8
2	C	329	ALA	2.8
2	C	186	ARG	2.8
1	D	844	LYS	2.8
1	D	806	ALA	2.7
2	C	308	THR	2.7
2	C	276	SER	2.7
1	D	809	VAL	2.6
2	C	337	LEU	2.5
2	C	205	SER	2.5
2	B	185	TRP	2.4
2	B	315	GLY	2.4
2	C	187	ARG	2.4
2	C	250	HIS	2.4
2	C	207	GLY	2.3
2	C	254	ARG	2.3
1	A	638	SER	2.3
1	D	810	ASN	2.2
2	B	317	LEU	2.2
2	C	322	ARG	2.2
1	D	748	ASP	2.2
2	B	329	ALA	2.2
1	A	630	LYS	2.1
2	C	377	TYR	2.1
2	C	353	SER	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	212	GLY	2.1
3	F	422	DG	2.0
2	C	217	GLN	2.0
2	C	262	GLN	2.0
2	B	253	ASP	2.0
2	C	318	GLN	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
3	PYO	E	427	19/20	0.95	0.16	73,88,98,103	0
3	PYO	F	427	19/20	0.96	0.15	79,89,104,119	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

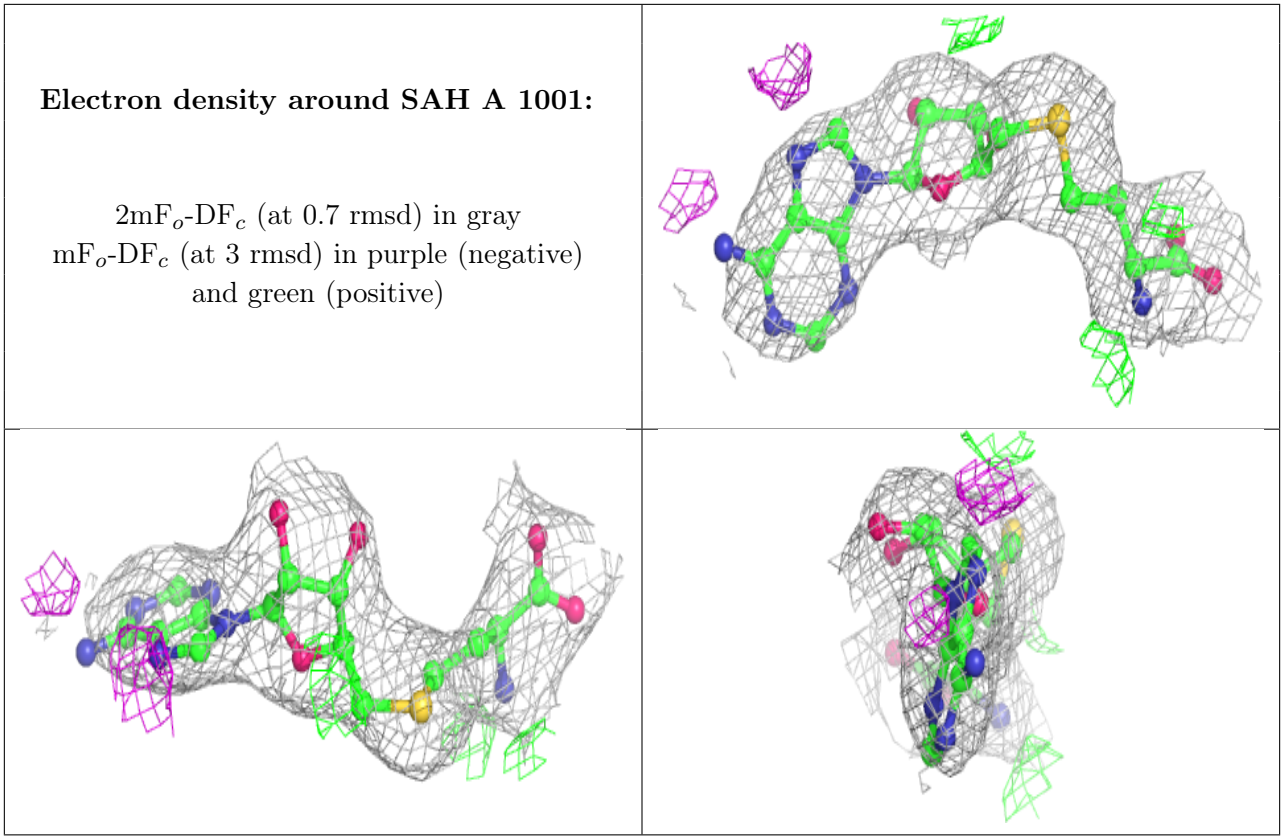
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SAH	A	1001	26/26	0.90	0.21	73,87,98,119	0
4	SAH	D	1001	26/26	0.95	0.16	63,87,102,104	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.

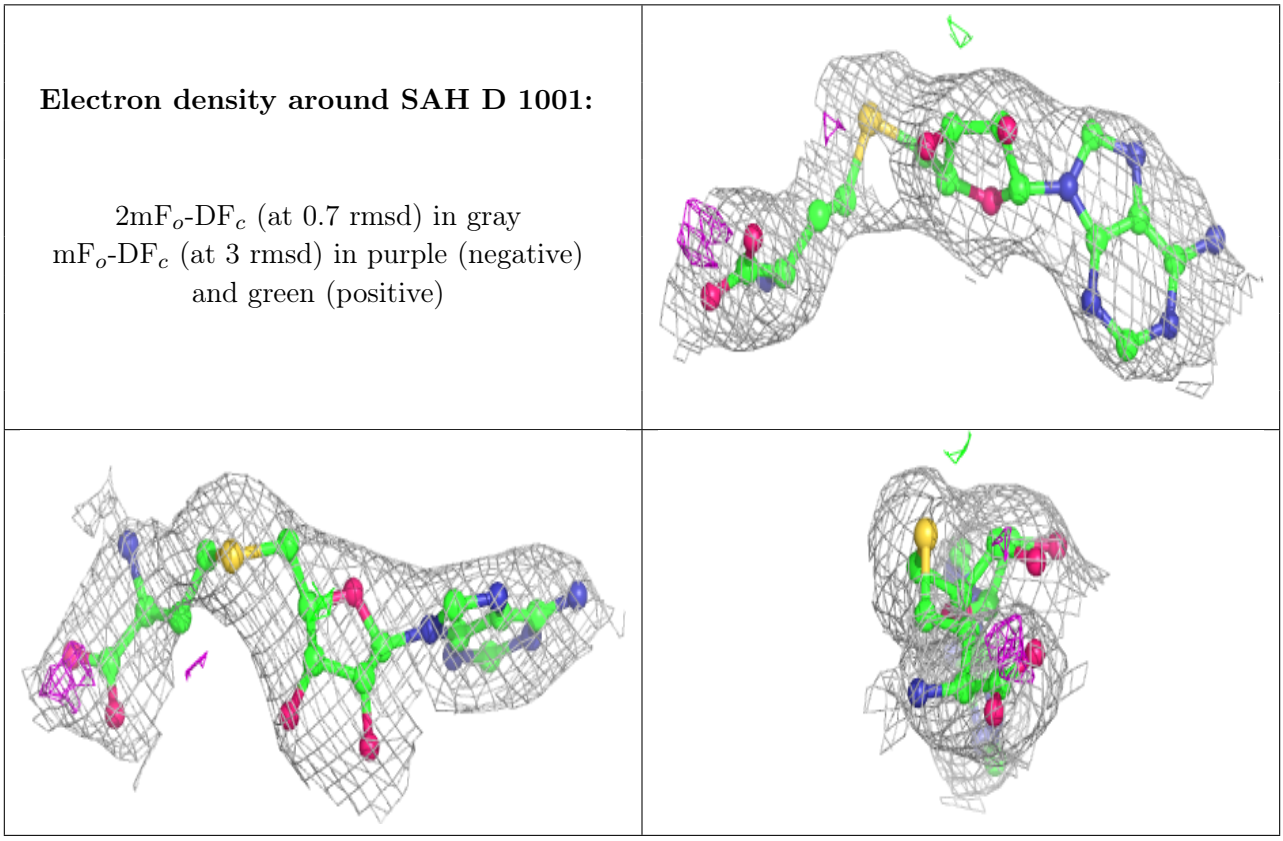
Electron density around SAH A 1001:

$2mF_o$-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 D 1001:

$2mF_o$-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.