



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:18 AM UTC

PDB ID : 3HCD / pdb_00003hcd
Title : Crystal Structure of hPNMT in Complex With Noradrenaline and AdoHcy
Authors : Drinkwater, N.; Martin, J.L.
Deposited on : 2009-05-06
Resolution : 2.39 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

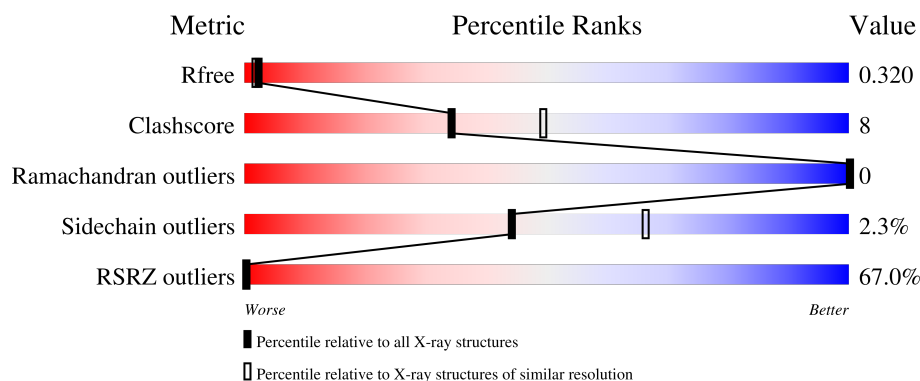
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	289	71% 72% 16% • 11%
1	B	289	51% 75% 17% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4421 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 Phenylethanolamine N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	1	0	0
			2016	1280	358	369	9			
1	B	268	Total	C	N	O	S	0	1	0
			2089	1324	371	385	9			

There are 14 discrepancies between the modelled and reference sequences:

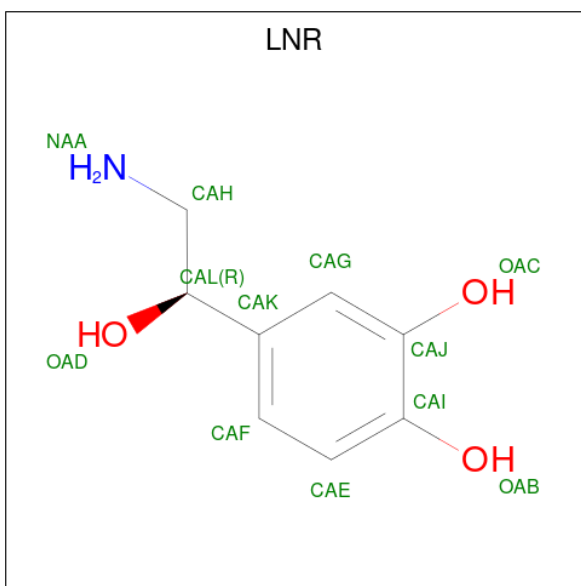
Chain	Residue	Modelled	Actual	Comment	Reference
A	283	GLU	-	expression tag	UNP P11086
A	284	HIS	-	expression tag	UNP P11086
A	285	HIS	-	expression tag	UNP P11086
A	286	HIS	-	expression tag	UNP P11086
A	287	HIS	-	expression tag	UNP P11086
A	288	HIS	-	expression tag	UNP P11086
A	289	HIS	-	expression tag	UNP P11086
B	283	GLU	-	expression tag	UNP P11086
B	284	HIS	-	expression tag	UNP P11086
B	285	HIS	-	expression tag	UNP P11086
B	286	HIS	-	expression tag	UNP P11086
B	287	HIS	-	expression tag	UNP P11086
B	288	HIS	-	expression tag	UNP P11086
B	289	HIS	-	expression tag	UNP P11086

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).



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

- Molecule 3 is L-NOREPINEPHRINE (CCD ID: LNR) (formula: $C_8H_{11}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 12	C 8	N 1	O 3	0	0
3	B	1	Total 12	C 8	N 1	O 3	0	0

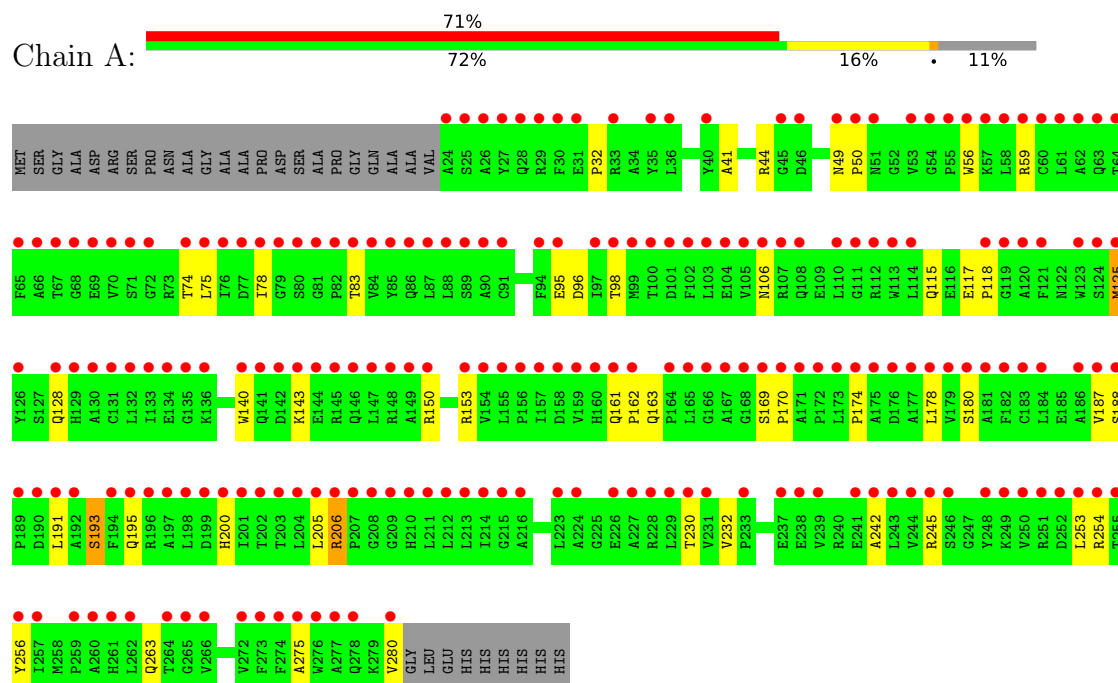
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	114	Total 114	O 114	0	0
4	B	126	Total 126	O 126	0	0

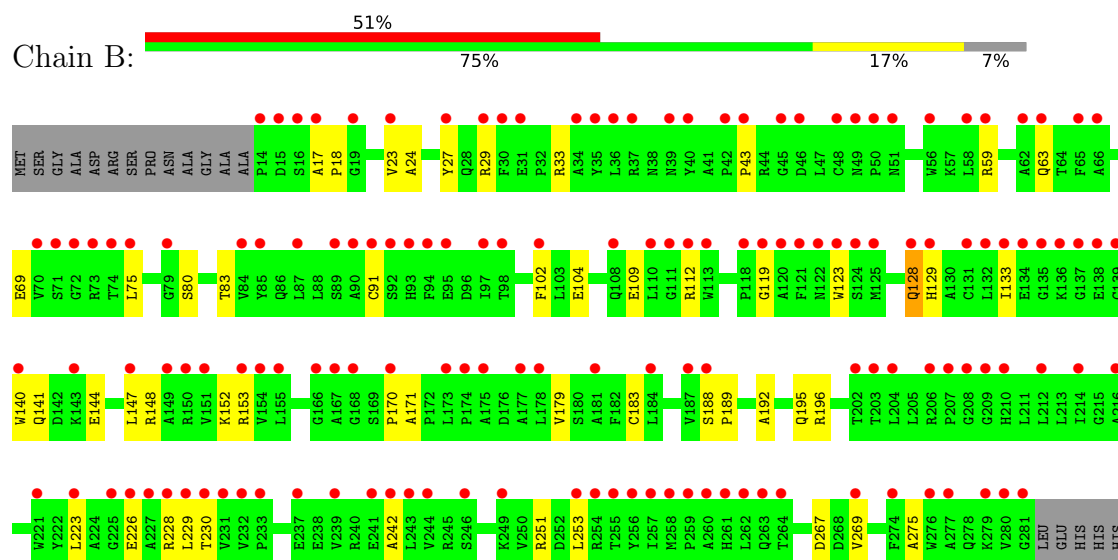
3 Residue-property plots

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: Phenylethanolamine N-methyltransferase



• Molecule 1: Phenylethanolamine N-methyltransferase



HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	93.65Å 93.65Å 187.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.78 – 2.39 34.78 – 2.39	Depositor EDS
% Data completeness (in resolution range)	91.2 (34.78-2.39) 99.9 (34.78-2.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.32 (at 2.40Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.181 , 0.230 0.321 , 0.320	Depositor DCC
R_{free} test set	3386 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4421	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: SAH, LNR

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	0.57	0/2067	0.90	6/2813 (0.2%)
1	B	0.66	1/2145 (0.0%)	0.87	0/2920
All	All	0.61	1/4212 (0.0%)	0.88	6/5733 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	183	CYS	CA-C	7.17	1.57	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	ASN	CA-C-N	7.38	127.40	119.28
1	A	49	ASN	C-N-CA	7.38	127.40	119.28
1	A	163	GLN	CA-C-N	5.61	125.28	119.05
1	A	163	GLN	C-N-CA	5.61	125.28	119.05
1	A	41	ALA	CA-C-N	-5.49	115.65	119.66
1	A	41	ALA	C-N-CA	-5.49	115.65	119.66

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	2016	0	1983	34	0
1	B	2089	0	2053	32	0
2	A	26	0	19	2	0
2	B	26	0	20	2	0
3	A	12	0	11	1	0
3	B	12	0	11	0	0
4	A	114	0	0	6	0
4	B	126	0	0	3	0
All	All	4421	0	4097	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 8.

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)
1:A:125:MET:HE2	1:B:141:GLN:HE22	1.13	1.06
1:A:125:MET:CE	1:B:141:GLN:HE22	1.86	0.89
1:B:29:ARG:HH21	1:B:226:GLU:HB3	1.41	0.85
1:A:125:MET:HB2	4:A:400:HOH:O	1.76	0.84
1:A:125:MET:HE2	1:B:141:GLN:NE2	1.93	0.81
1:B:75:LEU:HD11	1:B:179:VAL:HG23	1.66	0.77
1:B:195:GLN:HE22	1:B:242:ALA:HA	1.50	0.75
1:B:29:ARG:NH2	1:B:226:GLU:HB3	2.05	0.71
1:A:254:ARG:NH2	4:A:504:HOH:O	2.36	0.58
1:A:115:GLN:HB2	1:A:117:GLU:HG3	1.86	0.57
1:A:98:THR:HG23	1:A:153:ARG:HG3	1.87	0.56
1:A:143:LYS:HD3	4:A:320:HOH:O	2.04	0.56
1:B:69:GLU:OE1	1:B:251:ARG:NH2	2.38	0.56
1:A:125:MET:CE	1:B:141:GLN:NE2	2.61	0.54
1:A:83:THR:OG1	2:A:3001:SAH:HA	2.08	0.54
1:B:112:ARG:HH21	1:B:119:GLY:HA3	1.72	0.54
1:A:263:GLN:HG2	4:A:337:HOH:O	2.08	0.53
1:A:50:PRO:O	1:A:59:ARG:NH2	2.41	0.52
1:A:195:GLN:HE22	1:A:242:ALA:HA	1.75	0.51
1:B:170:PRO:O	1:B:171:ALA:C	2.54	0.51
1:B:17:ALA:HB3	1:B:18:PRO:HD3	1.93	0.50
1:B:253:LEU:HD13	1:B:275:ALA:HB2	1.94	0.50
1:A:253:LEU:HD13	1:A:275:ALA:HB2	1.94	0.50
1:B:128[A]:GLN:HE21	1:B:128[A]:GLN:HA	1.76	0.49
1:B:128[B]:GLN:HG2	1:B:140:TRP:CD1	2.47	0.48
1:B:148:ARG:HD2	4:B:414:HOH:O	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:GLN:HA	1:A:161:GLN:OE1	2.12	0.48
1:A:32:PRO:HG3	1:A:106:ASN:ND2	2.29	0.47
1:B:91:CYS:HB3	1:B:147:LEU:HD13	1.96	0.47
1:A:75:LEU:C	1:A:75:LEU:HD23	2.39	0.47
1:A:188:SER:HB3	1:A:193:SER:HB2	1.96	0.46
1:A:280:VAL:O	1:A:280:VAL:HG13	2.15	0.46
1:B:83:THR:HA	1:B:123:TRP:CZ2	2.51	0.46
1:B:129:HIS:ND1	4:B:445:HOH:O	2.35	0.46
1:B:43:PRO:HD2	4:B:426:HOH:O	2.14	0.46
1:A:187:VAL:HG11	2:A:3001:SAH:C5	2.45	0.45
1:B:102:PHE:HB2	2:B:3002:SAH:C4	2.45	0.45
1:A:74:THR:HG22	1:A:96:ASP:HB3	1.98	0.45
1:B:27:TYR:CE2	1:B:229:LEU:HD22	2.52	0.45
1:A:174:PRO:HG2	1:A:206:ARG:HB2	2.00	0.44
1:A:245:ARG:HE	1:A:245:ARG:HB2	1.62	0.43
1:A:195:GLN:NE2	1:A:245:ARG:HD2	2.34	0.43
1:B:59:ARG:HG2	1:B:63:GLN:NE2	2.33	0.43
1:B:188:SER:HA	1:B:189:PRO:HD3	1.90	0.43
1:B:192:ALA:O	1:B:196:ARG:HG3	2.18	0.43
1:A:56:TRP:CE2	1:A:256:TYR:HB2	2.54	0.43
1:A:128:GLN:HG2	1:A:140:TRP:CD1	2.54	0.43
1:A:44:ARG:HG3	4:A:294:HOH:O	2.18	0.43
1:A:178:LEU:HG	1:A:205:LEU:HD13	2.00	0.43
1:B:33:ARG:NH2	1:B:109:GLU:OE2	2.51	0.43
1:A:117:GLU:HB3	1:A:118:PRO:CD	2.50	0.42
1:A:162:PRO:HA	1:A:200:HIS:CD2	2.54	0.41
1:B:23:VAL:O	1:B:24:ALA:C	2.63	0.41
1:A:78:ILE:HB	1:A:180:SER:HB2	2.03	0.41
3:A:2001:LNR:HAHA	3:A:2001:LNR:HAG	1.81	0.41
1:A:169:SER:HA	1:A:170:PRO:HD3	1.94	0.41
1:B:267:ASP:OD2	1:B:269:VAL:HG12	2.21	0.41
1:A:95:GLU:HA	1:A:150:ARG:HD3	2.03	0.41
1:B:223:LEU:HD21	1:B:228:ARG:HD2	2.01	0.41
1:B:152:LYS:O	1:B:153:ARG:HB3	2.19	0.41
1:B:80:SER:O	2:B:3002:SAH:HA	2.20	0.41
1:A:125:MET:HG3	4:A:441:HOH:O	2.21	0.40
1:B:144:GLU:O	1:B:148:ARG:HG3	2.21	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	255/289 (88%)	247 (97%)	8 (3%)	0	100	100
1	B	267/289 (92%)	262 (98%)	5 (2%)	0	100	100
All	All	522/578 (90%)	509 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	212/233 (91%)	206 (97%)	6 (3%)	38	60
1	B	219/233 (94%)	214 (98%)	5 (2%)	44	66
All	All	431/466 (92%)	420 (97%)	11 (3%)	44	63

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	MET
1	A	191	LEU
1	A	193	SER
1	A	206	ARG
1	A	230	THR
1	A	232	VAL
1	B	104	GLU
1	B	128[A]	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	128[B]	GLN
1	B	133	ILE
1	B	230	THR

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	106	ASN
1	A	129	HIS
1	A	195	GLN
1	B	106	ASN
1	B	108	GLN
1	B	141	GLN
1	B	146	GLN
1	B	195	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	LNR	B	2002	-	12,12,12	1.02	0	16,16,16	0.89	0
2	SAH	A	3001	-	27,28,28	2.41	9 (33%)	36,40,40	2.33	13 (36%)
2	SAH	B	3002	-	27,28,28	2.06	7 (25%)	36,40,40	2.33	14 (38%)
3	LNR	A	2001	-	12,12,12	1.07	1 (8%)	16,16,16	1.04	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
3	LNR	B	2002	-	-	4/6/6/6	0/1/1/1
2	SAH	A	3001	-	-	5/15/31/31	0/3/3/3
2	SAH	B	3002	-	-	5/15/31/31	0/3/3/3
3	LNR	A	2001	-	-	5/6/6/6	0/1/1/1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3001	SAH	O-C	5.94	1.39	1.22
2	B	3002	SAH	C6-N6	5.70	1.48	1.34
2	A	3001	SAH	C2'-C3'	-5.38	1.38	1.53
2	B	3002	SAH	C2'-C3'	-4.86	1.40	1.53
2	A	3001	SAH	OXT-C	-4.27	1.17	1.30
2	A	3001	SAH	C6-N6	3.73	1.43	1.34
2	A	3001	SAH	C8-N7	3.68	1.38	1.31
2	A	3001	SAH	C2'-C1'	-3.55	1.42	1.53
2	B	3002	SAH	C8-N7	3.38	1.38	1.31
2	B	3002	SAH	C2'-C1'	-3.36	1.42	1.53
2	A	3001	SAH	C5-C4	-2.93	1.33	1.39
2	A	3001	SAH	O4'-C4'	-2.91	1.38	1.45
2	B	3002	SAH	OXT-C	2.44	1.38	1.30
3	A	2001	LNR	OAC-CAJ	2.34	1.41	1.36
2	B	3002	SAH	O4'-C4'	-2.34	1.39	1.45
2	B	3002	SAH	C2-N1	2.26	1.38	1.33
2	A	3001	SAH	C8-N9	-2.04	1.34	1.37

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3001	SAH	N3-C2-N1	-6.68	118.47	128.58
2	A	3001	SAH	C5-C4-N3	-5.71	118.86	126.72
2	B	3002	SAH	N3-C2-N1	-5.36	120.47	128.58
2	B	3002	SAH	N9-C8-N7	-5.33	106.38	113.94
2	A	3001	SAH	C2-N3-C4	4.54	122.92	111.83
2	B	3002	SAH	C5-N7-C8	4.47	110.47	103.45
2	B	3002	SAH	C5-C4-N3	-3.97	121.26	126.72
2	A	3001	SAH	N9-C8-N7	-3.93	108.36	113.94
2	B	3002	SAH	C4-C5-N7	-3.80	106.24	110.58
2	A	3001	SAH	C4'-O4'-C1'	-3.39	101.97	109.47
2	B	3002	SAH	C4-N9-C8	3.31	109.21	105.74
2	A	3001	SAH	N3-C4-N9	3.24	132.68	127.17
2	B	3002	SAH	CB-CA-N	3.16	118.36	110.12
2	A	3001	SAH	O4'-C4'-C5'	-3.07	100.92	108.83
2	B	3002	SAH	C6-C5-C4	2.99	121.26	117.18
2	A	3001	SAH	C5-N7-C8	2.66	107.63	103.45
2	B	3002	SAH	C2-N3-C4	2.56	118.09	111.83
2	A	3001	SAH	C5-C4-N9	2.43	108.46	105.81
2	A	3001	SAH	C5-C6-N6	-2.42	117.29	123.29
2	B	3002	SAH	C4'-C5'-SD	2.38	122.27	113.78
2	B	3002	SAH	N3-C4-N9	2.27	131.03	127.17
2	B	3002	SAH	C3'-C2'-C1'	2.27	105.75	101.46
2	B	3002	SAH	C2-N1-C6	2.22	122.38	118.73
2	B	3002	SAH	O3'-C3'-C4'	-2.16	104.88	111.08
2	A	3001	SAH	C5-C6-N1	2.13	122.92	117.51
2	A	3001	SAH	O2'-C2'-C3'	2.07	118.44	111.82
2	A	3001	SAH	C4-C5-N7	-2.03	108.26	110.58

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2001	LNR	CAG-CAK-CAL-CAH
3	A	2001	LNR	CAF-CAK-CAL-CAH
3	B	2002	LNR	CAG-CAK-CAL-CAH
3	A	2001	LNR	NAA-CAH-CAL-OAD
3	B	2002	LNR	CAF-CAK-CAL-CAH
2	A	3001	SAH	O-C-CA-CB
2	B	3002	SAH	C2'-C1'-N9-C8
2	B	3002	SAH	O-C-CA-CB
2	A	3001	SAH	C2'-C1'-N9-C8
2	B	3002	SAH	CB-CG-SD-C5'
3	A	2001	LNR	CAF-CAK-CAL-OAD

Continued on next page...

Continued from previous page...

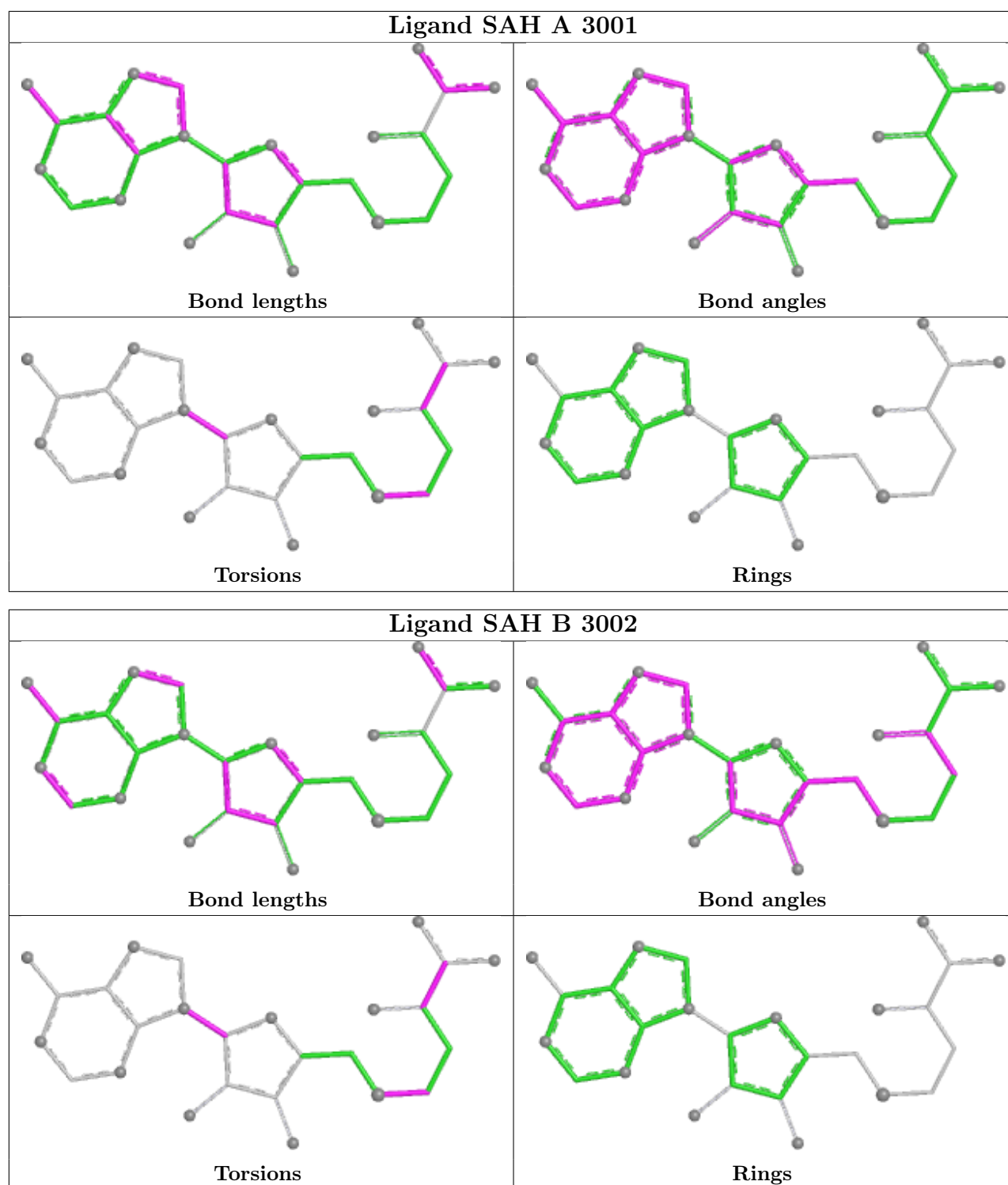
Mol	Chain	Res	Type	Atoms
3	B	2002	LNR	CAG-CAK-CAL-OAD
3	B	2002	LNR	CAF-CAK-CAL-OAD
2	A	3001	SAH	C2'-C1'-N9-C4
3	A	2001	LNR	CAG-CAK-CAL-OAD
2	A	3001	SAH	CB-CG-SD-C5'
2	B	3002	SAH	C2'-C1'-N9-C4
2	B	3002	SAH	O4'-C1'-N9-C8
2	A	3001	SAH	O4'-C1'-N9-C8

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3001	SAH	2	0
2	B	3002	SAH	2	0
3	A	2001	LNR	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 ⓘ

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	257/289 (88%)	2.85	206 (80%) 0 0	33, 51, 82, 113	4 (1%)
1	B	268/289 (92%)	2.22	146 (54%) 0 0	22, 46, 71, 112	6 (2%)
All	All	525/578 (90%)	2.53	352 (67%) 0 0	22, 48, 78, 113	10 (1%)

All (352) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	24	ALA	7.9
1	B	281	GLY	7.6
1	A	280	VAL	6.5
1	A	184	LEU	6.3
1	A	177	ALA	5.9
1	A	167	ALA	5.5
1	A	45	GLY	5.3
1	A	88	LEU	5.3
1	B	227	ALA	5.1
1	A	181	ALA	5.0
1	A	189	PRO	4.9
1	A	192	ALA	4.8
1	A	274	PHE	4.8
1	A	172	PRO	4.8
1	A	68	GLY	4.7
1	A	170	PRO	4.7
1	A	110	LEU	4.7
1	A	126	TYR	4.7
1	A	108	GLN	4.6
1	A	58	LEU	4.6
1	A	147	LEU	4.6
1	A	157	ILE	4.6
1	A	40	TYR	4.5
1	A	133	ILE	4.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	14	PRO	4.4
1	A	204	LEU	4.4
1	A	103	LEU	4.4
1	B	94	PHE	4.4
1	A	81	GLY	4.3
1	A	171	ALA	4.3
1	B	46	ASP	4.3
1	A	90	ALA	4.3
1	B	260	ALA	4.2
1	A	105	VAL	4.2
1	B	95	GLU	4.2
1	B	261	HIS	4.2
1	A	111	GLY	4.2
1	A	26	ALA	4.2
1	B	137	GLY	4.1
1	A	106	ASN	4.1
1	B	170	PRO	4.1
1	A	28	GLN	4.1
1	A	78	ILE	4.1
1	A	212	LEU	4.0
1	B	37	ARG	4.0
1	B	122	ASN	4.0
1	B	123	TRP	4.0
1	A	136	LYS	4.0
1	A	249	LYS	4.0
1	A	248	TYR	4.0
1	A	162	PRO	4.0
1	A	83	THR	4.0
1	A	100	THR	4.0
1	A	54	GLY	4.0
1	A	61	LEU	3.9
1	B	45	GLY	3.9
1	B	257	ILE	3.9
1	A	259	PRO	3.9
1	B	108	GLN	3.9
1	A	173	LEU	3.9
1	B	167	ALA	3.9
1	B	269	VAL	3.8
1	B	280	VAL	3.8
1	A	65	PHE	3.8
1	B	263	GLN	3.8
1	A	46	ASP	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	43	PRO	3.8
1	A	76	ILE	3.8
1	A	214	ILE	3.8
1	A	211	LEU	3.8
1	A	265	GLY	3.8
1	A	82	PRO	3.7
1	B	262	LEU	3.7
1	A	102	PHE	3.7
1	A	75	LEU	3.7
1	A	187	VAL	3.7
1	A	70	VAL	3.7
1	A	275	ALA	3.7
1	A	97	ILE	3.6
1	B	256	TYR	3.6
1	A	254	ARG	3.6
1	B	230	THR	3.6
1	A	80	SER	3.6
1	A	213	LEU	3.6
1	B	229	LEU	3.6
1	A	91	CYS	3.6
1	A	101	ASP	3.6
1	A	179	VAL	3.6
1	A	207	PRO	3.6
1	A	67	THR	3.6
1	B	73	ARG	3.5
1	A	35	TYR	3.5
1	A	98	THR	3.5
1	A	154	VAL	3.5
1	B	243	LEU	3.5
1	A	121	PHE	3.5
1	B	66	ALA	3.5
1	A	276	TRP	3.5
1	B	237	GLU	3.5
1	B	92	SER	3.4
1	A	36	LEU	3.4
1	A	155	LEU	3.4
1	B	29	ARG	3.4
1	A	264	THR	3.4
1	B	210	HIS	3.4
1	A	239	VAL	3.4
1	B	216	ALA	3.4
1	B	131	CYS	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	201	ILE	3.4
1	A	99	MET	3.4
1	A	79	GLY	3.4
1	B	177	ALA	3.3
1	A	245	ARG	3.3
1	A	202	THR	3.3
1	A	161	GLN	3.3
1	A	227	ALA	3.3
1	B	226	GLU	3.3
1	B	140	TRP	3.3
1	B	174	PRO	3.2
1	A	261	HIS	3.2
1	A	273	PHE	3.2
1	B	154	VAL	3.2
1	B	119	GLY	3.2
1	B	254	ARG	3.2
1	A	205	LEU	3.2
1	A	50	PRO	3.2
1	A	206	ARG	3.2
1	A	119	GLY	3.2
1	B	135	GLY	3.2
1	A	210	HIS	3.2
1	B	110	LEU	3.2
1	B	223	LEU	3.2
1	B	30	PHE	3.2
1	B	59	ARG	3.2
1	A	176	ASP	3.2
1	B	124	SER	3.1
1	A	168	GLY	3.1
1	A	253	LEU	3.1
1	B	203	THR	3.1
1	B	255	THR	3.1
1	B	111	GLY	3.1
1	B	168	GLY	3.1
1	B	208	GLY	3.1
1	A	53	VAL	3.1
1	A	266	VAL	3.1
1	A	27	TYR	3.1
1	B	279	LYS	3.1
1	A	190	ASP	3.1
1	B	19	GLY	3.1
1	A	277	ALA	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	239	VAL	3.1
1	B	70	VAL	3.1
1	B	118	PRO	3.1
1	A	200	HIS	3.0
1	A	71	SER	3.0
1	B	125	MET	3.0
1	B	181	ALA	3.0
1	B	277	ALA	3.0
1	A	84	VAL	3.0
1	A	262	LEU	3.0
1	B	133	ILE	3.0
1	B	15	ASP	3.0
1	A	94	PHE	2.9
1	A	223	LEU	2.9
1	A	278	GLN	2.9
1	B	72	GLY	2.9
1	A	229	LEU	2.9
1	A	85	TYR	2.9
1	B	93	HIS	2.9
1	A	197	ALA	2.9
1	A	175	ALA	2.9
1	A	243	LEU	2.9
1	B	121	PHE	2.9
1	B	173	LEU	2.9
1	A	164	PRO	2.8
1	B	244	VAL	2.8
1	B	264	THR	2.8
1	A	188	SER	2.8
1	A	118	PRO	2.8
1	B	35	TYR	2.8
1	A	29	ARG	2.8
1	B	139	CYS	2.8
1	A	166	GLY	2.8
1	B	241	GLU	2.8
1	B	149	ALA	2.8
1	B	151	VAL	2.8
1	A	252	ASP	2.8
1	A	72	GLY	2.8
1	B	16	SER	2.8
1	B	91	CYS	2.8
1	B	147	LEU	2.8
1	A	66	ALA	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	242	ALA	2.8
1	A	215	GLY	2.7
1	B	188	SER	2.7
1	B	221	TRP	2.7
1	A	131	CYS	2.7
1	A	178	LEU	2.7
1	B	232	VAL	2.7
1	A	158	ASP	2.7
1	B	97	ILE	2.7
1	A	180	SER	2.7
1	B	71	SER	2.7
1	A	153	ARG	2.7
1	A	149	ALA	2.7
1	A	272	VAL	2.7
1	B	209	GLY	2.7
1	A	125	MET	2.7
1	A	196	ARG	2.7
1	B	184	LEU	2.7
1	A	30	PHE	2.7
1	A	238	GLU	2.7
1	B	202	THR	2.7
1	B	207	PRO	2.7
1	A	33	ARG	2.7
1	B	212	LEU	2.7
1	A	62	ALA	2.6
1	A	146	GLN	2.6
1	A	57	LYS	2.6
1	B	27	TYR	2.6
1	A	77	ASP	2.6
1	A	64	THR	2.6
1	A	169	SER	2.6
1	A	87	LEU	2.6
1	B	129	HIS	2.6
1	B	204	LEU	2.6
1	A	56	TRP	2.6
1	A	128	GLN	2.6
1	A	194	PHE	2.6
1	A	59	ARG	2.6
1	A	25	SER	2.6
1	B	63	GLN	2.6
1	A	104	GLU	2.6
1	A	113	TRP	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	144	GLU	2.6
1	B	113	TRP	2.6
1	B	65	PHE	2.6
1	B	231	VAL	2.6
1	B	233	PRO	2.6
1	A	112	ARG	2.6
1	B	34	ALA	2.6
1	A	156	PRO	2.5
1	B	50	PRO	2.5
1	A	244	VAL	2.5
1	B	85	TYR	2.5
1	A	132	LEU	2.5
1	A	120	ALA	2.5
1	A	55	PRO	2.5
1	B	274	PHE	2.5
1	B	84	VAL	2.5
1	B	128[A]	GLN	2.5
1	A	228	ARG	2.5
1	B	40	TYR	2.5
1	B	206	ARG	2.5
1	A	114	LEU	2.5
1	A	143	LYS	2.5
1	A	174	PRO	2.5
1	B	143	LYS	2.5
1	A	145	ARG	2.4
1	B	228	ARG	2.4
1	A	199	ASP	2.4
1	A	195	GLN	2.4
1	A	107	ARG	2.4
1	A	130	ALA	2.4
1	B	259	PRO	2.4
1	B	48	CYS	2.4
1	A	159	VAL	2.4
1	A	86	GLN	2.4
1	A	148	ARG	2.4
1	B	138	GLU	2.4
1	A	186	ALA	2.4
1	A	208	GLY	2.4
1	B	246	SER	2.4
1	B	136	LYS	2.4
1	A	250	VAL	2.4
1	B	58	LEU	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	276	TRP	2.4
1	A	251	ARG	2.4
1	B	49	ASN	2.4
1	B	90	ALA	2.4
1	B	120	ALA	2.4
1	B	258	MET	2.4
1	B	253	LEU	2.4
1	A	134	GLU	2.4
1	A	216	ALA	2.3
1	A	231	VAL	2.3
1	B	214	ILE	2.3
1	A	198	LEU	2.3
1	A	49	ASN	2.3
1	A	256	TYR	2.3
1	A	209	GLY	2.3
1	A	260	ALA	2.3
1	A	255	THR	2.3
1	A	165	LEU	2.3
1	B	42	PRO	2.3
1	A	123	TRP	2.3
1	B	56	TRP	2.3
1	B	17	ALA	2.3
1	B	112	ARG	2.3
1	A	183	CYS	2.3
1	B	225	GLY	2.2
1	A	31	GLU	2.2
1	A	129	HIS	2.2
1	A	203	THR	2.2
1	B	74	THR	2.2
1	B	155	LEU	2.2
1	B	153	ARG	2.2
1	A	135	GLY	2.2
1	B	166	GLY	2.2
1	A	257	ILE	2.2
1	A	51	ASN	2.2
1	B	39	ASN	2.2
1	A	160	HIS	2.2
1	A	237	GLU	2.2
1	A	150	ARG	2.2
1	B	87	LEU	2.2
1	B	51	ASN	2.2
1	A	241	GLU	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	63	GLN	2.2
1	A	242	ALA	2.2
1	B	62	ALA	2.2
1	B	150	ARG	2.1
1	B	36	LEU	2.1
1	B	23	VAL	2.1
1	A	233	PRO	2.1
1	A	141	GLN	2.1
1	A	60	CYS	2.1
1	A	89	SER	2.1
1	B	175	ALA	2.1
1	A	191	LEU	2.1
1	A	142	ASP	2.1
1	B	134	GLU	2.1
1	B	187	VAL	2.1
1	A	124	SER	2.1
1	A	230	THR	2.1
1	B	89	SER	2.1
1	A	69	GLU	2.1
1	B	31	GLU	2.1
1	A	74	THR	2.1
1	A	246	SER	2.1
1	A	224	ALA	2.1
1	A	182	PHE	2.1
1	B	79	GLY	2.1
1	A	140	TRP	2.1
1	B	132	LEU	2.0
1	B	102	PHE	2.0
1	B	249	LYS	2.0
1	A	95	GLU	2.0
1	A	226	GLU	2.0
1	B	98	THR	2.0
1	B	75	LEU	2.0
1	B	178	LEU	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

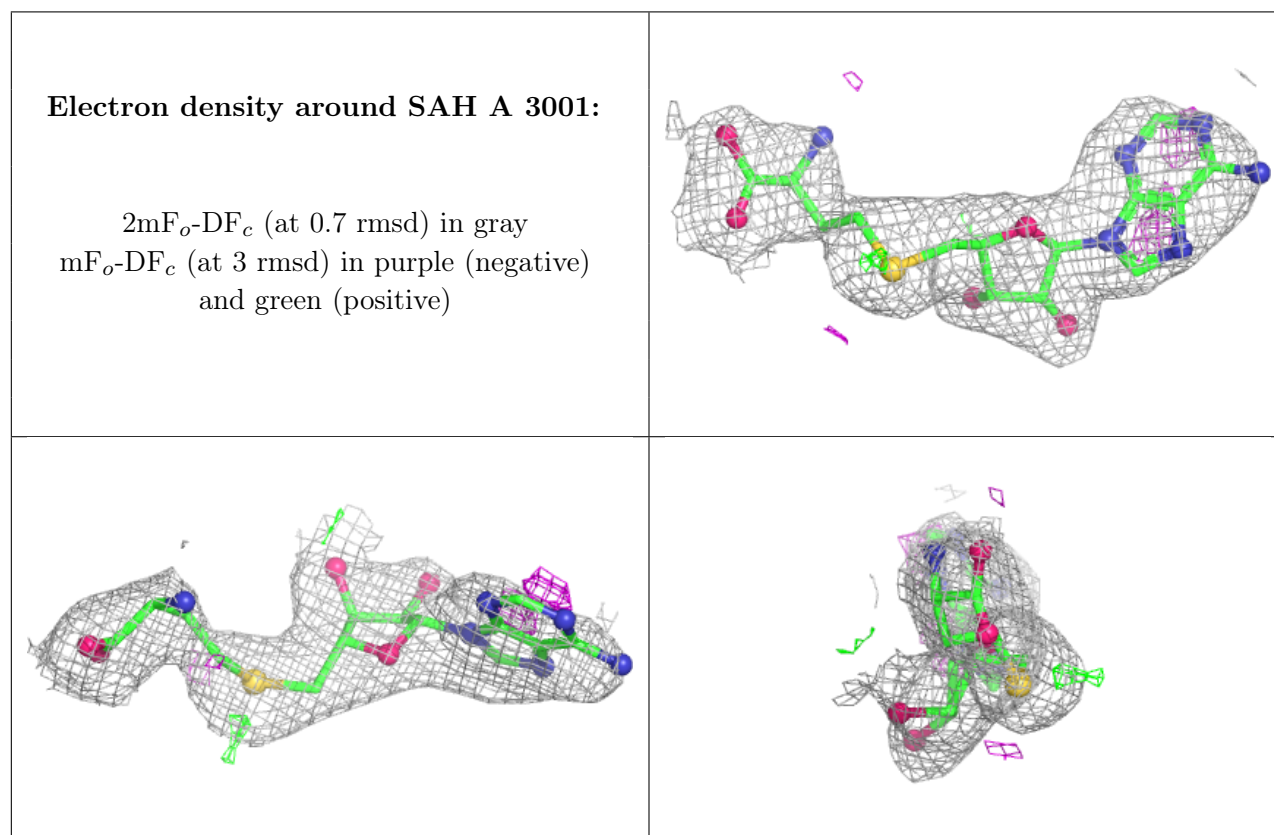
There are no oligosaccharides in this entry.

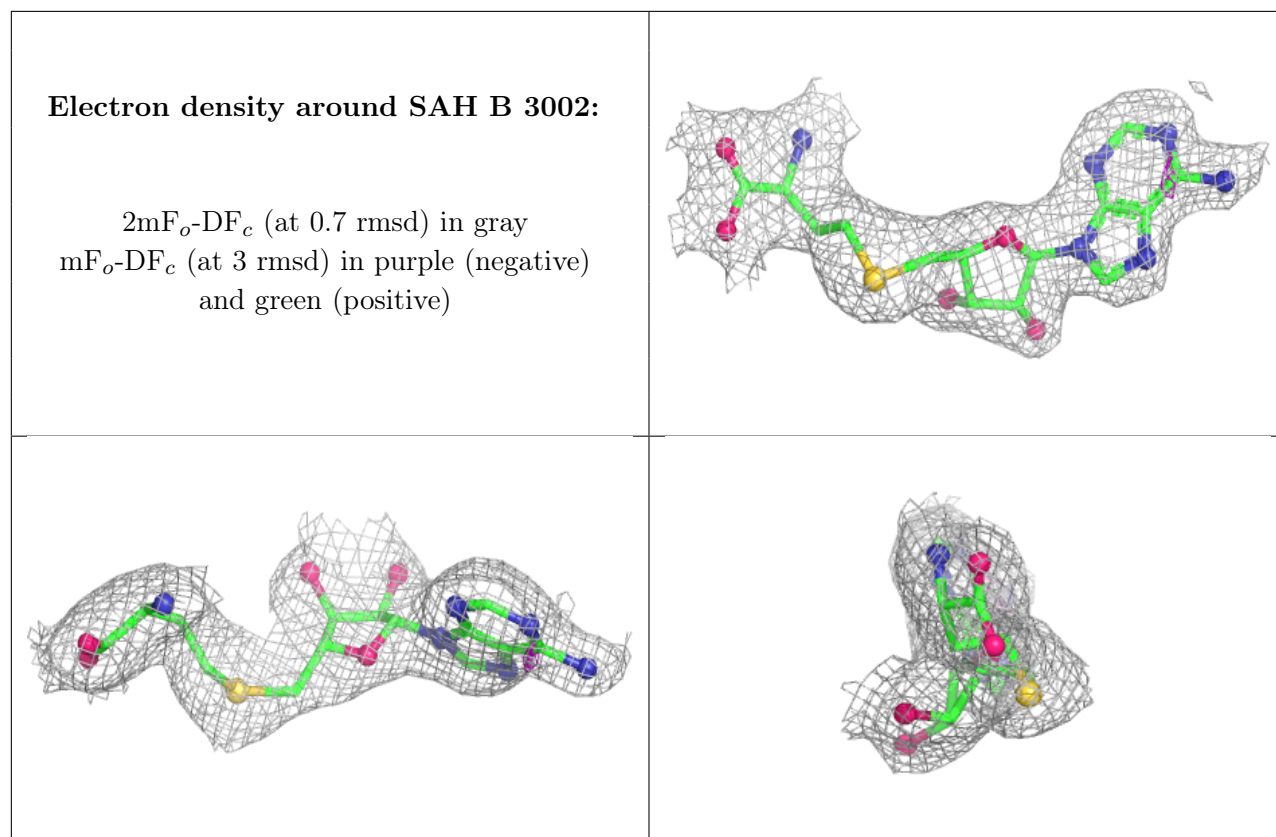
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	LNR	A	2001	12/12	0.61	0.24	46,49,53,54	0
3	LNR	B	2002	12/12	0.62	0.24	48,52,53,54	0
2	SAH	A	3001	26/26	0.83	0.16	41,54,59,62	0
2	SAH	B	3002	26/26	0.91	0.11	30,40,47,47	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.