Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2023 – 04:48 PM EDT

PDB ID	:	7TWM
Title	:	Structure of a borosin methyltransferase from Mycena rosella with peptide CspL(MroMCspL) in complex with SAH
Authors	:	Zheng, Y.; Ongpipattanakul, C.; Nair, S.K.
Deposited on	:	2022-02-07
Resolution	:	1.93 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:

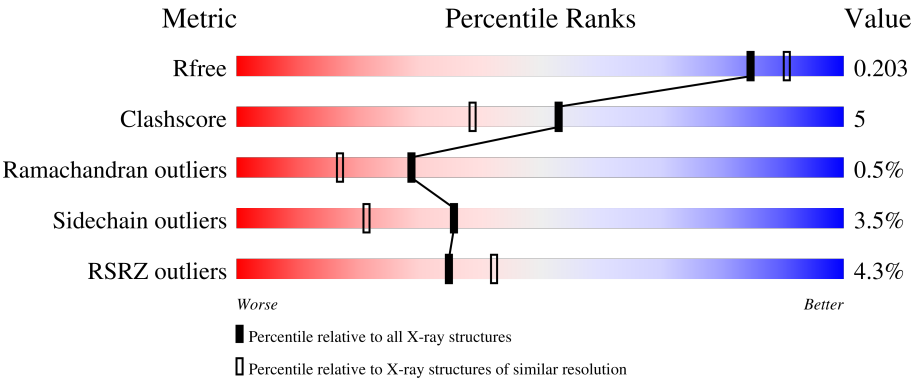
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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	402	3% 84% 8% • 7%
1	B	402	4% 84% 12% • •
1	C	402	5% 80% 11% • 8%
1	D	402	4% 85% 11% • •

2 Entry composition

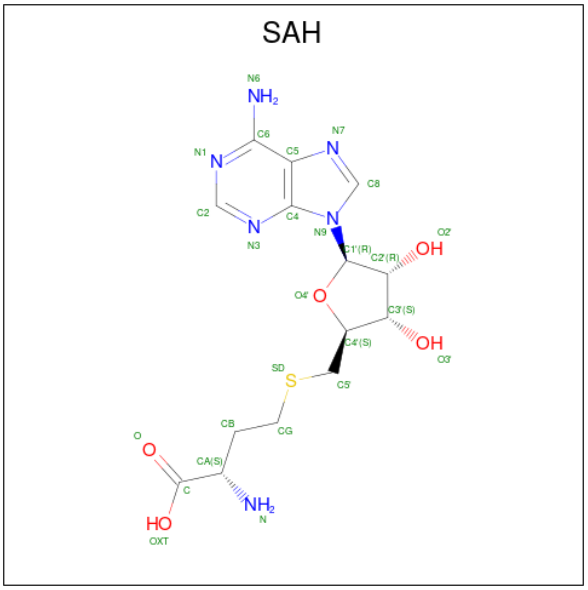
There are 3 unique types of molecules in this entry. The entry contains 12715 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MroMCspL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	1	0
			2885	1840	491	542	12			
1	B	391	Total	C	N	O	S	0	2	0
			3029	1938	513	565	13			
1	C	369	Total	C	N	O	S	0	1	0
			2854	1819	486	537	12			
1	D	387	Total	C	N	O	S	0	1	0
			2986	1906	509	559	12			

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



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		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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 water.

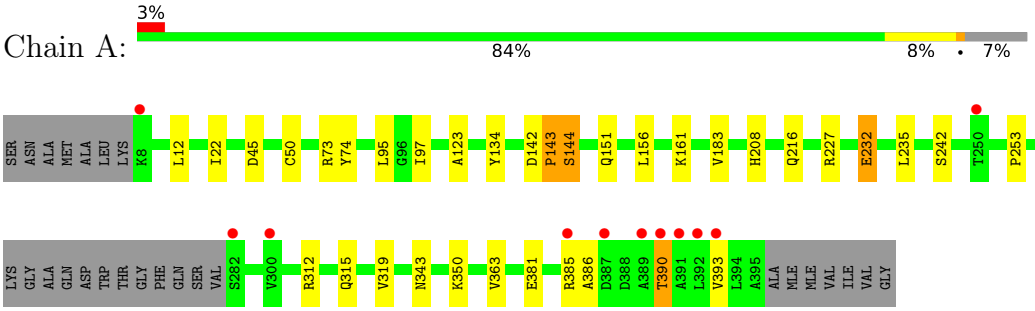
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	224	Total	O	0	0
			224	224		
3	B	213	Total	O	0	0
			213	213		
3	C	187	Total	O	0	0
			187	187		
3	D	233	Total	O	0	0
			233	233		

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.

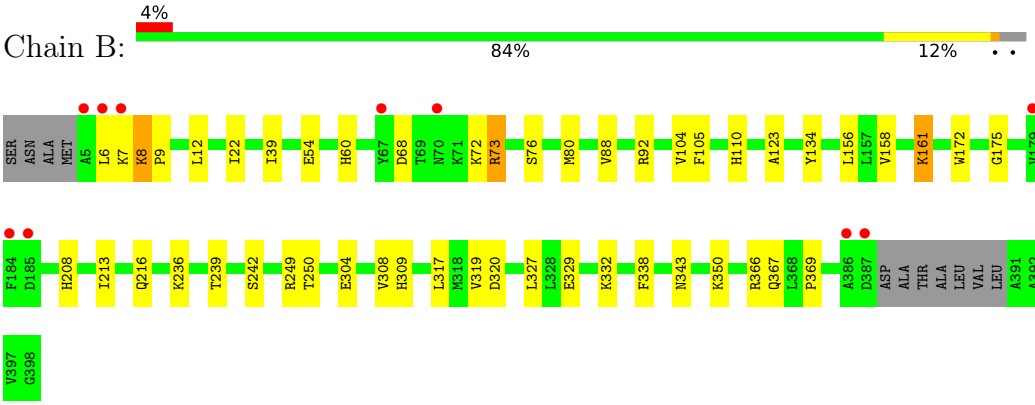
• Molecule 1: MroMCspL

Chain A:



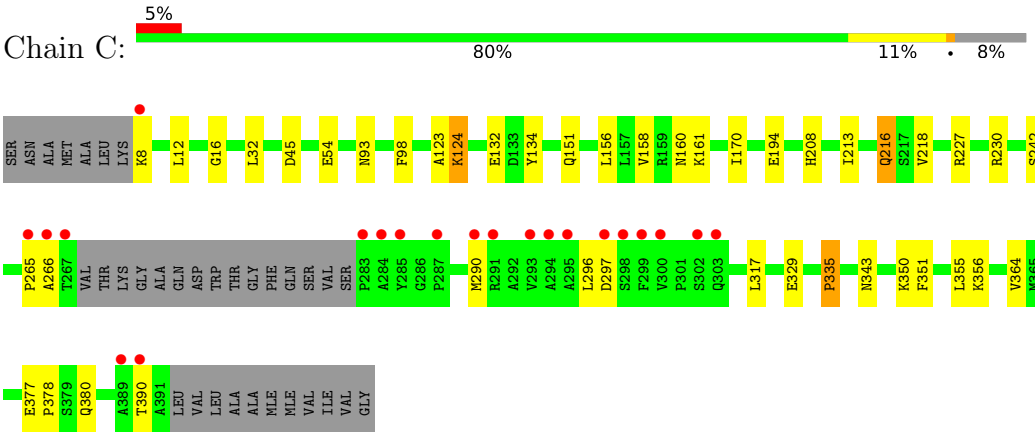
• Molecule 1: MroMCspL

Chain B:

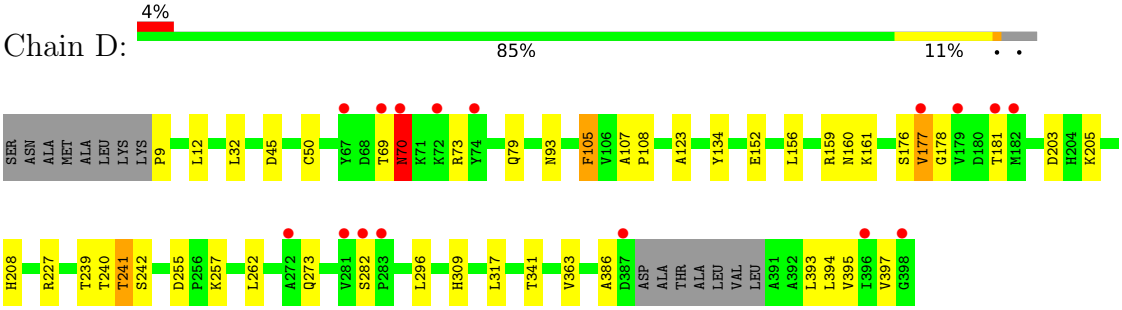


• Molecule 1: MroMCspL

Chain C:



• Molecule 1: MroMCspL



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	190.96Å 190.96Å 93.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 1.93 82.69 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.00-1.93) 100.0 (82.69-1.93)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.26 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.174 , 0.202 0.175 , 0.203	Depositor DCC
R_{free} test set	7170 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	26.7	Xtriage
Anisotropy	0.298	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.020 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	12715	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, MLE

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	0.31	0/2949	0.61	1/3999 (0.0%)
1	B	0.29	0/3081	0.59	0/4177
1	C	0.30	0/2919	0.61	0/3959
1	D	0.30	0/3034	0.59	1/4116 (0.0%)
All	All	0.30	0/11983	0.60	2/16251 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	9	PRO	N-CA-CB	6.01	110.51	103.30
1	A	143	PRO	N-CA-C	-5.15	98.72	112.10

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	2885	0	2882	35	0
1	B	3029	0	3052	49	0
1	C	2854	0	2853	31	0
1	D	2986	0	2983	35	0
2	A	26	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	26	0	19	0	0
2	C	26	0	19	0	0
2	D	26	0	19	0	0
3	A	224	0	0	12	0
3	B	213	0	0	4	0
3	C	187	0	0	7	0
3	D	233	0	0	10	0
All	All	12715	0	11846	127	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 (127) 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:D:50:CYS:HB3	3:D:778:HOH:O	1.27	1.26
1:A:50:CYS:HB3	3:A:794:HOH:O	1.11	1.25
1:A:144:SER:N	3:A:601:HOH:O	1.80	1.11
1:C:317:LEU:HG	3:C:769:HOH:O	1.49	1.08
1:D:317:LEU:HG	3:D:816:HOH:O	1.56	1.05
1:A:143:PRO:HA	3:A:601:HOH:O	1.60	1.01
1:A:143:PRO:CA	3:A:601:HOH:O	2.08	1.00
1:D:239:THR:HG23	1:D:241:THR:H	1.26	0.96
1:A:50:CYS:SG	1:B:308:VAL:HG21	2.07	0.94
1:B:8:LYS:HA	3:B:789:HOH:O	1.69	0.92
3:A:666:HOH:O	1:B:110:HIS:HE1	1.51	0.90
1:A:142:ASP:OD1	1:A:143:PRO:O	1.87	0.89
1:C:218:VAL:HG13	3:C:757:HOH:O	1.72	0.89
1:D:93:ASN:HB3	3:D:817:HOH:O	1.76	0.83
1:A:315:GLN:NE2	1:B:54:GLU:OE2	2.15	0.80
1:D:69:THR:O	1:D:70:ASN:HB2	1.82	0.80
1:A:161:LYS:HE2	3:B:606:HOH:O	1.84	0.76
1:A:232:GLU:H	1:A:232:GLU:CD	1.86	0.76
1:A:50:CYS:SG	1:B:308:VAL:CG2	2.73	0.76
1:D:156:LEU:HD12	1:D:161:LYS:HB2	1.67	0.75
1:B:73:ARG:HA	1:B:73:ARG:HE	1.51	0.74
1:D:208:HIS:HE1	1:D:242:SER:OG	1.70	0.74
1:D:205:LYS:CB	3:D:818:HOH:O	2.37	0.73
1:A:253:PRO:O	3:A:602:HOH:O	2.07	0.70
1:A:74:TYR:HB2	1:B:396:ILE:HD11	1.73	0.70
1:B:68:ASP:H	1:B:73:ARG:HH22	1.37	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:ASN:HB2	3:C:637:HOH:O	1.94	0.67
1:A:312[B]:ARG:NH1	1:B:54:GLU:OE2	2.23	0.67
1:C:366:ARG:O	1:C:367:GLN:HG3	1.94	0.67
1:D:177:VAL:C	3:D:612:HOH:O	2.33	0.67
1:C:208:HIS:HD2	3:C:654:HOH:O	1.78	0.67
1:A:208:HIS:HD2	3:A:646:HOH:O	1.76	0.66
1:A:73:ARG:NH2	1:B:396:ILE:HG22	2.11	0.65
1:B:8:LYS:N	1:B:9:PRO:CD	2.60	0.64
1:A:312[B]:ARG:HH12	1:B:54:GLU:CD	2.01	0.64
1:A:74:TYR:HB2	1:B:396:ILE:CD1	2.29	0.62
1:D:208:HIS:HD2	3:D:629:HOH:O	1.82	0.62
1:B:7:LYS:C	1:B:9:PRO:HD3	2.19	0.62
1:B:317:LEU:HD11	1:B:338:PHE:HE1	1.65	0.61
1:A:312[B]:ARG:NH2	1:C:54:GLU:OE2	2.34	0.61
1:B:208:HIS:HD2	3:B:626:HOH:O	1.84	0.61
1:B:309:HIS:HD2	1:B:367:GLN:NE2	2.00	0.60
1:D:177:VAL:O	1:D:177:VAL:HG13	2.02	0.60
1:B:8:LYS:N	1:B:9:PRO:HD3	2.16	0.59
3:A:666:HOH:O	1:B:110:HIS:CE1	2.38	0.59
1:C:213:ILE:HG23	3:C:619:HOH:O	2.02	0.59
1:C:208:HIS:HE1	1:C:242:SER:OG	1.87	0.57
1:D:203:ASP:OD1	1:D:227:ARG:NH1	2.30	0.57
1:D:208:HIS:CE1	1:D:242:SER:OG	2.56	0.57
1:B:208:HIS:HE1	1:B:242:SER:OG	1.87	0.57
1:B:366:ARG:O	1:B:367:GLN:HG3	2.06	0.56
1:C:156:LEU:HD12	1:C:161:LYS:HB2	1.86	0.56
1:C:160:ASN:HD21	1:D:255:ASP:HB2	1.70	0.56
1:B:6:LEU:HB3	1:B:9:PRO:HG2	1.87	0.56
1:C:296:LEU:HG	1:D:79:GLN:HG2	1.88	0.56
1:C:132:GLU:HG2	1:C:170:ILE:HD13	1.87	0.55
1:A:315:GLN:NE2	1:B:54:GLU:CD	2.61	0.54
1:A:343:ASN:HD22	1:A:350:LYS:NZ	2.04	0.54
3:A:703:HOH:O	1:B:332:LYS:HE2	2.06	0.54
1:A:208:HIS:HE1	1:A:242:SER:OG	1.91	0.54
1:A:381:GLU:O	1:A:385:ARG:HB3	2.08	0.54
1:D:273:GLN:OE1	1:D:282:SER:HB2	2.10	0.52
1:C:158:VAL:HG21	1:D:397:VAL:HG11	1.91	0.51
1:B:6:LEU:HD12	1:B:329:GLU:OE2	2.11	0.51
1:C:12:LEU:O	1:C:123:ALA:HA	2.10	0.50
1:A:95:LEU:HD21	1:A:97:ILE:HD11	1.94	0.50
1:B:249:ARG:HG2	1:B:250:THR:HG23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:239:THR:HG23	1:D:241:THR:N	2.10	0.49
1:B:105:PHE:HE2	1:B:172:TRP:CD2	2.30	0.49
1:B:343:ASN:HD22	1:B:350:LYS:NZ	2.10	0.49
1:A:363:VAL:HG21	1:A:386:ALA:HB2	1.93	0.49
1:A:227:ARG:NH2	3:A:605:HOH:O	2.45	0.49
1:D:208:HIS:HE1	1:D:242:SER:HG	1.60	0.49
1:A:22:ILE:HD13	1:B:319:VAL:HG22	1.95	0.48
1:C:194:GLU:CG	1:C:230:ARG:HH22	2.26	0.48
1:A:50:CYS:CB	3:A:794:HOH:O	1.95	0.48
1:C:377:GLU:HG3	1:C:378:PRO:HD2	1.96	0.48
1:B:104:VAL:O	1:B:105:PHE:HB2	2.14	0.48
1:B:320:ASP:HB3	1:B:327[B]:LEU:CD2	2.43	0.48
1:D:107:ALA:N	1:D:108:PRO:HD2	2.29	0.48
1:C:343:ASN:HD22	1:C:350:LYS:NZ	2.12	0.47
1:B:92:ARG:NH2	1:D:341:THR:O	2.48	0.47
1:C:252:ALA:O	1:D:159:ARG:NH1	2.45	0.47
1:C:160:ASN:HD21	1:D:255:ASP:CB	2.28	0.46
1:A:142:ASP:C	1:A:143:PRO:O	2.50	0.45
1:A:183:VAL:HG22	3:A:677:HOH:O	2.17	0.45
1:C:160:ASN:ND2	1:D:255:ASP:HB2	2.32	0.45
1:B:156:LEU:HD12	1:B:161:LYS:HB2	1.98	0.45
1:B:317:LEU:HD11	1:B:338:PHE:CE1	2.47	0.45
1:B:175:GLY:HA3	1:B:239:THR:O	2.16	0.45
1:A:343:ASN:HD22	1:A:350:LYS:HZ1	1.64	0.45
1:D:309:HIS:HD2	3:D:788:HOH:O	2.00	0.45
1:D:105:PHE:CZ	1:D:152:GLU:HG3	2.52	0.44
1:B:12:LEU:O	1:B:123:ALA:HA	2.17	0.44
1:A:73:ARG:CZ	1:B:396:ILE:HG22	2.47	0.44
1:C:208:HIS:HE1	1:C:242:SER:CB	2.31	0.44
1:B:76:SER:O	1:B:80:MET:HG3	2.18	0.44
1:D:240:THR:HA	3:D:722:HOH:O	2.17	0.44
1:D:393:MLE:HA	1:D:394:MLE:HN1	1.66	0.43
1:B:12:LEU:HB2	1:B:88:VAL:HG21	1.99	0.43
1:A:319:VAL:HG22	1:B:22:ILE:HD13	2.00	0.43
1:C:366:ARG:C	1:C:367:GLN:HG3	2.39	0.43
1:D:12:LEU:O	1:D:123:ALA:HA	2.18	0.43
1:C:351:PHE:CE2	1:C:380:GLN:HG3	2.54	0.43
1:D:50:CYS:CB	3:D:778:HOH:O	2.12	0.43
1:A:312[B]:ARG:NH2	1:B:54:GLU:OE2	2.50	0.42
1:B:393:MLE:HA	1:B:394:MLE:HN1	1.74	0.42
1:C:351:PHE:CD2	1:C:380:GLN:HG3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:ASP:O	1:B:181:THR:C	2.57	0.42
1:B:320:ASP:HB3	1:B:327[B]:LEU:HD22	2.01	0.42
1:A:12:LEU:O	1:A:123:ALA:HA	2.18	0.42
1:D:176:SER:OG	1:D:181:THR:HA	2.20	0.42
1:B:213:ILE:HG23	3:B:650:HOH:O	2.19	0.41
1:C:335:PRO:HG3	1:C:356:LYS:HE3	2.01	0.41
1:D:363:VAL:HG21	1:D:386:ALA:HB2	2.02	0.41
1:A:50:CYS:SG	1:B:308:VAL:HG22	2.58	0.41
1:C:194:GLU:HG2	1:C:230:ARG:HH22	1.85	0.41
1:C:16:GLY:HA2	1:C:98:PHE:O	2.20	0.41
1:B:73:ARG:HE	1:B:73:ARG:CA	2.26	0.41
1:C:124:LYS:HE3	3:C:744:HOH:O	2.21	0.41
1:D:296:LEU:C	1:D:296:LEU:HD23	2.41	0.41
1:B:304:GLU:OE2	1:B:369:PRO:HD2	2.21	0.41
1:C:32:LEU:HD11	3:C:781:HOH:O	2.20	0.41
1:C:216:GLN:H	1:C:216:GLN:HE21	1.69	0.41
1:D:178:GLY:N	3:D:612:HOH:O	2.53	0.41
1:B:39:ILE:O	1:B:60:HIS:HA	2.22	0.40
1:C:158:VAL:HG12	1:D:262:LEU:CD1	2.51	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	368/402 (92%)	356 (97%)	10 (3%)	2 (0%)	29	17
1	B	387/402 (96%)	369 (95%)	16 (4%)	2 (0%)	29	17
1	C	366/402 (91%)	353 (96%)	11 (3%)	2 (0%)	29	17
1	D	382/402 (95%)	372 (97%)	8 (2%)	2 (0%)	29	17
All	All	1503/1608 (94%)	1450 (96%)	45 (3%)	8 (0%)	29	17

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	8	LYS
1	D	70	ASN
1	C	265	PRO
1	C	266	ALA
1	B	181	THR
1	A	390	THR
1	A	144	SER
1	D	177	VAL

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	307/327 (94%)	298 (97%)	9 (3%)	42	28
1	B	321/327 (98%)	312 (97%)	9 (3%)	43	29
1	C	304/327 (93%)	289 (95%)	15 (5%)	25	10
1	D	314/327 (96%)	304 (97%)	10 (3%)	39	25
All	All	1246/1308 (95%)	1203 (96%)	43 (4%)	36	21

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ASP
1	A	134	TYR
1	A	151	GLN
1	A	156	LEU
1	A	216	GLN
1	A	232	GLU
1	A	235	LEU
1	A	390	THR
1	A	393	VAL
1	B	72	LYS
1	B	73	ARG
1	B	134	TYR

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Mol	Chain	Res	Type
1	B	158	VAL
1	B	161	LYS
1	B	180	ASP
1	B	216	GLN
1	B	236	LYS
1	B	396	ILE
1	C	8	LYS
1	C	45	ASP
1	C	124	LYS
1	C	134	TYR
1	C	151	GLN
1	C	216	GLN
1	C	227	ARG
1	C	257	LYS
1	C	290	MET
1	C	297	ASP
1	C	329	GLU
1	C	335	PRO
1	C	355	LEU
1	C	364	VAL
1	C	390	THR
1	D	32	LEU
1	D	45	ASP
1	D	70	ASN
1	D	73	ARG
1	D	105	PHE
1	D	134	TYR
1	D	160	ASN
1	D	241	THR
1	D	257	LYS
1	D	395	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	173	GLN
1	A	186	ASN
1	A	208	HIS
1	A	216	GLN
1	A	303	GLN
1	A	315	GLN
1	A	343	ASN

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Mol	Chain	Res	Type
1	B	190	HIS
1	B	208	HIS
1	B	216	GLN
1	B	309	HIS
1	B	343	ASN
1	B	367	GLN
1	C	160	ASN
1	C	208	HIS
1	C	216	GLN
1	C	237	GLN
1	C	343	ASN
1	D	93	ASN
1	D	173	GLN
1	D	186	ASN
1	D	208	HIS
1	D	237	GLN
1	D	309	HIS
1	D	343	ASN
1	D	367	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	$\#\|Z\| > 2$
1	MLE	D	394	1	7,8,9	0.54	0	6,9,11	1.10	0
1	MLE	B	393	1	7,8,9	0.46	0	6,9,11	1.01	0
1	MLE	B	394	1	7,8,9	0.59	0	6,9,11	1.08	0
1	MLE	D	393	1	7,8,9	0.42	0	6,9,11	0.98	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
1	MLE	D	394	1	-	2/5/8/10	-
1	MLE	B	393	1	-	0/5/8/10	-
1	MLE	B	394	1	-	3/5/8/10	-
1	MLE	D	393	1	-	0/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	394	MLE	O-C-CA-CB
1	D	394	MLE	O-C-CA-CB
1	B	394	MLE	CA-CB-CG-CD1
1	B	394	MLE	CA-CB-CG-CD2
1	D	394	MLE	CA-CB-CG-CD1

There are no ring outliers.

4 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	394	MLE	1	0
1	B	393	MLE	1	0
1	B	394	MLE	1	0
1	D	393	MLE	1	0

5.5 Carbohydrates (i)

There are no monosaccharides 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	$\#\|Z\| > 2$
2	SAH	C	500	-	24,28,28	0.65	0	25,40,40	0.93	3 (12%)
2	SAH	B	500	-	24,28,28	0.67	1 (4%)	25,40,40	1.10	2 (8%)
2	SAH	D	500	-	24,28,28	0.65	0	25,40,40	0.90	2 (8%)
2	SAH	A	500	-	24,28,28	0.64	0	25,40,40	1.04	3 (12%)

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	C	500	-	-	1/11/31/31	0/3/3/3
2	SAH	B	500	-	-	4/11/31/31	0/3/3/3
2	SAH	D	500	-	-	4/11/31/31	0/3/3/3
2	SAH	A	500	-	-	1/11/31/31	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	SAH	OXT-C	-2.13	1.23	1.30

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	500	SAH	OXT-C-O	-3.40	116.38	124.09
2	A	500	SAH	OXT-C-CA	2.73	122.70	113.38
2	D	500	SAH	C5-C6-N6	2.47	124.10	120.35
2	A	500	SAH	OXT-C-O	-2.45	118.52	124.09
2	C	500	SAH	OXT-C-O	-2.42	118.60	124.09
2	C	500	SAH	C5-C6-N6	2.31	123.87	120.35
2	D	500	SAH	OXT-C-O	-2.29	118.90	124.09
2	C	500	SAH	OXT-C-CA	2.26	121.07	113.38
2	B	500	SAH	C5-C6-N6	2.25	123.77	120.35
2	A	500	SAH	C5-C6-N6	2.11	123.57	120.35

There are no chirality outliers.

All (10) torsion outliers are listed below:

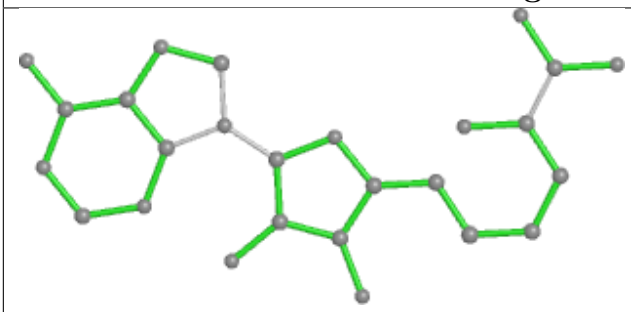
Mol	Chain	Res	Type	Atoms
2	B	500	SAH	C-CA-CB-CG
2	D	500	SAH	C-CA-CB-CG
2	B	500	SAH	N-CA-CB-CG
2	D	500	SAH	N-CA-CB-CG
2	B	500	SAH	O-C-CA-CB
2	B	500	SAH	OXT-C-CA-CB
2	D	500	SAH	O-C-CA-CB
2	D	500	SAH	OXT-C-CA-CB
2	A	500	SAH	OXT-C-CA-CB
2	C	500	SAH	OXT-C-CA-CB

There are no ring outliers.

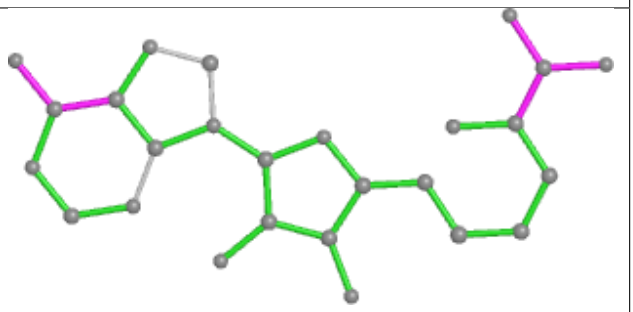
No monomer is involved in short contacts.

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 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.

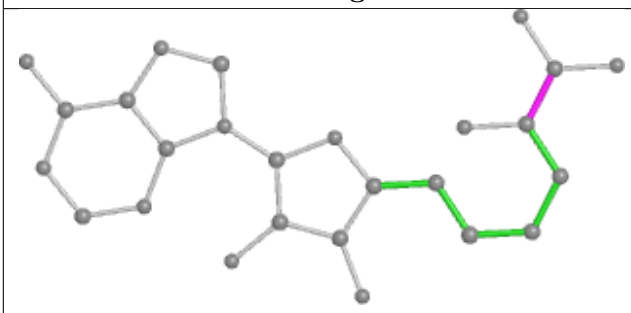
Ligand SAH C 500



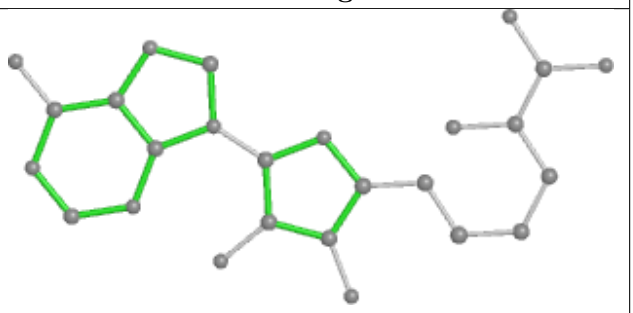
Bond lengths



Bond angles

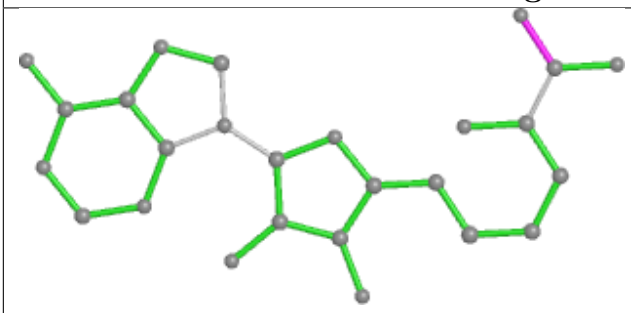


Torsions

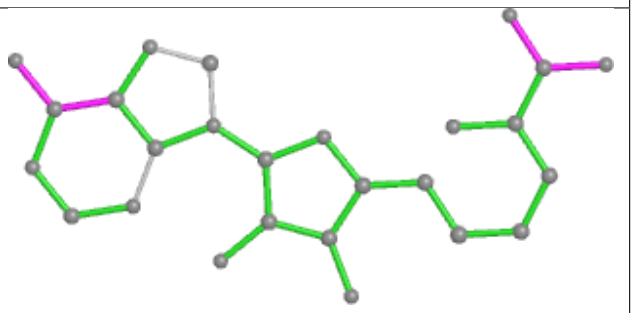


Rings

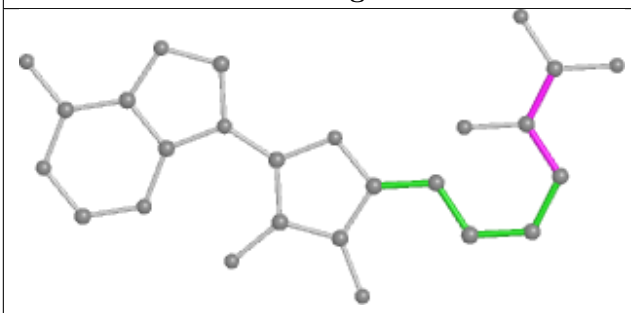
Ligand SAH B 500



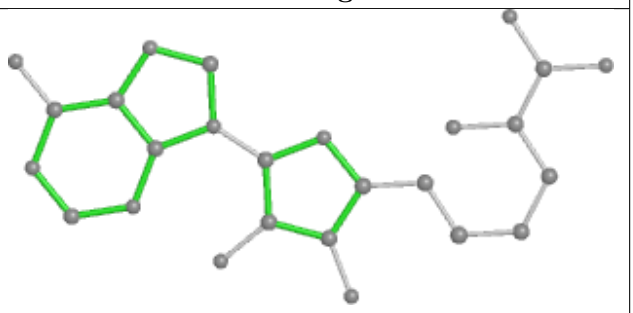
Bond lengths



Bond angles

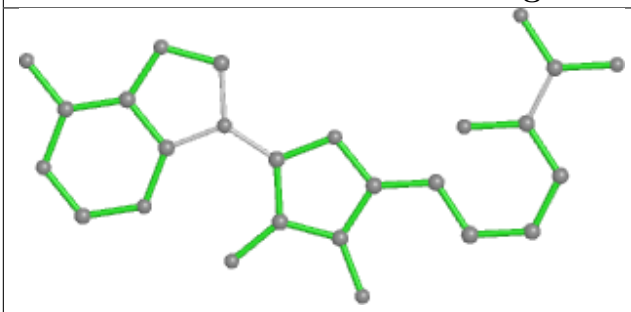


Torsions

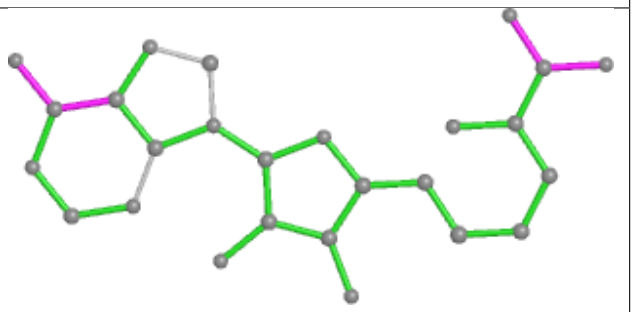


Rings

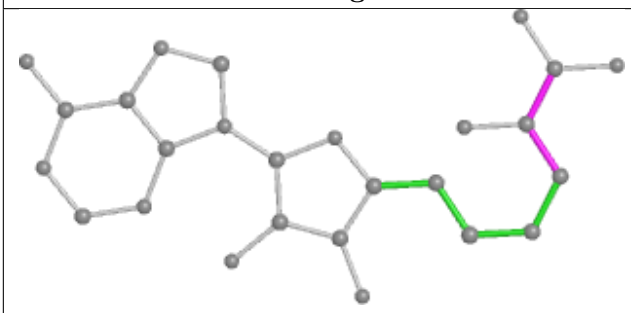
Ligand SAH D 500



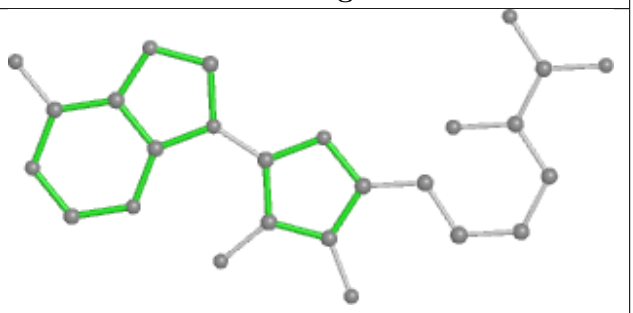
Bond lengths



Bond angles

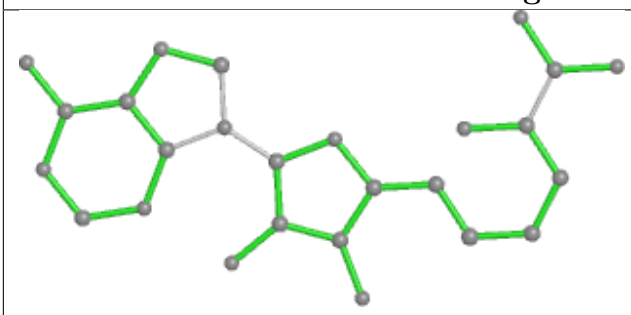


Torsions

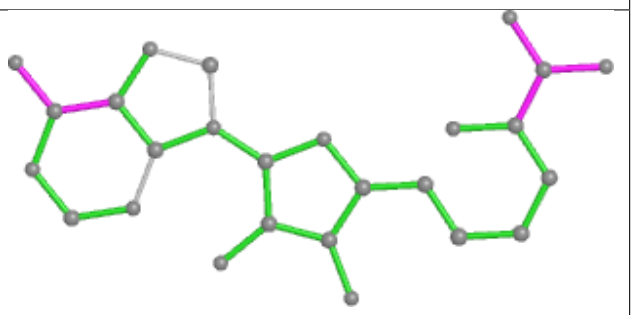


Rings

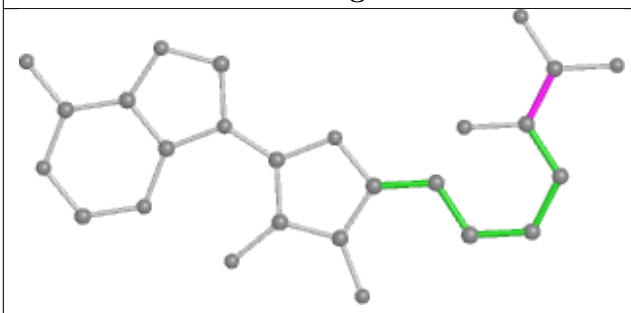
Ligand SAH A 500



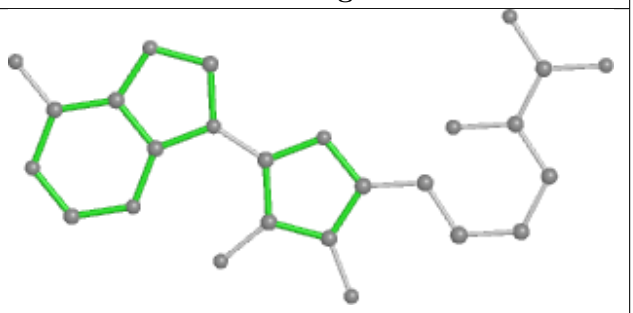
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	373/402 (92%)	-0.13	12 (3%)	47	55	17, 29, 64, 114	0
1	B	389/402 (96%)	0.01	15 (3%)	39	47	18, 31, 63, 149	0
1	C	369/402 (91%)	-0.09	22 (5%)	21	28	19, 30, 71, 125	0
1	D	385/402 (95%)	-0.10	16 (4%)	36	43	20, 30, 58, 92	0
All	All	1516/1608 (94%)	-0.08	65 (4%)	35	42	17, 30, 65, 149	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	6	LEU	13.2
1	C	267	THR	12.2
1	B	182	MET	10.7
1	B	5	ALA	10.5
1	B	7	LYS	10.5
1	B	181	THR	10.0
1	A	392	LEU	8.9
1	C	266	ALA	6.0
1	B	386	ALA	5.7
1	A	391	ALA	5.6
1	C	287	PRO	5.2
1	D	70	ASN	5.2
1	B	183	VAL	5.0
1	D	281	VAL	4.8
1	B	184	PHE	4.6
1	D	398	GLY	4.6
1	C	300	VAL	4.5
1	B	180	ASP	4.4
1	C	290	MET	4.4
1	C	283	PRO	4.2
1	C	299	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	182	MET	4.2
1	A	389	ALA	4.2
1	A	385	ARG	3.8
1	A	390	THR	3.7
1	B	387	ASP	3.7
1	A	282	SER	3.5
1	C	390	THR	3.5
1	B	67	TYR	3.5
1	A	300	VAL	3.4
1	C	265	PRO	3.3
1	A	8	LYS	3.2
1	D	74	TYR	3.1
1	D	177	VAL	3.0
1	B	185	ASP	3.0
1	C	298	SER	3.0
1	D	282	SER	3.0
1	C	291	ARG	3.0
1	A	393	VAL	3.0
1	C	293	VAL	2.9
1	B	70	ASN	2.9
1	C	294	ALA	2.8
1	D	69	THR	2.8
1	C	302	SER	2.7
1	D	396	ILE	2.7
1	C	389	ALA	2.6
1	D	67	TYR	2.6
1	A	250	THR	2.6
1	C	284	ALA	2.6
1	C	8	LYS	2.5
1	D	283	PRO	2.4
1	C	297	ASP	2.4
1	C	285	TYR	2.3
1	B	179	VAL	2.2
1	D	72	LYS	2.2
1	A	266	ALA	2.2
1	B	396	ILE	2.2
1	C	295	ALA	2.1
1	C	373	ALA	2.1
1	C	303	GLN	2.1
1	D	179	VAL	2.1
1	A	387	ASP	2.1
1	D	181	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	272	ALA	2.0
1	D	387	ASP	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, 95^{th} 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
1	MLE	B	394	9/10	0.95	0.11	23,27,31,31	0
1	MLE	D	393	9/10	0.96	0.11	26,31,34,35	0
1	MLE	D	394	9/10	0.96	0.10	24,28,31,33	0
1	MLE	B	393	9/10	0.97	0.09	25,26,29,31	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

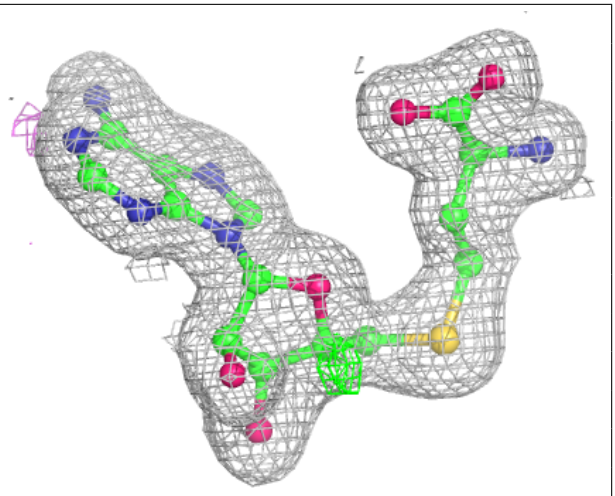
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

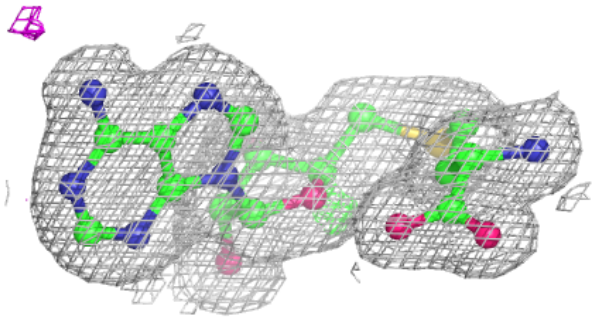
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SAH	A	500	26/26	0.98	0.10	19,21,22,23	0
2	SAH	B	500	26/26	0.98	0.08	18,22,25,27	0
2	SAH	C	500	26/26	0.98	0.08	20,23,24,25	0
2	SAH	D	500	26/26	0.98	0.07	20,23,27,27	0

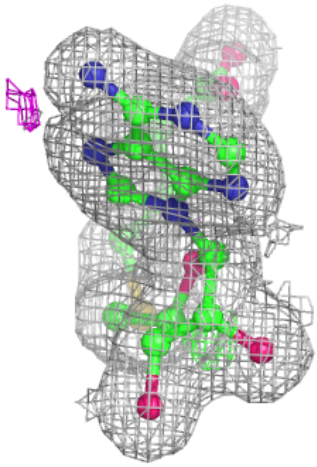
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SAH A 500:

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

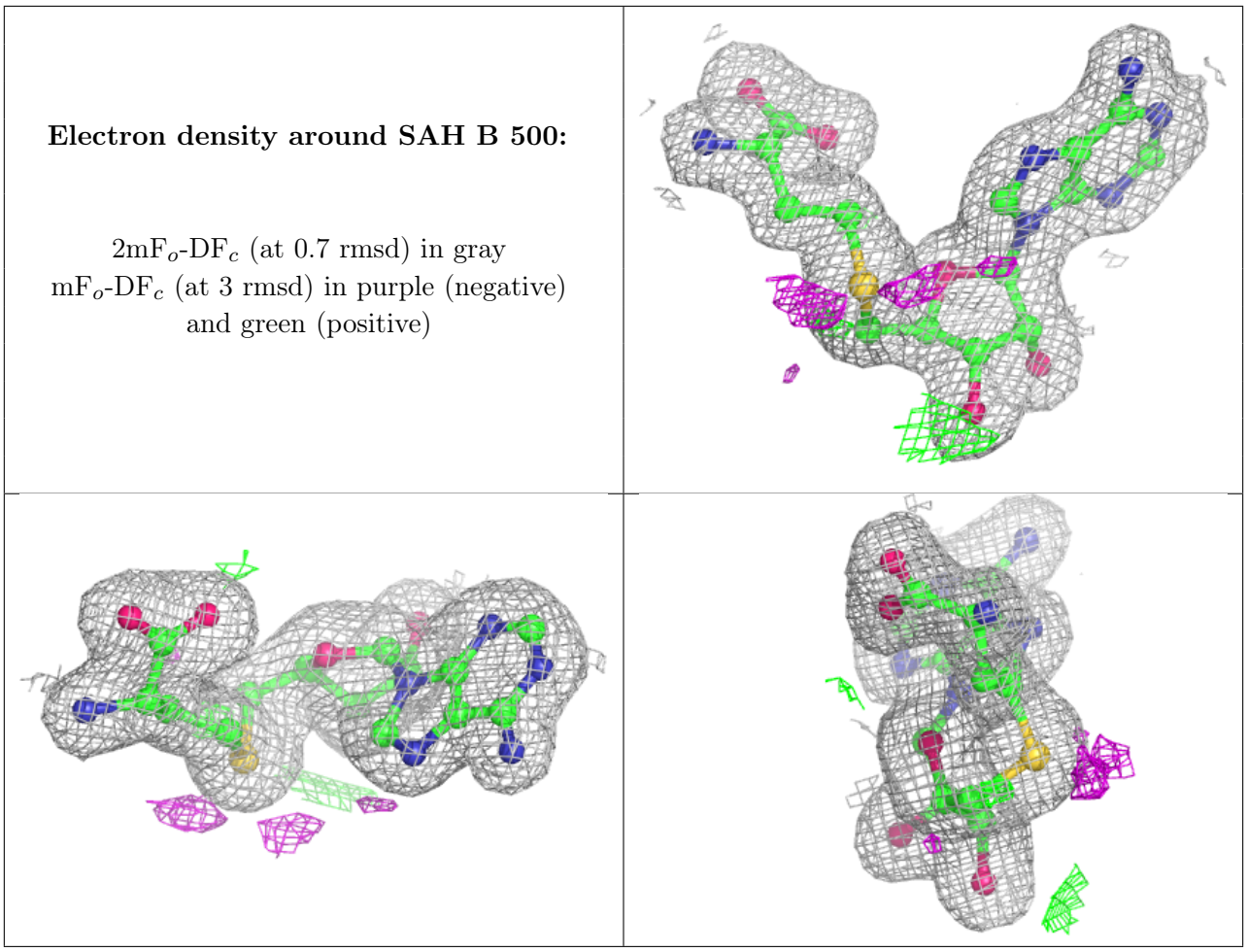






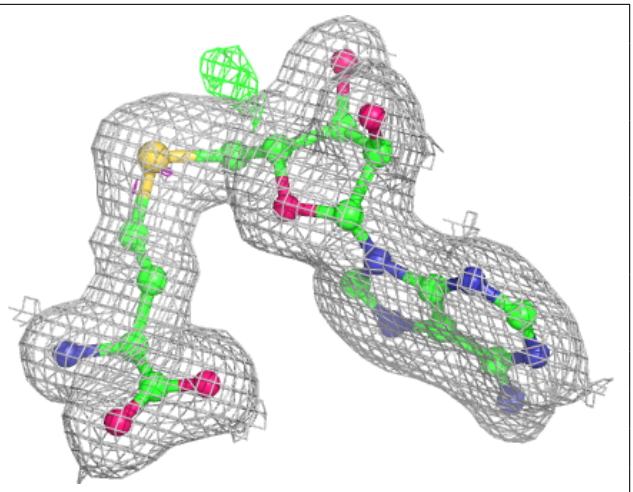
Electron density around SAH B 500:

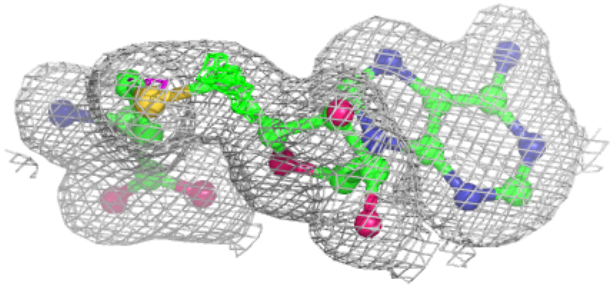
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

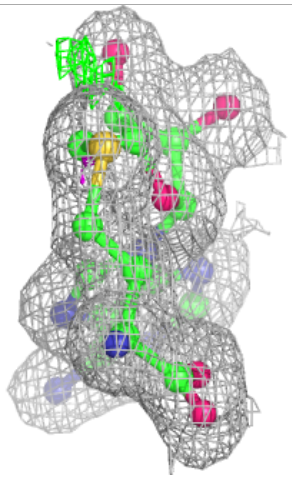


Electron density around SAH C 500:

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

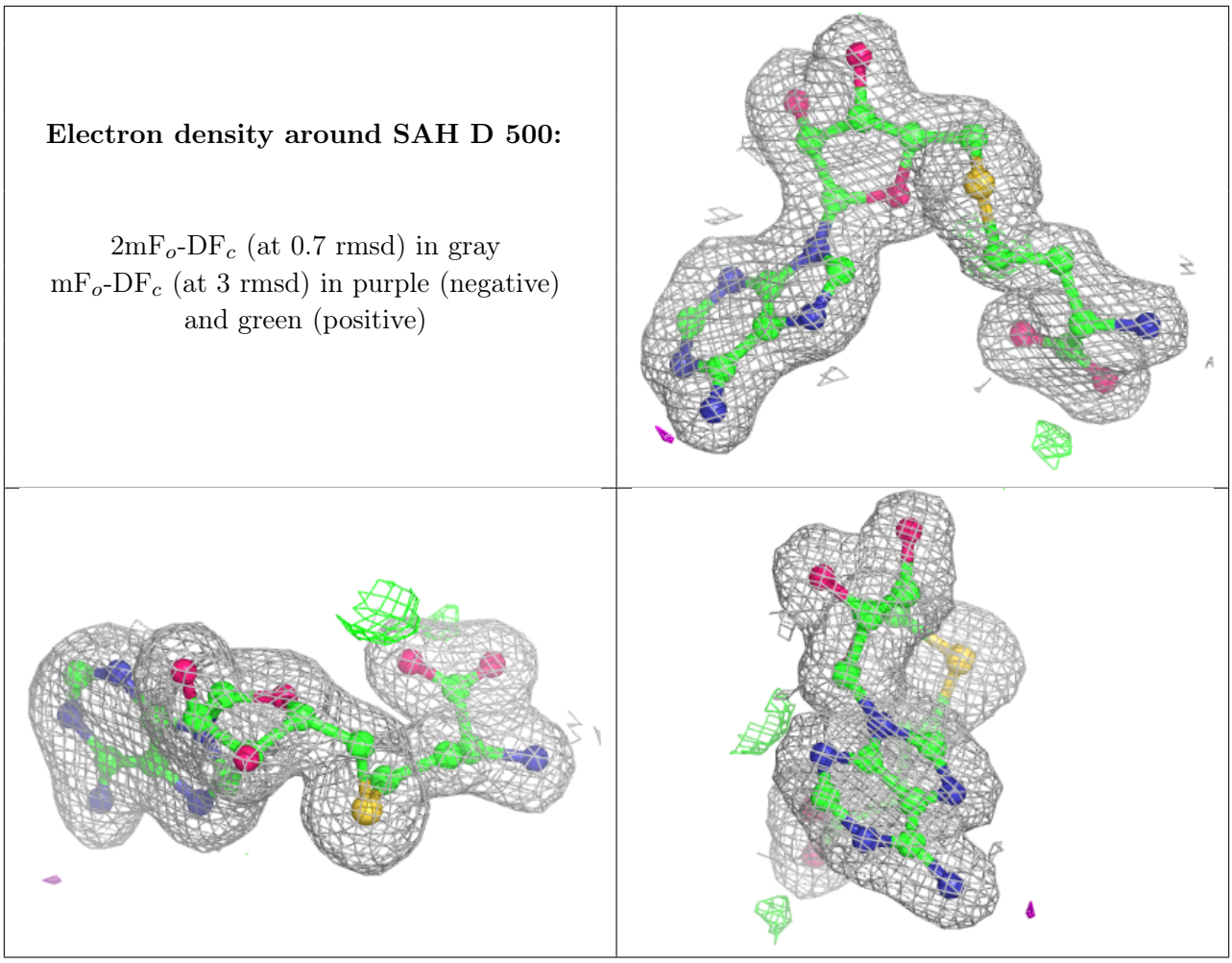






Electron density around SAH D 500:

$2mF_o$-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.