



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:15 AM UTC

PDB ID : 6QZZ / pdb_00006qzz
Title : full length OphA V404E in complex with SAH
Authors : Song, H.; Naismith, J.H.
Deposited on : 2019-03-12
Resolution : 1.85 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

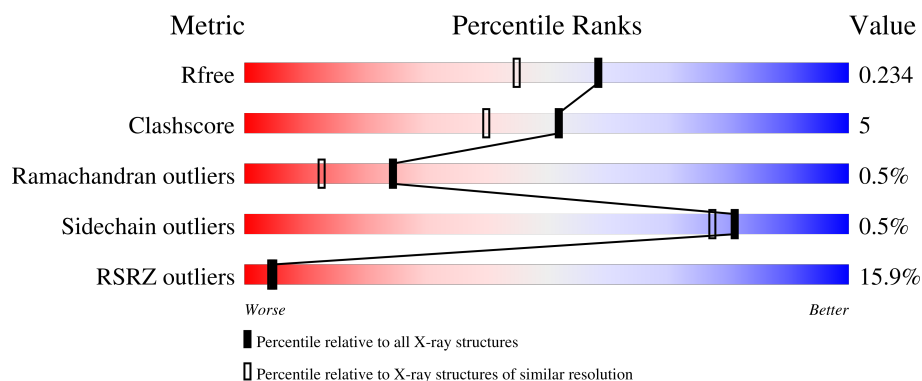
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	416	17% 85% 8% 6%
2	B	416	12% 85% 8% 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6521 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.

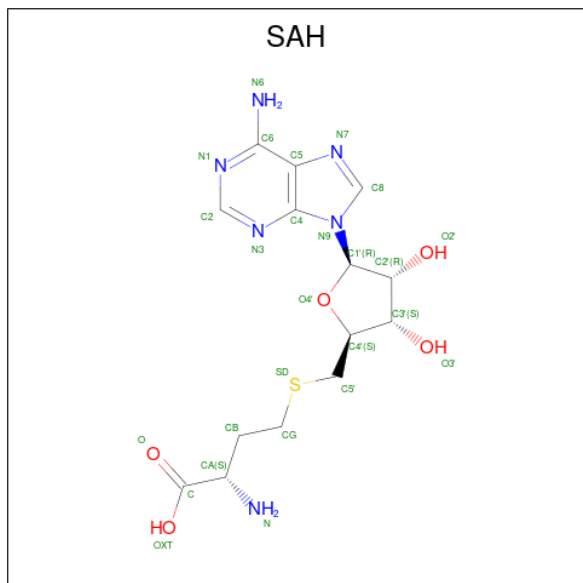
- Molecule 1 is a protein called Peptide N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	4	0
			3081	1963	527	574	17			

- Molecule 2 is a protein called Peptide N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	392	Total	C	N	O	S	0	3	0
			3064	1951	521	575	17			

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



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

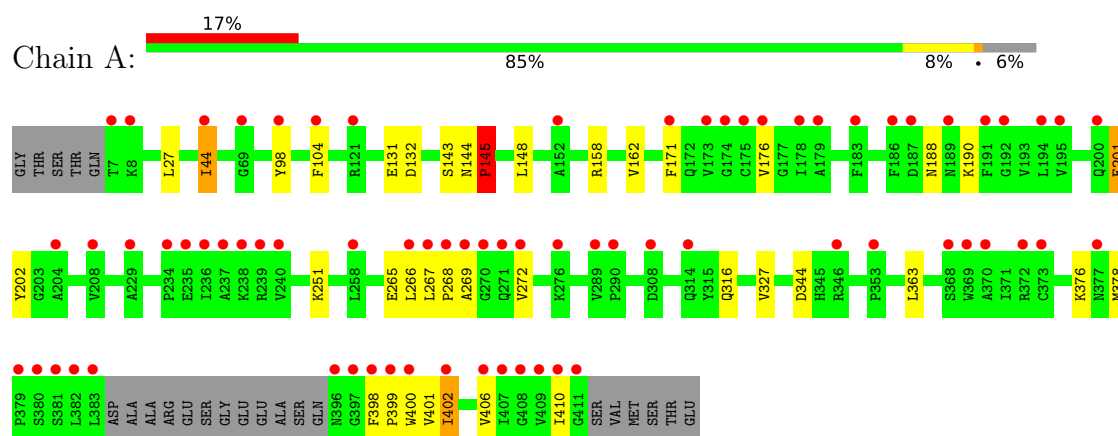
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	159	Total 159	O 159	0	0
4	B	165	Total 165	O 165	0	0

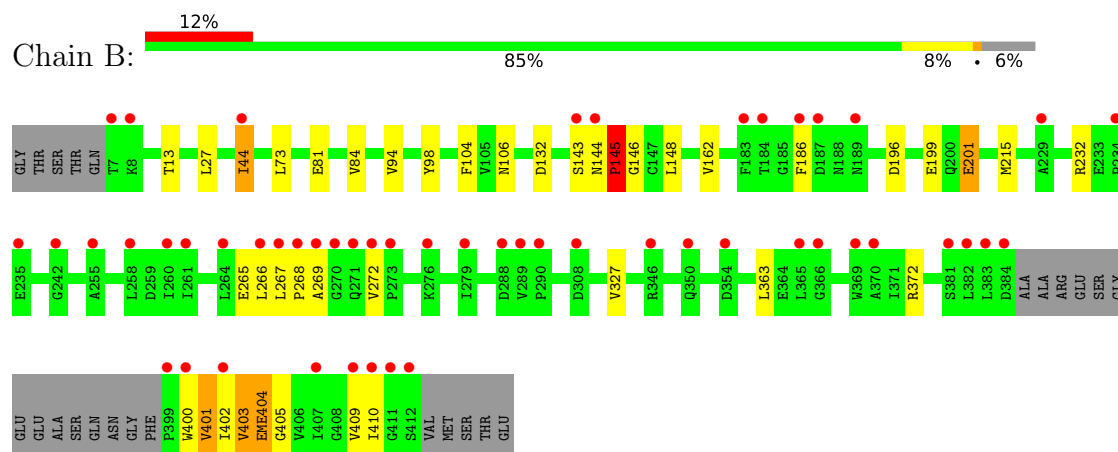
3 Residue-property plots

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: Peptide N-methyltransferase



• Molecule 2: Peptide N-methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	164.00Å 91.72Å 85.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.05 – 1.85 80.05 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (80.05-1.85) 99.9 (80.05-1.85)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.206 , 0.225 0.215 , 0.234	Depositor DCC
R_{free} test set	5568 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6521	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 85.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0908e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SAH, MVA, EME

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	1.01	2/3145 (0.1%)	1.31	1/4276 (0.0%)
2	B	1.02	1/3108 (0.0%)	1.32	5/4225 (0.1%)
All	All	1.02	3/6253 (0.0%)	1.32	6/8501 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	2
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	201	GLU	C-O	12.60	1.40	1.24
2	B	201	GLU	C-O	12.19	1.39	1.24
1	A	344	ASP	C-O	6.37	1.29	1.23

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	145	PRO	N-CA-CB	-5.91	96.09	102.60
1	A	145	PRO	N-CA-CB	-5.50	96.54	102.60
2	B	145	PRO	N-CD-CG	-5.40	97.33	103.80
2	B	146	GLY	CA-C-O	-5.22	118.06	122.29
2	B	410	ILE	CA-C-N	5.18	125.85	119.99
2	B	410	ILE	C-N-CA	5.18	125.85	119.99

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	266	LEU	Peptide
2	B	186	PHE	Peptide
2	B	266	LEU	Peptide

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	3081	0	3053	41	0
2	B	3064	0	3033	40	0
3	A	26	0	19	0	0
3	B	26	0	19	0	0
4	A	159	0	0	0	0
4	B	165	0	0	0	0
All	All	6521	0	6124	63	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 5.

All (63) 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:44:ILE:HG13	2:B:98[B]:TYR:CE1	2.14	0.82
1:A:104:PHE:CZ	1:A:171[B]:PHE:HD2	2.01	0.79
2:B:44:ILE:HG13	2:B:98[B]:TYR:CZ	2.23	0.72
1:A:402:ILE:HG13	2:B:106:ASN:OD1	1.92	0.69
2:B:402:ILE:O	2:B:402:ILE:HG23	1.92	0.68
1:A:104:PHE:CZ	1:A:171[B]:PHE:CD2	2.82	0.68
1:A:406:VAL:O	1:A:410:ILE:HG12	1.95	0.66
1:A:104:PHE:CD2	2:B:143:SER:HB3	2.31	0.65
1:A:202:TYR:O	1:A:251:LYS:NZ	2.29	0.65
1:A:376:LYS:HB2	1:A:378:MET:HE3	1.80	0.64
1:A:143:SER:HB3	2:B:104:PHE:CD2	2.34	0.63
1:A:131:GLU:HB2	1:A:171[B]:PHE:HZ	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:VAL:HG23	1:A:190:LYS:HB2	1.82	0.61
1:A:104:PHE:CE1	1:A:171[B]:PHE:CD2	2.88	0.60
2:B:44:ILE:HG21	2:B:215:MET:HE3	1.84	0.60
1:A:401:MVA:HN2	1:A:401:MVA:HG22	1.85	0.58
1:A:44:ILE:CG1	2:B:402:ILE:HG21	2.37	0.55
2:B:272:VAL:HG13	2:B:409:VAL:HG13	1.87	0.55
2:B:199:GLU:CD	2:B:232:ARG:HH22	2.14	0.55
2:B:372:ARG:HD2	2:B:400:TRP:CH2	2.43	0.54
2:B:267:LEU:O	2:B:269:ALA:N	2.41	0.53
1:A:402:ILE:CG1	2:B:106:ASN:OD1	2.55	0.53
1:A:267:LEU:O	1:A:269:ALA:N	2.43	0.52
2:B:81:GLU:HA	2:B:84:VAL:HG22	1.91	0.51
2:B:265:GLU:HA	2:B:267:LEU:HG	1.92	0.51
1:A:399:PRO:CG	2:B:44:ILE:HD13	2.41	0.50
2:B:162:VAL:HG21	2:B:201:GLU:HB3	1.94	0.50
1:A:265:GLU:HA	1:A:267:LEU:HG	1.93	0.50
1:A:162:VAL:HG21	1:A:201:GLU:HB3	1.94	0.50
1:A:272:VAL:HA	1:A:410:ILE:HD11	1.93	0.49
1:A:376:LYS:CB	1:A:378:MET:HE3	2.42	0.48
1:A:398:PHE:N	1:A:399:PRO:CD	2.77	0.48
1:A:27:LEU:HD23	2:B:27:LEU:HD23	1.96	0.47
2:B:404:EME:C7	2:B:405:GLY:N	2.76	0.47
1:A:104:PHE:CE2	2:B:143:SER:HB3	2.50	0.46
1:A:132:ASP:OD2	2:B:132:ASP:OD2	2.32	0.46
1:A:148:LEU:HG	2:B:148:LEU:HG	1.96	0.45
1:A:104:PHE:CD2	2:B:143:SER:CB	2.98	0.45
1:A:44:ILE:HD12	1:A:98:TYR:CZ	2.51	0.45
1:A:104:PHE:CE2	2:B:143:SER:CB	2.99	0.45
1:A:399:PRO:O	2:B:98[A]:TYR:OH	2.14	0.45
2:B:401:MVA:HN2	2:B:401:MVA:HG22	1.99	0.45
1:A:400:TRP:HA	1:A:401:MVA:HN1	1.80	0.44
1:A:44:ILE:CG2	2:B:400:TRP:CE3	3.01	0.44
1:A:316:GLN:HB3	1:A:378:MET:CE	2.49	0.43
2:B:327:VAL:HG11	2:B:363:LEU:HD11	2.01	0.43
1:A:398:PHE:N	1:A:399:PRO:HD3	2.33	0.43
2:B:44:ILE:HG21	2:B:215:MET:CE	2.47	0.43
2:B:400:TRP:HA	2:B:401:MVA:HN1	1.78	0.43
1:A:176:VAL:HG22	1:A:188:ASN:OD1	2.19	0.42
1:A:143:SER:HB3	2:B:104:PHE:CE2	2.55	0.42
2:B:199:GLU:OE2	2:B:232:ARG:NH2	2.48	0.42
1:A:143:SER:CB	2:B:104:PHE:CD2	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:LYS:CB	1:A:378:MET:CE	2.98	0.42
2:B:13:THR:O	2:B:94:VAL:HA	2.21	0.41
1:A:44:ILE:HG12	2:B:402:ILE:HG21	2.03	0.41
1:A:327:VAL:HG11	1:A:363:LEU:HD11	2.03	0.41
2:B:73:LEU:HD12	2:B:73:LEU:HA	1.98	0.41
1:A:144[A]:ASN:HA	1:A:145:PRO:HA	1.88	0.41
1:A:158:ARG:NH2	2:B:409:VAL:HG23	2.36	0.40
2:B:144[A]:ASN:HA	2:B:145:PRO:HA	1.88	0.40
2:B:402:ILE:HA	2:B:403:MVA:HN1	1.89	0.40
2:B:196:ASP:OD1	2:B:232:ARG:NH1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	392/416 (94%)	373 (95%)	17 (4%)	2 (0%)	24	13
2	B	388/416 (93%)	369 (95%)	17 (4%)	2 (0%)	24	13
All	All	780/832 (94%)	742 (95%)	34 (4%)	4 (0%)	24	13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	PRO
2	B	268	PRO
2	B	145	PRO
1	A	145	PRO

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	329/343 (96%)	327 (99%)	2 (1%)	78	73
2	B	326/341 (96%)	325 (100%)	1 (0%)	86	85
All	All	655/684 (96%)	652 (100%)	3 (0%)	81	77

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ILE
1	A	402	ILE
2	B	44	ILE

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	64	GLN
1	A	284	GLN
2	B	64	GLN
2	B	172	GLN
2	B	284	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](#)

4 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	EME	B	404	2	8,9,10	0.87	0	7,10,12	1.40	1 (14%)
1	MVA	A	401	1	6,7,8	0.61	0	6,8,10	0.99	0
2	MVA	B	403	2	6,7,8	0.62	0	6,8,10	1.21	1 (16%)
2	MVA	B	401	2	6,7,8	0.82	0	6,8,10	1.68	2 (33%)

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	EME	B	404	2	-	4/6/9/11	-
1	MVA	A	401	1	-	4/6/8/10	-
2	MVA	B	403	2	-	2/6/8/10	-
2	MVA	B	401	2	-	4/6/8/10	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	MVA	CB-CA-C	-2.90	109.21	112.96
2	B	403	MVA	O-C-CA	-2.67	117.80	124.86
2	B	401	MVA	O-C-CA	-2.27	118.85	124.86
2	B	404	EME	OE1-CD-CG	2.02	120.39	114.00

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	401	MVA	N-CA-CB-CG1
1	A	401	MVA	N-CA-CB-CG2
1	A	401	MVA	C-CA-CB-CG1
1	A	401	MVA	C-CA-CB-CG2
2	B	401	MVA	N-CA-CB-CG1
2	B	401	MVA	N-CA-CB-CG2
2	B	401	MVA	C-CA-CB-CG1

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Mol	Chain	Res	Type	Atoms
2	B	401	MVA	C-CA-CB-CG2
2	B	403	MVA	O-C-CA-CB
2	B	404	EME	O-C-CA-CB
2	B	404	EME	C-CA-CB-CG
2	B	404	EME	N-CA-CB-CG
2	B	404	EME	CA-CB-CG-CD
2	B	403	MVA	CB-CA-N-CN

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	404	EME	1	0
1	A	401	MVA	2	0
2	B	403	MVA	1	0
2	B	401	MVA	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
3	SAH	B	501	-	27,28,28	0.55	1 (3%)	36,40,40	0.67	1 (2%)
3	SAH	A	501	-	27,28,28	0.67	1 (3%)	36,40,40	0.70	1 (2%)

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	SAH	B	501	-	-	2/15/31/31	0/3/3/3
3	SAH	A	501	-	-	2/15/31/31	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	SAH	OXT-C	-2.44	1.22	1.30
3	B	501	SAH	OXT-C	-2.43	1.22	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	SAH	OXT-C-O	-2.55	118.29	124.08
3	B	501	SAH	OXT-C-O	-2.24	119.01	124.08

There are no chirality outliers.

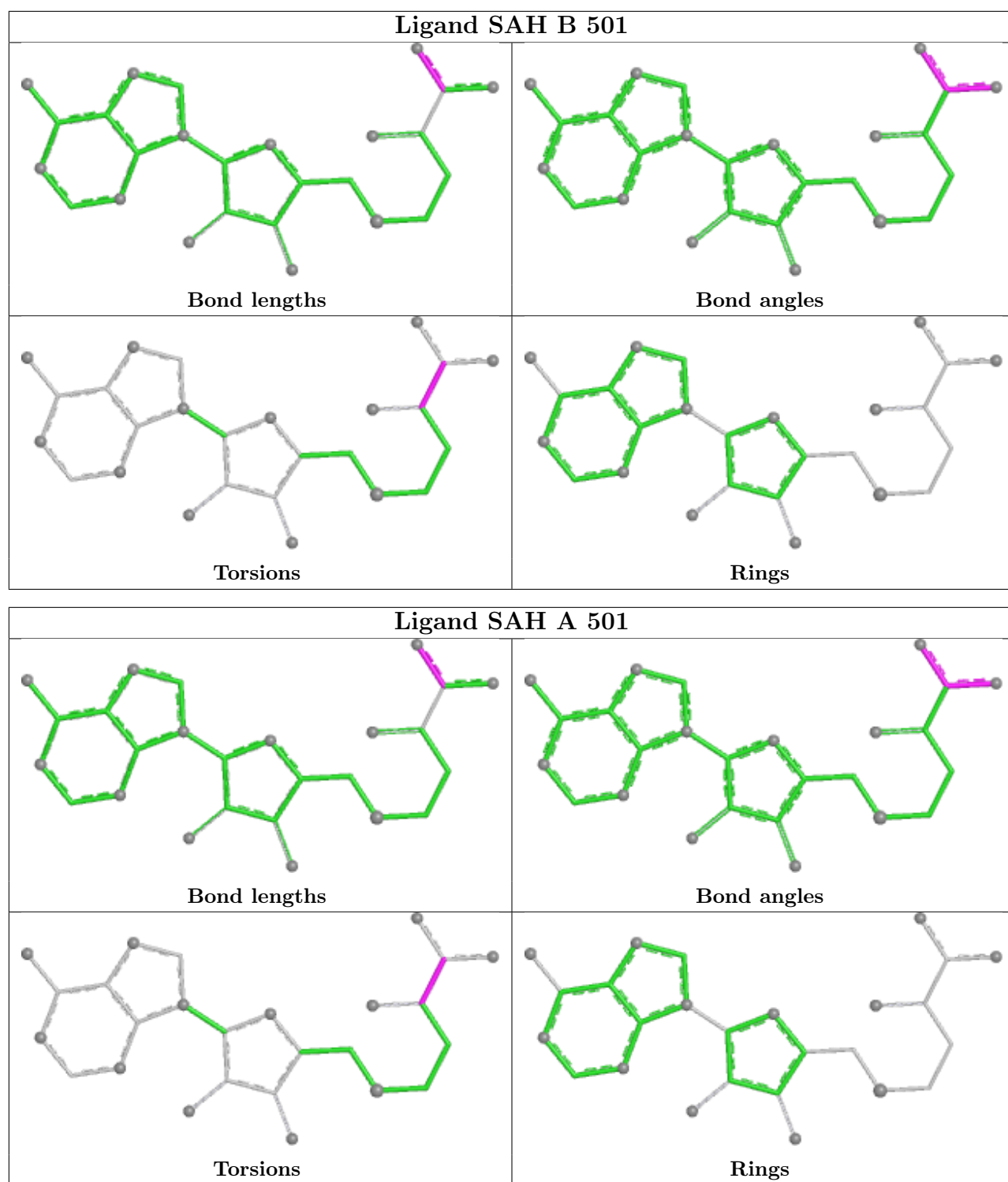
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	SAH	O-C-CA-CB
3	A	501	SAH	O-C-CA-CB
3	A	501	SAH	OXT-C-CA-CB
3	B	501	SAH	OXT-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	392/416 (94%)	1.09	72 (18%) 3 3	16, 48, 84, 113	4 (1%)
2	B	389/416 (93%)	0.86	52 (13%) 7 6	15, 45, 80, 126	3 (0%)
All	All	781/832 (93%)	0.98	124 (15%) 5 4	15, 46, 82, 126	7 (0%)

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	398	PHE	8.0
2	B	400	TRP	7.9
1	A	267	LEU	7.2
2	B	267	LEU	7.2
1	A	186	PHE	6.5
1	A	400	TRP	6.4
1	A	383	LEU	5.9
2	B	402	ILE	5.4
1	A	369	TRP	5.3
1	A	409	VAL	5.2
1	A	268	PRO	5.1
2	B	399	PRO	5.1
2	B	289	VAL	5.1
1	A	289	VAL	5.0
1	A	410	ILE	5.0
2	B	268	PRO	5.0
1	A	7	THR	4.9
2	B	410	ILE	4.8
2	B	411	GLY	4.7
2	B	7	THR	4.5
1	A	397	GLY	4.5
2	B	409	VAL	4.5
1	A	121[A]	ARG	4.4
1	A	411	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	399	PRO	4.2
1	A	346	ARG	4.0
2	B	412	SER	4.0
2	B	407	ILE	3.9
2	B	272	VAL	3.8
1	A	236	ILE	3.7
1	A	240	VAL	3.7
2	B	186	PHE	3.7
1	A	407	ILE	3.7
1	A	381	SER	3.6
1	A	104	PHE	3.6
2	B	44	ILE	3.6
2	B	346	ARG	3.6
1	A	44	ILE	3.5
1	A	379	PRO	3.5
1	A	396	ASN	3.4
1	A	382	LEU	3.4
1	A	229	ALA	3.4
2	B	264	LEU	3.4
1	A	234	PRO	3.4
2	B	258	LEU	3.3
1	A	402	ILE	3.3
2	B	242	GLY	3.3
1	A	238	LYS	3.2
2	B	266	LEU	3.2
1	A	276	LYS	3.1
2	B	354	ASP	3.1
1	A	270	GLY	3.0
1	A	179	ALA	3.0
1	A	175	CYS	2.9
2	B	383	LEU	2.9
1	A	187	ASP	2.9
2	B	260	ILE	2.9
2	B	270	GLY	2.9
1	A	237	ALA	2.8
2	B	269	ALA	2.8
1	A	290	PRO	2.8
1	A	152	ALA	2.7
1	A	353	PRO	2.7
2	B	276	LYS	2.7
1	A	406	VAL	2.7
1	A	183	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	192	GLY	2.6
1	A	98	TYR	2.6
2	B	308	ASP	2.6
1	A	173	VAL	2.6
1	A	408	GLY	2.6
1	A	373	CYS	2.6
2	B	8	LYS	2.6
1	A	368	SER	2.6
2	B	290	PRO	2.6
1	A	176	VAL	2.6
1	A	380	SER	2.6
2	B	369	TRP	2.5
2	B	189	ASN	2.5
1	A	189	ASN	2.5
1	A	69	GLY	2.5
1	A	372	ARG	2.4
2	B	234	PRO	2.4
2	B	381	SER	2.4
1	A	178	ILE	2.4
2	B	255	ALA	2.4
2	B	184	THR	2.4
1	A	239	ARG	2.3
1	A	235	GLU	2.3
1	A	271	GLN	2.3
2	B	261	ILE	2.3
1	A	272	VAL	2.3
2	B	288	ASP	2.3
1	A	258	LEU	2.3
1	A	8	LYS	2.3
1	A	204	ALA	2.3
2	B	271	GLN	2.3
2	B	365	LEU	2.3
1	A	191	PHE	2.2
2	B	273	PRO	2.2
2	B	279	ILE	2.2
1	A	266	LEU	2.2
1	A	200	GLN	2.2
1	A	171[A]	PHE	2.2
1	A	314	GLN	2.2
2	B	384	ASP	2.2
2	B	350	GLN	2.2
1	A	308	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	269	ALA	2.2
2	B	187	ASP	2.1
2	B	183	PHE	2.1
1	A	370	ALA	2.1
2	B	143	SER	2.1
1	A	194	LEU	2.1
2	B	229	ALA	2.1
2	B	235	GLU	2.0
2	B	144[A]	ASN	2.0
2	B	382	LEU	2.0
2	B	370	ALA	2.0
1	A	174	GLY	2.0
1	A	377	ASN	2.0
2	B	366	GLY	2.0
1	A	195	VAL	2.0
1	A	208	VAL	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	MVA	B	401	8/9	0.77	0.28	59,64,71,73	0
2	MVA	B	403	8/9	0.84	0.24	41,47,67,71	0
2	EME	B	404	10/11	0.90	0.25	40,54,109,128	0
1	MVA	A	401	8/9	0.94	0.12	35,41,51,58	0

6.3 Carbohydrates [i](#)

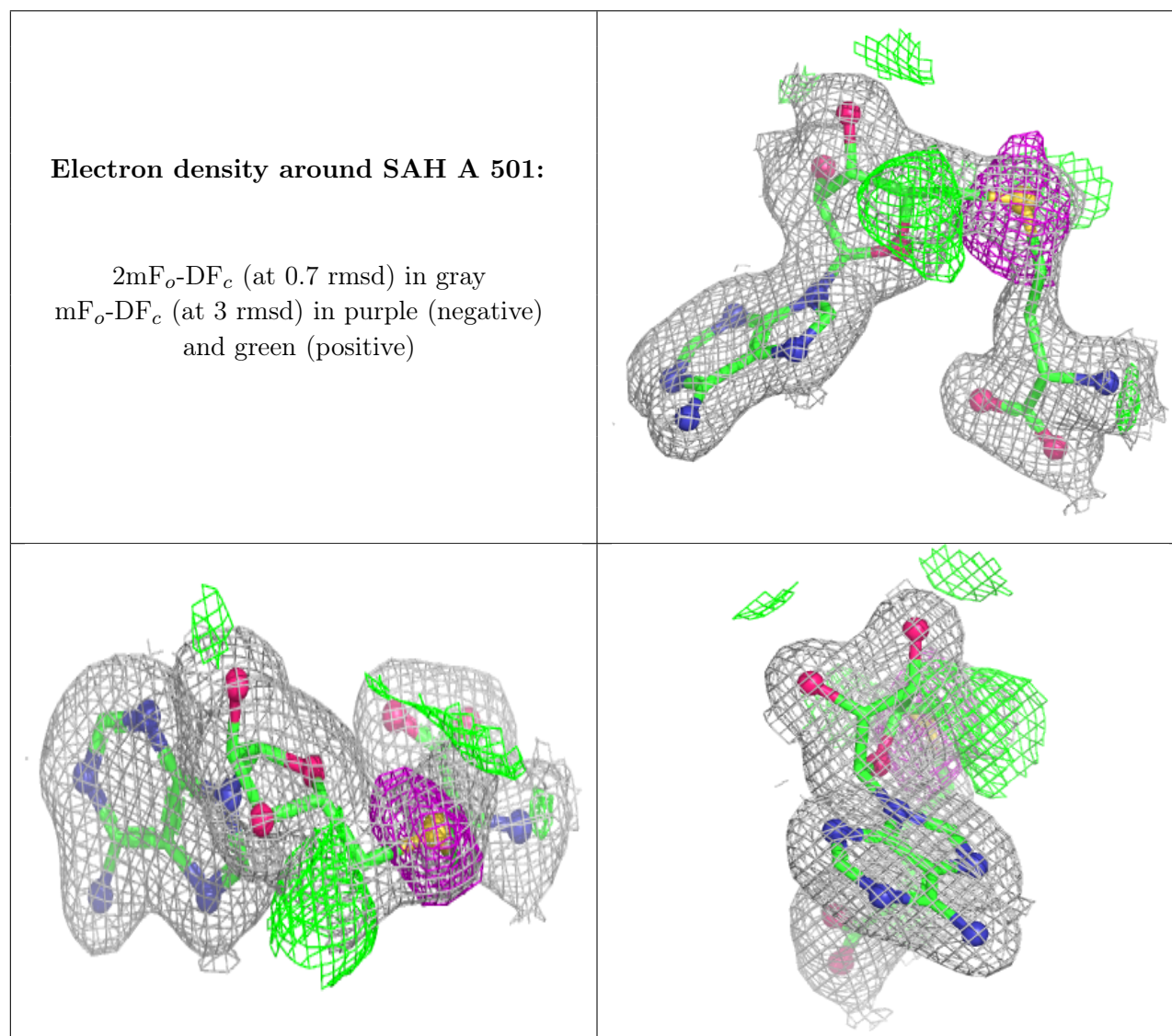
There are no oligosaccharides in this entry.

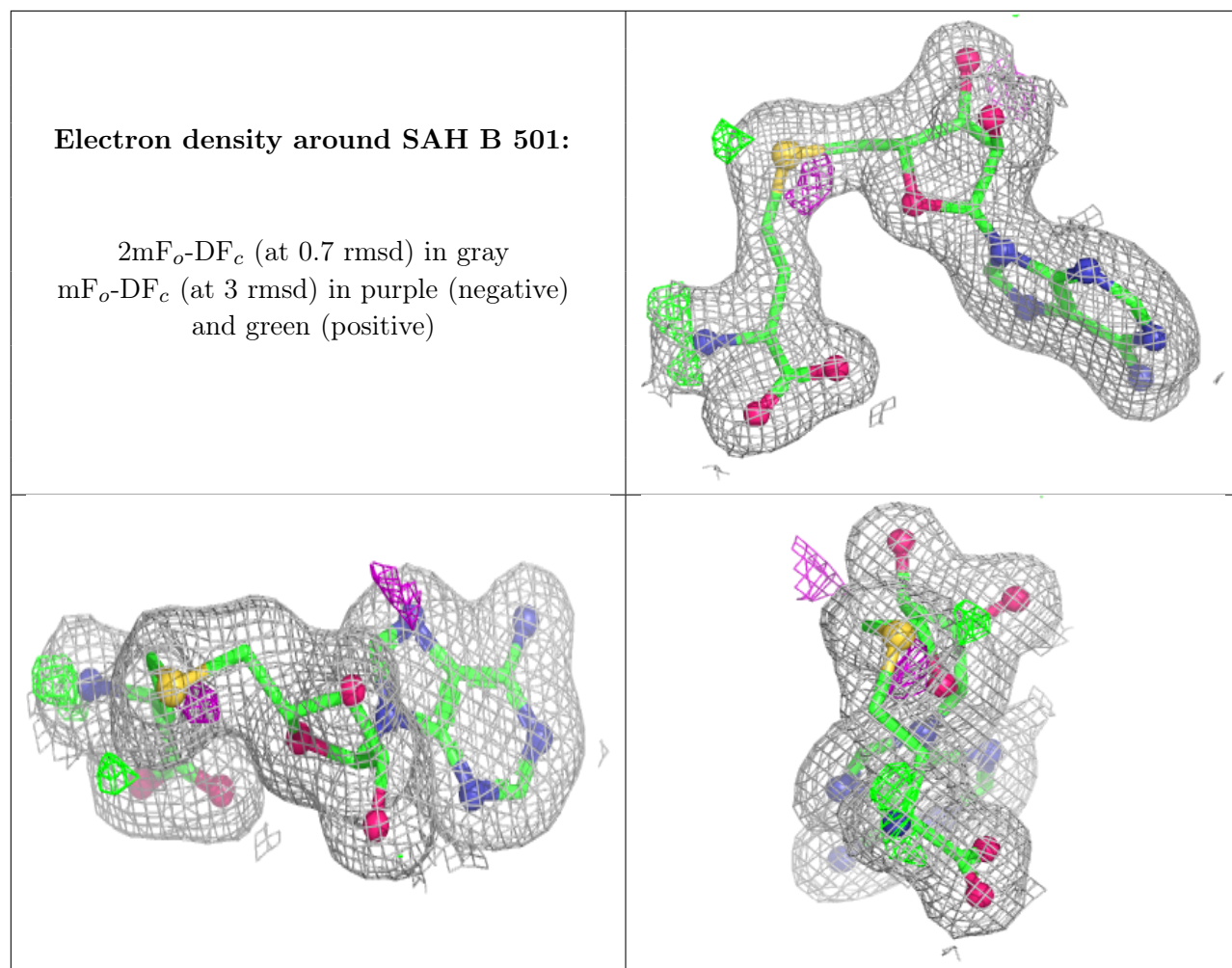
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
3	SAH	A	501	26/26	0.91	0.10	27,33,43,46	0
3	SAH	B	501	26/26	0.96	0.07	28,32,36,37	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.