



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 07:41 PM UTC

PDB ID : 3LBF / pdb_00003lbf
Title : Crystal structure of Protein L-isoaspartyl methyltransferase from Escherichia coli
Authors : Fang, P.; Li, X.; Wang, J.; Niu, L.; Teng, M.
Deposited on : 2010-01-08
Resolution : 1.80 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

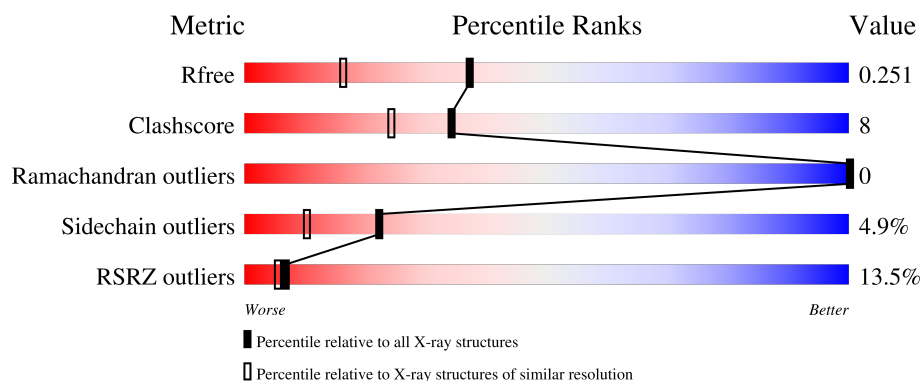
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	210	5% 82% 16% ..
1	B	210	10% 80% 17% ..
1	C	210	6% 87% 10% ..
1	D	210	31% 78% 14% 7%

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
3	PO4	C	209	-	-	X	-
4	GOL	A	212	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6657 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.

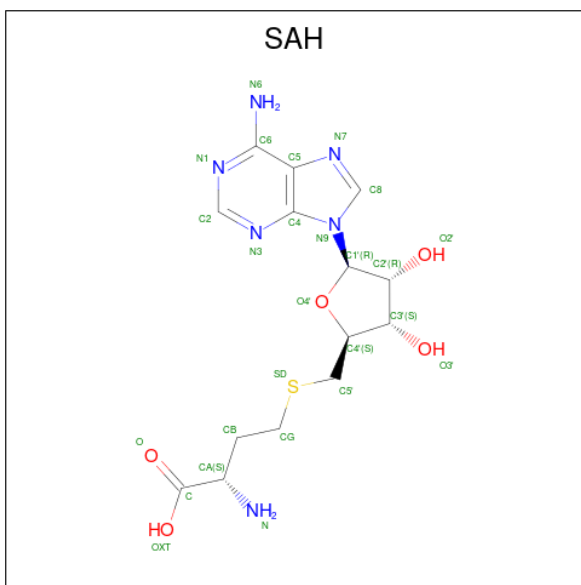
- Molecule 1 is a protein called Protein-L-isoaspartate O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	2	0
			1594	1014	288	288	4			
1	B	207	Total	C	N	O	S	0	4	0
			1579	1008	279	288	4			
1	C	207	Total	C	N	O	S	0	1	0
			1577	1001	283	289	4			
1	D	196	Total	C	N	O	S	0	1	0
			1407	898	243	262	4			

There are 8 discrepancies between the modelled and reference sequences:

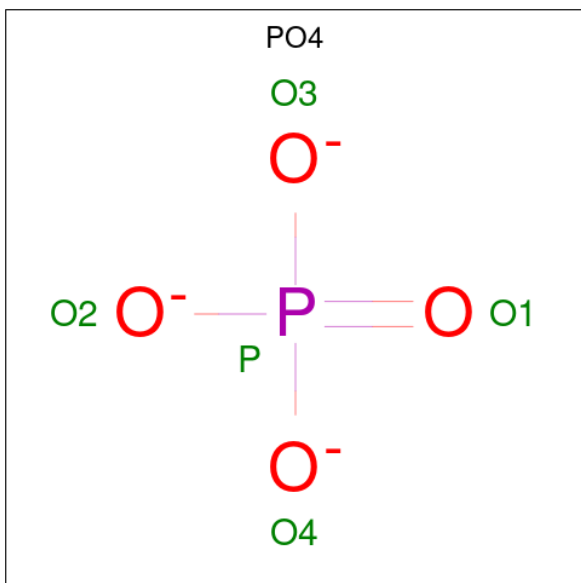
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP P0A7A5
A	0	LEU	-	expression tag	UNP P0A7A5
B	-1	SER	-	expression tag	UNP P0A7A5
B	0	LEU	-	expression tag	UNP P0A7A5
C	-1	SER	-	expression tag	UNP P0A7A5
C	0	LEU	-	expression tag	UNP P0A7A5
D	-1	SER	-	expression tag	UNP P0A7A5
D	0	LEU	-	expression tag	UNP P0A7A5

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



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

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	115	Total O 115 115	0	0
5	B	110	Total O 110 110	0	0
5	C	87	Total O 87 87	0	0

Continued on next page...

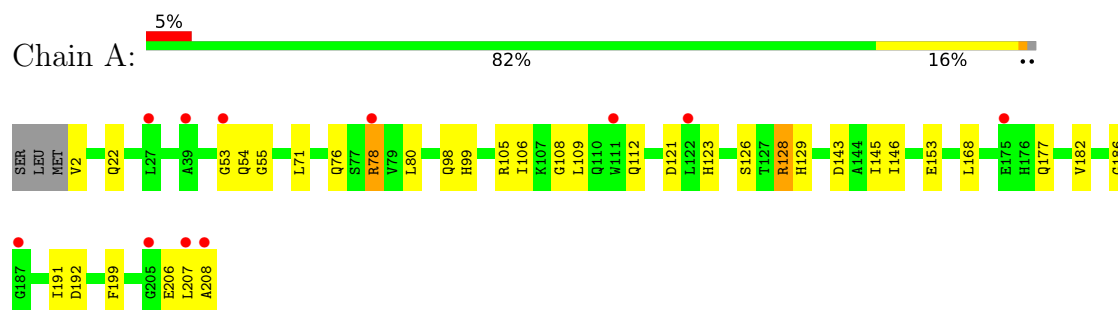
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	48	Total	O	0	0
			48	48		

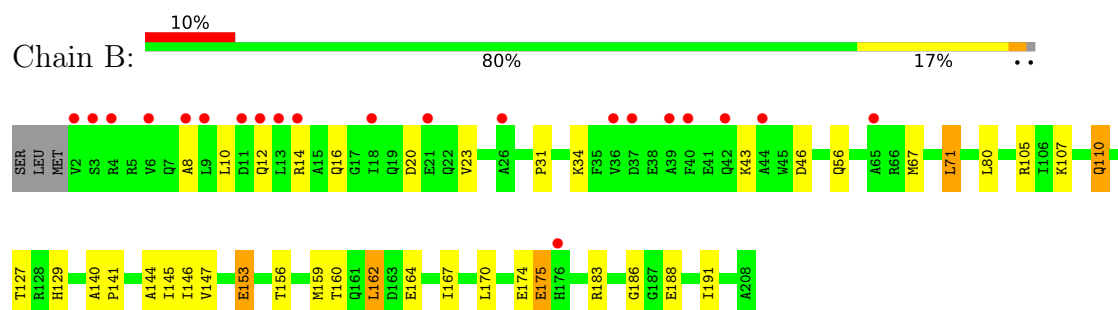
3 Residue-property plots

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.

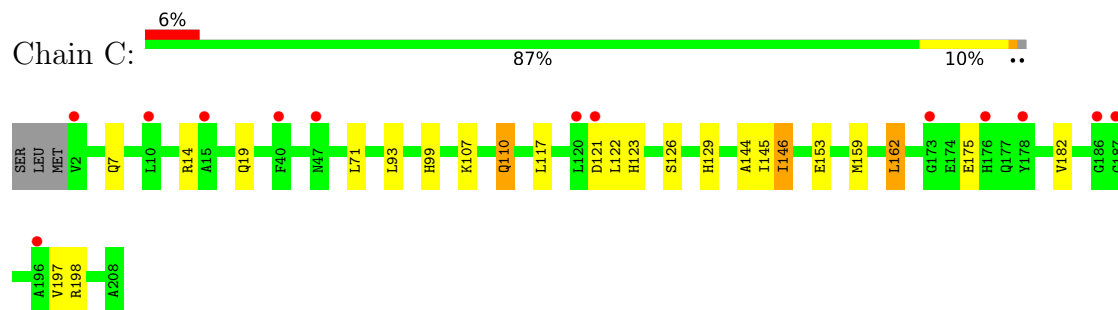
- Molecule 1: Protein-L-isoaspartate O-methyltransferase



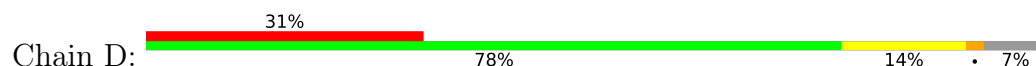
- Molecule 1: Protein-L-isoaspartate O-methyltransferase

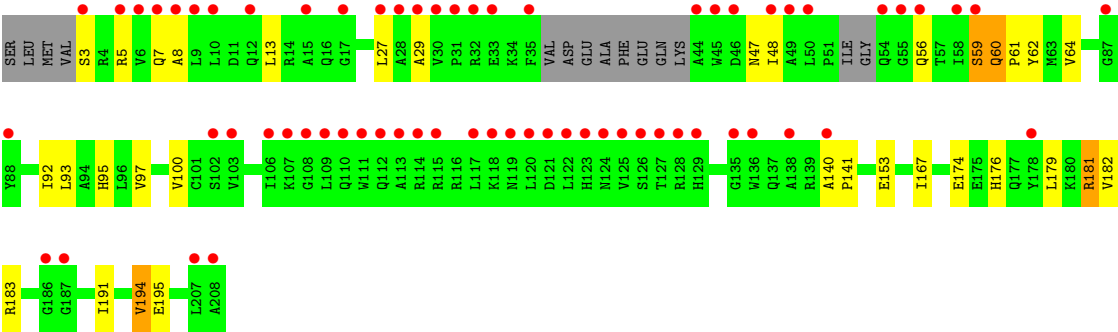


- Molecule 1: Protein-L-isoaspartate O-methyltransferase



- Molecule 1: Protein-L-isoaspartate O-methyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	52.30Å 55.06Å 67.49Å 74.00° 74.70° 85.57°	Depositor
Resolution (Å)	25.00 – 1.80 25.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.2 (25.00-1.80) 96.2 (25.00-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.42 (at 1.80Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.213 , 0.247 0.218 , 0.251	Depositor DCC
R_{free} test set	3156 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6657	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.26% 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, GOL, PO4

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	0.63	1/1630 (0.1%)	0.90	5/2217 (0.2%)
1	B	0.59	0/1621	0.80	0/2206
1	C	0.55	0/1609	0.81	0/2191
1	D	0.74	2/1434 (0.1%)	0.90	3/1956 (0.2%)
All	All	0.63	3/6294 (0.0%)	0.85	8/8570 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	7	GLN	C-O	-5.16	1.18	1.24
1	A	53	GLY	C-O	-5.12	1.17	1.23
1	D	176	HIS	C-O	-5.03	1.18	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	GLY	N-CA-C	9.91	124.62	112.73
1	A	53	GLY	CA-C-N	-7.35	113.18	123.03
1	A	53	GLY	C-N-CA	-7.35	113.18	123.03
1	D	3	SER	CA-C-N	-5.79	114.58	123.04
1	D	3	SER	C-N-CA	-5.79	114.58	123.04
1	A	54	GLN	N-CA-C	5.53	117.61	108.49
1	A	55	GLY	N-CA-C	-5.34	108.26	115.36
1	D	195	GLU	N-CA-C	5.20	116.09	107.73

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	1594	0	1592	23	0
1	B	1579	0	1560	31	0
1	C	1577	0	1554	23	0
1	D	1407	0	1301	17	0
2	A	26	0	19	1	0
2	B	26	0	19	1	0
2	C	26	0	19	0	0
2	D	26	0	20	2	0
3	A	15	0	0	1	0
3	B	10	0	0	0	1
3	C	5	0	0	1	1
4	A	6	0	8	5	0
5	A	115	0	0	3	0
5	B	110	0	0	1	0
5	C	87	0	0	4	0
5	D	48	0	0	0	0
All	All	6657	0	6092	94	1

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 (94) 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:D:300:SAH:OXT	2:D:300:SAH:C	1.68	1.38
1:B:174:GLU:CB	1:B:175:GLU:OE2	1.95	1.14
1:B:174:GLU:HB2	1:B:175:GLU:OE2	1.44	1.12
1:A:78[A]:ARG:HD3	1:A:143:ASP:OD2	1.63	0.98
1:C:71:LEU:HD11	1:C:146[A]:ILE:HG12	1.44	0.98
1:C:121:ASP:HB3	5:C:424:HOH:O	1.64	0.96
1:B:67:MET:HE2	1:B:146[B]:ILE:HD11	1.49	0.95
1:B:175:GLU:H	1:B:175:GLU:CD	1.75	0.93
1:A:153:GLU:HG3	4:A:212:GOL:O3	1.71	0.89
1:A:128:ARG:HG3	1:A:128:ARG:HH11	1.38	0.86
1:A:177:GLN:HE22	1:A:199:PHE:H	1.24	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:GLU:HB3	1:B:175:GLU:OE2	1.75	0.85
1:C:93:LEU:HD11	1:C:146[A]:ILE:CD1	2.13	0.79
2:A:300:SAH:SD	5:A:273:HOH:O	2.41	0.79
1:B:67:MET:HE2	1:B:146[B]:ILE:CD1	2.18	0.74
1:A:129:HIS:HD2	3:A:209:PO4:O1	1.71	0.73
1:C:93:LEU:HD11	1:C:146[A]:ILE:HD13	1.72	0.72
1:B:175:GLU:OE2	1:B:175:GLU:N	2.25	0.69
1:C:107:LYS:NZ	1:C:110:GLN:HE22	1.89	0.69
1:B:71:LEU:HG	1:B:144:ALA:HB1	1.73	0.69
1:A:177:GLN:NE2	1:A:199:PHE:H	1.92	0.67
1:B:8:ALA:O	1:B:12:GLN:HG3	1.97	0.64
1:A:153:GLU:OE1	4:A:212:GOL:H31	1.98	0.64
1:B:175:GLU:CD	1:B:175:GLU:N	2.54	0.64
1:A:128:ARG:HG3	1:A:128:ARG:NH1	2.13	0.61
4:A:212:GOL:C3	1:B:156:THR:H	2.12	0.61
1:D:47:ASN:HD21	1:D:62:TYR:H	1.46	0.61
1:B:164:GLU:CD	1:B:186:GLY:H	2.09	0.59
1:C:19:GLN:HG3	5:C:421:HOH:O	2.02	0.59
1:C:123:HIS:NE2	5:C:424:HOH:O	2.31	0.58
1:A:106:ILE:HG12	1:A:208:ALA:HB3	1.86	0.58
1:C:129:HIS:HD2	3:C:209:PO4:O1	1.87	0.57
1:D:29:ALA:HB1	1:D:95:HIS:CE1	2.40	0.57
1:A:153:GLU:OE1	4:A:212:GOL:C3	2.51	0.57
1:A:192:ASP:OD2	1:B:188:GLU:HG2	2.04	0.57
1:B:167:ILE:HG12	1:B:183[B]:ARG:HG2	1.87	0.57
1:A:105:ARG:O	1:A:129:HIS:HE1	1.88	0.57
1:B:107:LYS:NZ	1:B:110:GLN:HE22	2.04	0.56
1:C:71:LEU:CD1	1:C:146[A]:ILE:HG12	2.29	0.55
1:D:47:ASN:HD22	1:D:61:PRO:HD2	1.71	0.55
1:C:93:LEU:CD1	1:C:146[A]:ILE:HD11	2.37	0.54
1:B:145:ILE:HD12	1:B:162:LEU:HD13	1.88	0.54
1:C:107:LYS:HZ1	1:C:110:GLN:HE22	1.55	0.54
1:D:140:ALA:HB1	1:D:141:PRO:HA	1.88	0.54
1:A:105:ARG:NH1	1:A:206:GLU:O	2.39	0.53
1:B:156:THR:O	1:B:160:THR:HG23	2.08	0.53
1:A:99:HIS:HE1	1:A:126:SER:OG	1.92	0.52
1:C:71:LEU:HD22	1:C:144:ALA:HB1	1.92	0.51
1:C:93:LEU:CD1	1:C:146[A]:ILE:CD1	2.88	0.51
1:C:175:GLU:H	1:C:175:GLU:CD	2.18	0.51
1:D:179:LEU:HD23	1:D:194:VAL:CG2	2.40	0.51
1:C:197:VAL:O	1:C:198:ARG:HD2	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:VAL:HB	1:B:170:LEU:HB2	1.93	0.50
1:D:5:ARG:O	1:D:8:ALA:HB3	2.12	0.50
1:D:179:LEU:HD23	1:D:194:VAL:HG21	1.92	0.50
1:D:167:ILE:HG23	1:D:181:ARG:HD2	1.93	0.50
2:D:300:SAH:C	2:D:300:SAH:HXT	2.12	0.49
4:A:212:GOL:H32	1:B:156:THR:H	1.77	0.48
1:A:105:ARG:O	1:A:129:HIS:CE1	2.66	0.47
1:D:56:GLN:N	1:D:56:GLN:CD	2.72	0.47
1:C:153:GLU:HG3	1:D:153:GLU:HB2	1.96	0.46
1:B:20:ASP:HB3	1:B:23:VAL:HB	1.97	0.46
1:C:99:HIS:HE1	1:C:126:SER:OG	1.99	0.46
1:B:56:GLN:HE21	2:B:300:SAH:H3'	1.81	0.45
1:B:153:GLU:HG2	5:B:255:HOH:O	2.15	0.45
1:A:191:ILE:HD11	1:B:191:ILE:HD11	1.98	0.45
1:B:14:ARG:C	1:B:16:GLN:N	2.74	0.45
1:B:164:GLU:OE1	1:B:186:GLY:N	2.49	0.45
1:D:167:ILE:CG2	1:D:181:ARG:HD2	2.46	0.45
1:A:22:GLN:HG2	5:A:299:HOH:O	2.17	0.45
1:B:31:PRO:HG2	1:B:34:LYS:HG3	1.99	0.45
1:D:93:LEU:O	1:D:97:VAL:HG22	2.16	0.45
1:C:107:LYS:HZ2	1:C:110:GLN:HE22	1.64	0.45
1:A:186:GLY:O	5:A:218:HOH:O	2.21	0.45
1:C:110:GLN:HG3	5:C:341:HOH:O	2.17	0.44
1:A:108:GLY:O	1:A:112:GLN:HG3	2.17	0.44
1:D:179:LEU:O	1:D:194:VAL:HG13	2.17	0.44
1:D:59[A]:SER:HB2	1:D:64:VAL:HG23	2.00	0.44
1:D:60:GLN:HE21	1:D:60:GLN:HB2	1.57	0.44
1:B:80:LEU:HB3	1:B:145:ILE:HG12	2.00	0.43
1:B:105:ARG:O	1:B:129:HIS:HE1	2.02	0.42
1:B:140:ALA:HB1	1:B:141:PRO:HA	2.00	0.42
1:C:99:HIS:CE1	1:C:126:SER:OG	2.72	0.42
1:A:121:ASP:OD1	1:A:123:HIS:HE1	2.03	0.42
1:D:27:LEU:HA	1:D:92:ILE:HD12	2.02	0.42
1:A:71:LEU:HD11	1:A:146:ILE:HB	2.02	0.42
1:C:159:MET:O	1:C:162:LEU:HB2	2.19	0.41
1:A:80:LEU:HB3	1:A:145:ILE:HG12	2.03	0.41
1:D:182:VAL:HG22	1:D:191:ILE:HG12	2.03	0.41
1:C:7:GLN:HE22	1:C:14:ARG:HH22	1.67	0.41
1:A:168:LEU:HB3	1:A:182:VAL:HB	2.03	0.40
1:B:159:MET:O	1:B:162:LEU:HB2	2.21	0.40
1:C:145:ILE:HD12	1:C:162:LEU:HD13	2.04	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:LYS:HA	1:B:46:ASP:OD1	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:209:PO4:O1	3:C:209:PO4:O3[1_556]	2.04	0.16

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	207/210 (99%)	198 (96%)	9 (4%)	0	100	100
1	B	209/210 (100%)	200 (96%)	9 (4%)	0	100	100
1	C	206/210 (98%)	198 (96%)	8 (4%)	0	100	100
1	D	191/210 (91%)	186 (97%)	5 (3%)	0	100	100
All	All	813/840 (97%)	782 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	161/174 (92%)	153 (95%)	8 (5%)	22	10
1	B	157/174 (90%)	150 (96%)	7 (4%)	24	12
1	C	157/174 (90%)	150 (96%)	7 (4%)	24	12
1	D	126/174 (72%)	116 (92%)	10 (8%)	11	3
All	All	601/696 (86%)	569 (95%)	32 (5%)	22	9

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	VAL
1	A	76	GLN
1	A	78[A]	ARG
1	A	78[B]	ARG
1	A	98	GLN
1	A	109	LEU
1	A	128	ARG
1	A	207	LEU
1	B	10	LEU
1	B	71	LEU
1	B	110	GLN
1	B	127	THR
1	B	153	GLU
1	B	162	LEU
1	B	175	GLU
1	C	110	GLN
1	C	117	LEU
1	C	122	LEU
1	C	146[A]	ILE
1	C	146[B]	ILE
1	C	162	LEU
1	C	182	VAL
1	D	13	LEU
1	D	48	ILE
1	D	59[A]	SER
1	D	59[B]	SER
1	D	60	GLN
1	D	100	VAL
1	D	174	GLU
1	D	181	ARG
1	D	183	ARG
1	D	194	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	98	GLN
1	A	99	HIS
1	A	110	GLN
1	A	119	ASN
1	A	123	HIS
1	A	129	HIS
1	A	177	GLN
1	B	7	GLN
1	B	56	GLN
1	B	89	GLN
1	B	99	HIS
1	B	110	GLN
1	B	112	GLN
1	B	119	ASN
1	B	129	HIS
1	B	134	GLN
1	C	7	GLN
1	C	12	GLN
1	C	56	GLN
1	C	89	GLN
1	C	99	HIS
1	C	110	GLN
1	C	119	ASN
1	C	129	HIS
1	C	134	GLN
1	D	47	ASN
1	D	56	GLN
1	D	60	GLN
1	D	95	HIS
1	D	129	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

11 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	SAH	D	300	-	27,28,28	2.67	5 (18%)	36,40,40	1.99	9 (25%)
2	SAH	A	300	-	27,28,28	1.39	6 (22%)	36,40,40	2.06	12 (33%)
3	PO4	A	211	-	4,4,4	0.91	0	6,6,6	0.68	0
3	PO4	A	210	-	4,4,4	0.92	0	6,6,6	0.31	0
3	PO4	A	209	-	4,4,4	0.88	0	6,6,6	0.21	0
3	PO4	C	209	-	4,4,4	1.07	0	6,6,6	0.51	0
3	PO4	B	210	-	4,4,4	0.85	0	6,6,6	0.79	0
2	SAH	B	300	-	27,28,28	1.33	3 (11%)	36,40,40	1.94	10 (27%)
3	PO4	B	209	-	4,4,4	1.09	0	6,6,6	0.78	0
4	GOL	A	212	-	5,5,5	0.60	0	5,5,5	0.80	0
2	SAH	C	300	-	27,28,28	1.42	4 (14%)	36,40,40	2.14	14 (38%)

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	SAH	D	300	-	-	3/15/31/31	0/3/3/3
2	SAH	A	300	-	-	1/15/31/31	0/3/3/3
2	SAH	B	300	-	-	2/15/31/31	0/3/3/3
4	GOL	A	212	-	-	3/4/4/4	-
2	SAH	C	300	-	-	2/15/31/31	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	300	SAH	OXT-C	11.89	1.68	1.30
2	D	300	SAH	C5-C4	4.52	1.47	1.39
2	A	300	SAH	C5-C4	3.98	1.46	1.39
2	C	300	SAH	C5-C4	3.88	1.46	1.39
2	B	300	SAH	C5-C4	3.85	1.46	1.39
2	C	300	SAH	C4-N9	-3.09	1.31	1.37
2	C	300	SAH	C8-N7	2.88	1.37	1.31
2	B	300	SAH	C4-N9	-2.76	1.32	1.37
2	C	300	SAH	C5-N7	-2.75	1.34	1.39
2	D	300	SAH	C5-C6	2.53	1.48	1.41
2	A	300	SAH	C5-C6	2.48	1.47	1.41
2	D	300	SAH	C5-N7	-2.38	1.34	1.39
2	A	300	SAH	OXT-C	-2.24	1.23	1.30
2	A	300	SAH	C4-N9	-2.22	1.33	1.37
2	A	300	SAH	C8-N7	2.21	1.35	1.31
2	B	300	SAH	OXT-C	-2.12	1.23	1.30
2	D	300	SAH	C8-N7	2.04	1.35	1.31
2	A	300	SAH	C5-N7	-2.01	1.35	1.39

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	300	SAH	C5-C4-N3	-5.74	118.81	126.72
2	A	300	SAH	C5-C4-N3	-5.50	119.14	126.72
2	D	300	SAH	N3-C4-N9	4.93	135.56	127.17
2	C	300	SAH	N3-C2-N1	-4.71	121.46	128.58
2	C	300	SAH	C5-C4-N3	-4.69	120.25	126.72
2	B	300	SAH	C5-C4-N3	-4.68	120.27	126.72
2	B	300	SAH	N3-C4-N9	4.44	134.71	127.17
2	B	300	SAH	C4-N9-C8	4.36	110.31	105.74
2	A	300	SAH	N3-C4-N9	4.19	134.29	127.17
2	C	300	SAH	N3-C4-N9	4.10	134.14	127.17
2	C	300	SAH	C4-N9-C8	4.08	110.02	105.74
2	A	300	SAH	C2-N3-C4	3.91	121.39	111.83
2	C	300	SAH	C2-N3-C4	3.74	120.97	111.83
2	A	300	SAH	N3-C2-N1	-3.69	122.99	128.58
2	D	300	SAH	C2-N3-C4	3.60	120.63	111.83
2	B	300	SAH	N3-C2-N1	-3.46	123.34	128.58
2	D	300	SAH	N3-C2-N1	-3.32	123.56	128.58
2	A	300	SAH	C4-C5-N7	-3.29	106.83	110.58
2	D	300	SAH	C4-C5-N7	-3.26	106.86	110.58
2	D	300	SAH	C4-N9-C8	3.25	109.15	105.74
2	B	300	SAH	C2-N3-C4	3.06	119.30	111.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	300	SAH	N9-C8-N7	-2.91	109.81	113.94
2	A	300	SAH	O4'-C1'-N9	2.85	113.56	108.09
2	A	300	SAH	C4-N9-C8	2.79	108.67	105.74
2	D	300	SAH	C5-N7-C8	2.74	107.75	103.45
2	B	300	SAH	N9-C8-N7	-2.69	110.12	113.94
2	C	300	SAH	C5'-SD-CG	-2.56	94.65	102.26
2	C	300	SAH	C2-N1-C6	2.54	122.91	118.73
2	D	300	SAH	OXT-C-O	-2.47	118.48	124.08
2	A	300	SAH	C5-N7-C8	2.41	107.25	103.45
2	D	300	SAH	N9-C8-N7	-2.35	110.61	113.94
2	A	300	SAH	OXT-C-O	-2.31	118.83	124.08
2	C	300	SAH	C4-N9-C1'	-2.31	121.24	126.63
2	C	300	SAH	CB-CA-C	-2.30	104.36	110.45
2	A	300	SAH	N9-C8-N7	-2.28	110.70	113.94
2	A	300	SAH	C6-C5-N7	2.28	136.48	132.09
2	B	300	SAH	C4-C5-N7	-2.24	108.02	110.58
2	C	300	SAH	C4-C5-N7	-2.16	108.11	110.58
2	B	300	SAH	C5'-SD-CG	-2.15	95.88	102.26
2	B	300	SAH	N6-C6-N1	2.15	123.16	118.38
2	C	300	SAH	N6-C6-N1	2.14	123.13	118.38
2	B	300	SAH	C5-C6-N6	-2.09	118.12	123.29
2	C	300	SAH	C6-C5-N7	2.05	136.04	132.09
2	A	300	SAH	C4'-C5'-SD	-2.03	106.54	113.78
2	C	300	SAH	C5-C6-N6	-2.02	118.28	123.29

There are no chirality outliers.

All (11) torsion outliers are listed below:

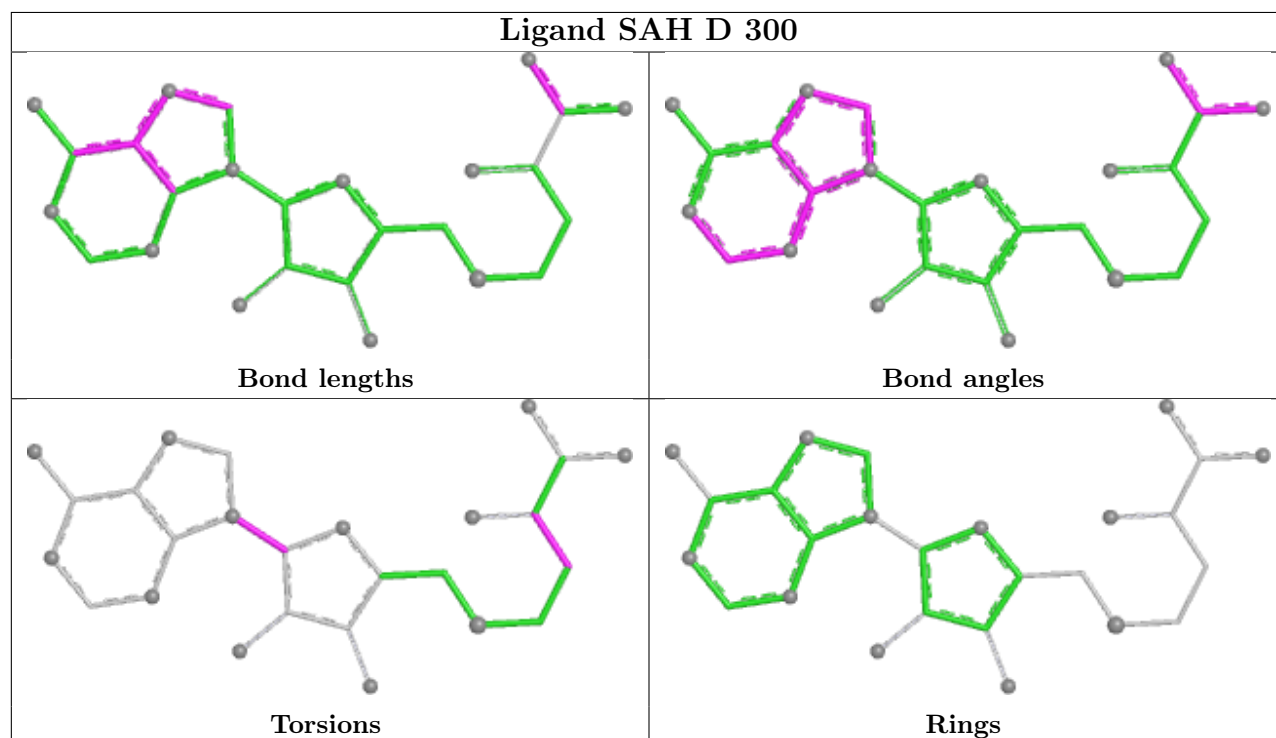
Mol	Chain	Res	Type	Atoms
2	D	300	SAH	N-CA-CB-CG
2	D	300	SAH	C-CA-CB-CG
2	C	300	SAH	CA-CB-CG-SD
4	A	212	GOL	O1-C1-C2-C3
4	A	212	GOL	C1-C2-C3-O3
4	A	212	GOL	O2-C2-C3-O3
2	A	300	SAH	CA-CB-CG-SD
2	B	300	SAH	C-CA-CB-CG
2	C	300	SAH	C2'-C1'-N9-C8
2	B	300	SAH	C2'-C1'-N9-C8
2	D	300	SAH	C2'-C1'-N9-C8

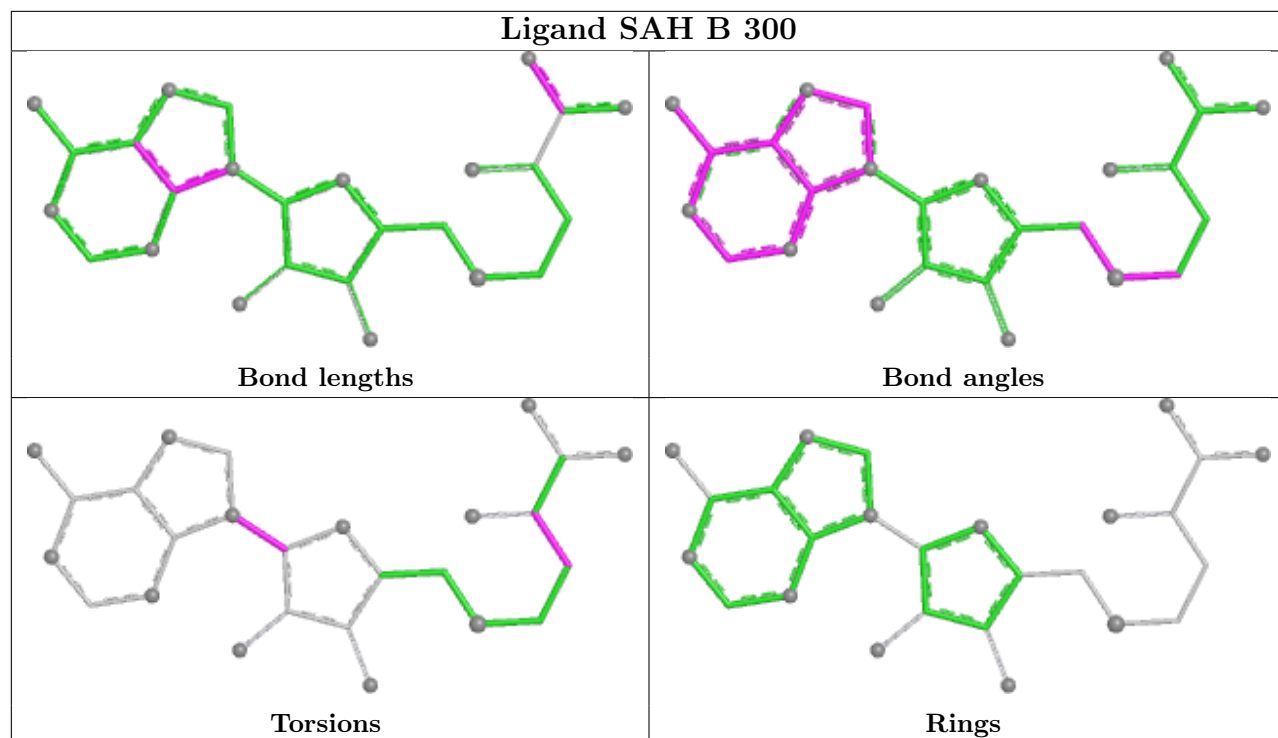
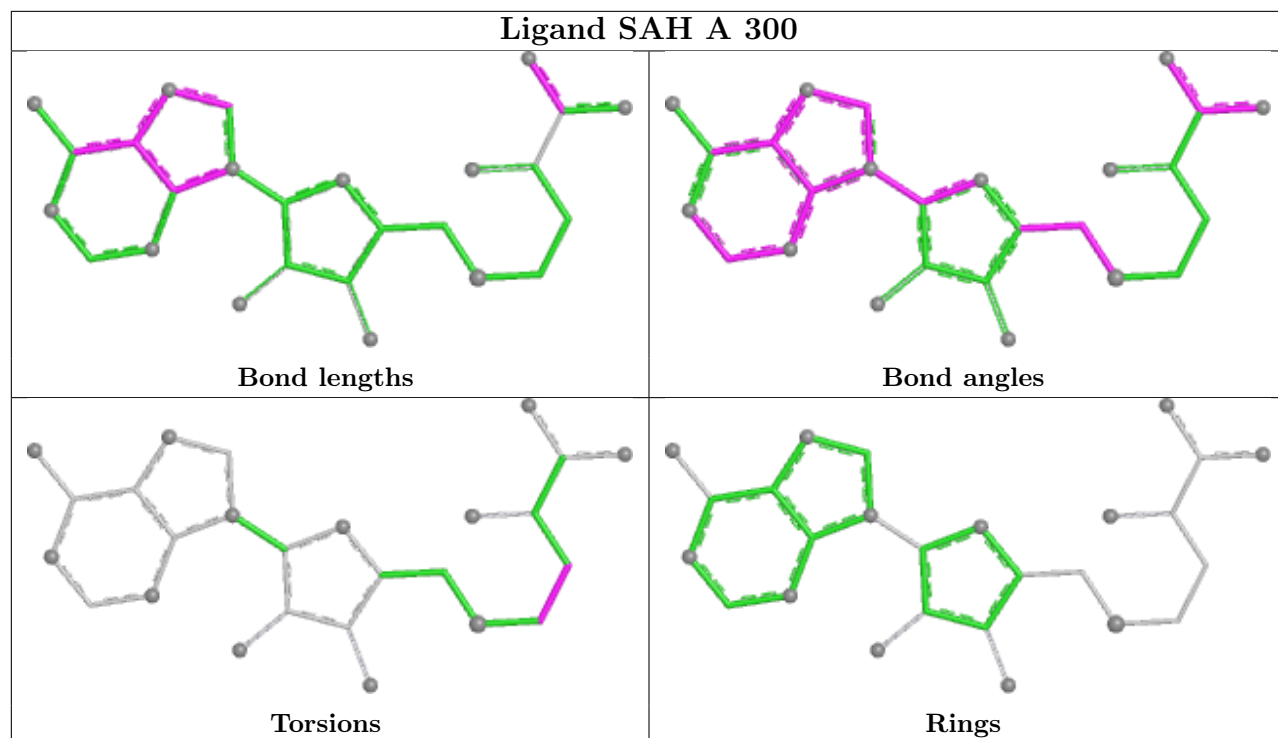
There are no ring outliers.

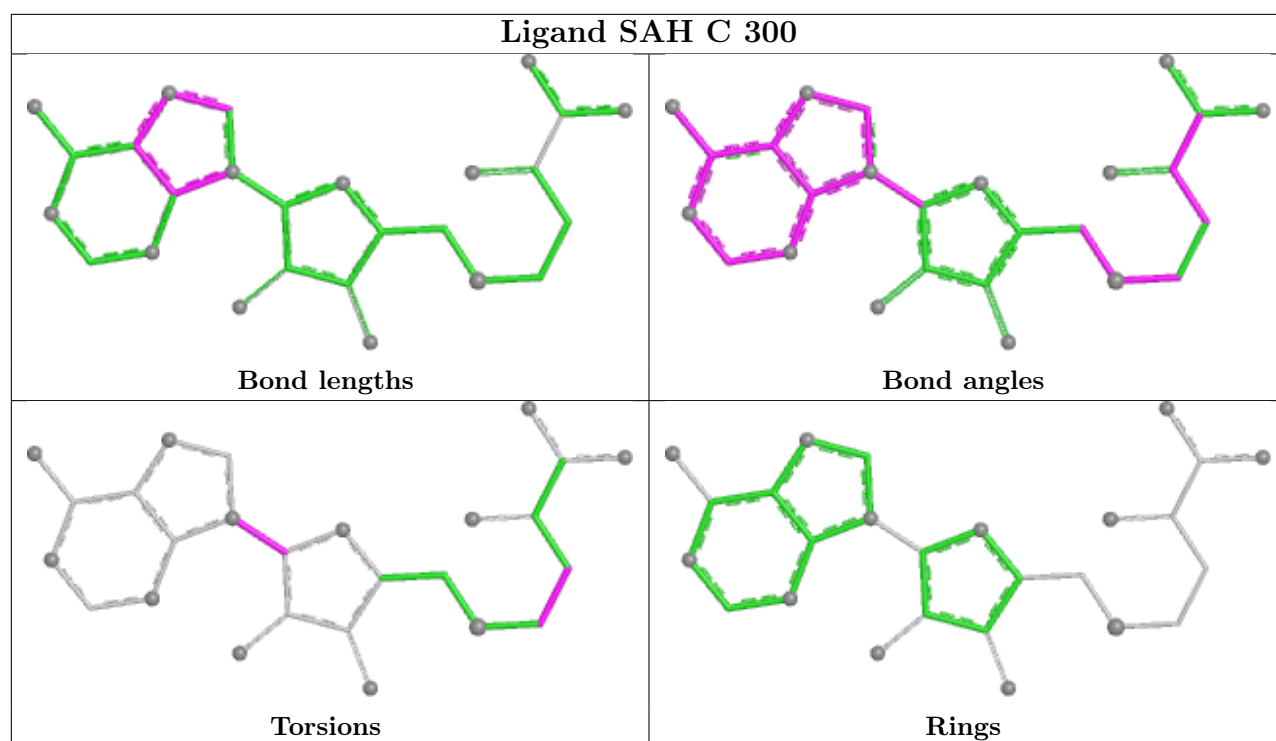
7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	300	SAH	2	0
2	A	300	SAH	1	0
3	A	209	PO4	1	0
3	C	209	PO4	1	1
2	B	300	SAH	1	0
3	B	209	PO4	0	1
4	A	212	GOL	5	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	207/210 (98%)	0.53	11 (5%) 32 31	18, 33, 52, 55	2 (0%)
1	B	207/210 (98%)	0.83	21 (10%) 12 11	14, 36, 63, 71	4 (1%)
1	C	207/210 (98%)	0.99	13 (6%) 26 24	18, 42, 55, 68	1 (0%)
1	D	196/210 (93%)	1.48	65 (33%) 1 1	23, 50, 90, 101	1 (0%)
All	All	817/840 (97%)	0.95	110 (13%) 7 5	14, 39, 73, 101	8 (0%)

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	45	TRP	6.5
1	C	196	ALA	6.0
1	A	53	GLY	4.9
1	B	37	ASP	4.8
1	D	119	ASN	4.8
1	D	44	ALA	4.8
1	D	49	ALA	4.5
1	B	2	VAL	4.1
1	D	111	TRP	4.1
1	D	3	SER	4.0
1	D	120	LEU	4.0
1	D	35	PHE	4.0
1	D	10	LEU	3.9
1	D	122	LEU	3.9
1	D	138	ALA	3.8
1	A	187	GLY	3.8
1	D	208	ALA	3.7
1	C	2	VAL	3.7
1	D	117	LEU	3.7
1	D	118	LYS	3.6
1	A	111	TRP	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	109	LEU	3.3
1	D	106	ILE	3.2
1	D	15	ALA	3.2
1	D	207	LEU	3.1
1	D	121	ASP	3.1
1	C	187	GLY	3.1
1	D	5	ARG	3.0
1	B	4	ARG	3.0
1	D	135	GLY	3.0
1	D	186	GLY	3.0
1	A	208	ALA	3.0
1	C	120	LEU	2.9
1	B	39	ALA	2.9
1	D	12	GLN	2.9
1	D	108	GLY	2.9
1	D	27	LEU	2.9
1	D	28	ALA	2.8
1	D	48	ILE	2.8
1	D	125	VAL	2.8
1	D	113	ALA	2.8
1	D	115	ARG	2.8
1	C	40	PHE	2.7
1	A	205	GLY	2.7
1	A	39	ALA	2.7
1	A	175	GLU	2.7
1	D	8	ALA	2.7
1	A	122	LEU	2.7
1	D	58	ILE	2.7
1	D	7	GLN	2.7
1	D	102	SER	2.7
1	D	6	VAL	2.7
1	B	36	VAL	2.7
1	B	40	PHE	2.6
1	D	114	ARG	2.6
1	B	9	LEU	2.6
1	B	14	ARG	2.6
1	D	46	ASP	2.6
1	B	11	ASP	2.6
1	B	21	GLU	2.6
1	D	9	LEU	2.5
1	B	26	ALA	2.5
1	D	128	ARG	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	140	ALA	2.5
1	D	110	GLN	2.5
1	B	18	ILE	2.4
1	D	107	LYS	2.4
1	D	54	GLN	2.4
1	D	29	ALA	2.4
1	D	55	GLY	2.4
1	D	103	VAL	2.4
1	D	187	GLY	2.4
1	A	78[A]	ARG	2.3
1	B	6	VAL	2.3
1	C	10	LEU	2.3
1	C	121	ASP	2.3
1	B	42	GLN	2.3
1	C	47	ASN	2.3
1	D	124	ASN	2.3
1	A	27	LEU	2.3
1	D	50	LEU	2.3
1	B	65	ALA	2.2
1	C	173	GLY	2.2
1	D	30	VAL	2.2
1	D	123	HIS	2.2
1	D	129	HIS	2.2
1	D	127	THR	2.2
1	B	13	LEU	2.2
1	C	186	GLY	2.2
1	D	31	PRO	2.2
1	C	176	HIS	2.2
1	B	44	ALA	2.2
1	C	178	TYR	2.2
1	B	176	HIS	2.2
1	D	136	TRP	2.2
1	D	17	GLY	2.2
1	B	3	SER	2.1
1	D	59[A]	SER	2.1
1	D	87	GLY	2.1
1	A	207	LEU	2.1
1	B	8	ALA	2.1
1	D	33	GLU	2.1
1	D	56	GLN	2.1
1	C	15	ALA	2.1
1	D	32	ARG	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	88	TYR	2.0
1	D	126	SER	2.0
1	B	12	GLN	2.0
1	D	112	GLN	2.0
1	D	178	TYR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

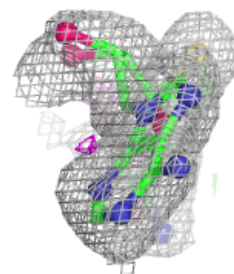
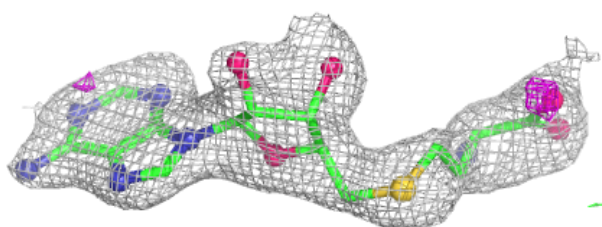
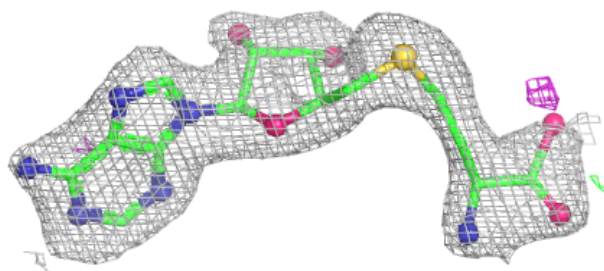
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PO4	B	210	5/5	0.76	0.14	78,79,80,83	0
4	GOL	A	212	6/6	0.78	0.56	196,206,221,222	0
3	PO4	C	209	5/5	0.84	0.26	84,86,89,94	0
3	PO4	A	210	5/5	0.88	0.11	45,47,49,50	0
2	SAH	D	300	26/26	0.90	0.11	48,53,58,58	0
3	PO4	A	211	5/5	0.91	0.10	50,53,55,55	0
3	PO4	B	209	5/5	0.92	0.21	71,74,77,78	0
3	PO4	A	209	5/5	0.93	0.10	49,51,52,52	0
2	SAH	B	300	26/26	0.94	0.09	23,28,32,33	0
2	SAH	A	300	26/26	0.95	0.07	26,29,33,33	0
2	SAH	C	300	26/26	0.95	0.08	30,33,36,37	0

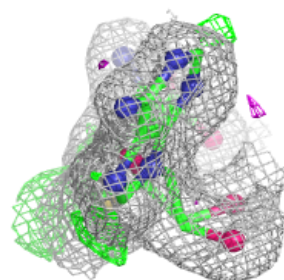
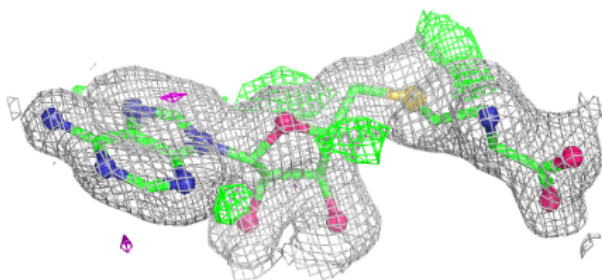
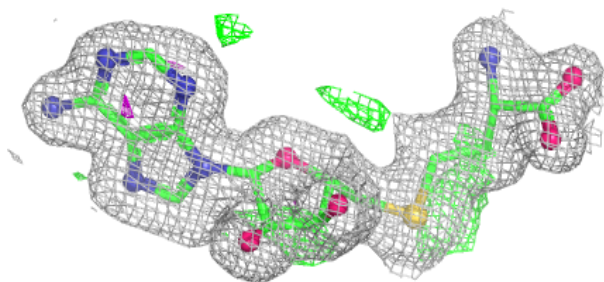
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SAH D 300:

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

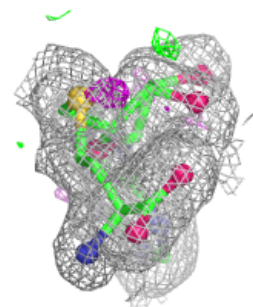
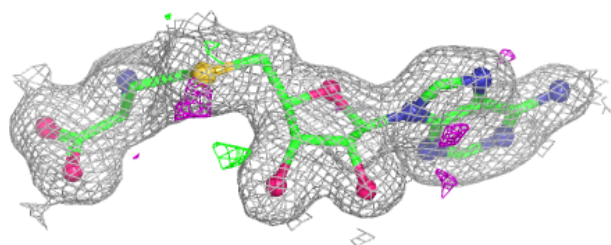
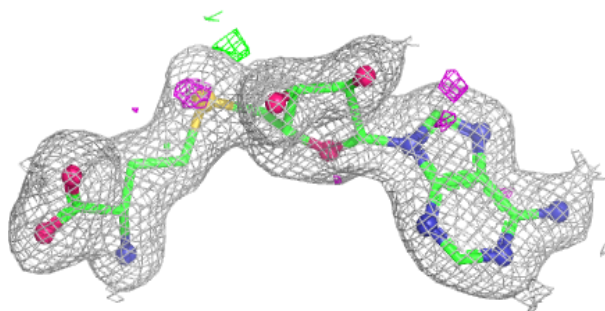
**Electron density around SAH B 300:**

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

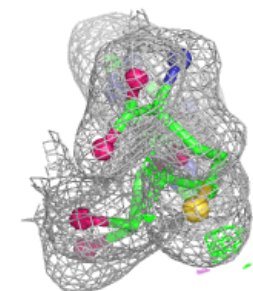
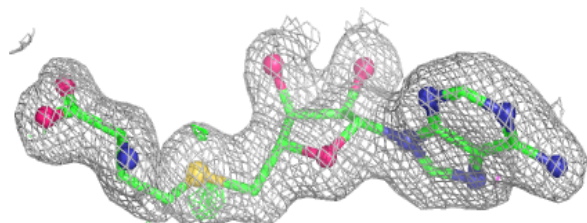
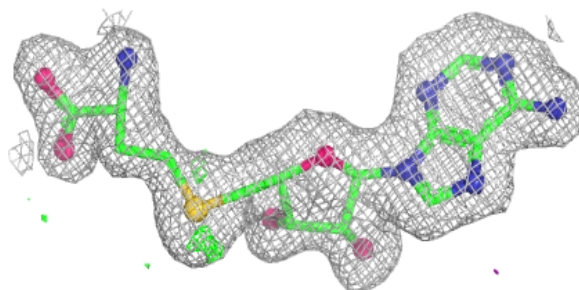


Electron density around SAH A 300:

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

**Electron density around SAH C 300:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.