



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 06:21 AM UTC

PDB ID : 7TWL / pdb_00007twl
Title : Structure of a borosin methyltransferase from *Mycena rosella* with peptide A2 (MroMA2) in complex with SAH
Authors : Zheng, Y.; Ongpipattanakul, C.; Nair, S.K.
Deposited on : 2022-02-07
Resolution : 1.86 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

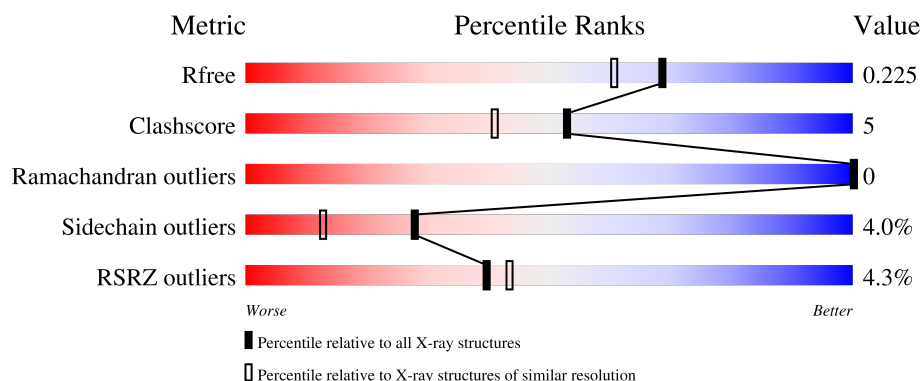
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	400	 4% 86% 10% ..
1	B	400	 2% 85% 10% ..
1	C	400	 7% 83% 12% ..
1	D	400	 4% 88% 8% ..

2 Entry composition [i](#)

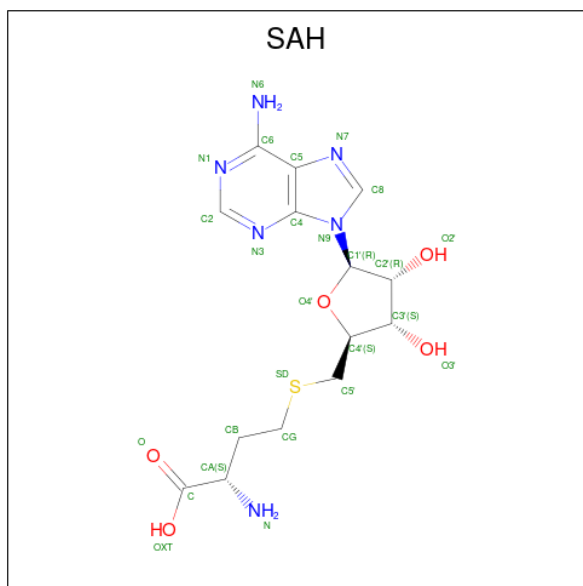
There are 3 unique types of molecules in this entry. The entry contains 12984 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MroMA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	3	0
			3012	1927	509	563	13			
1	B	388	Total	C	N	O	S	0	4	0
			3029	1936	518	562	13			
1	C	387	Total	C	N	O	S	0	5	0
			3015	1930	511	561	13			
1	D	389	Total	C	N	O	S	0	2	0
			3009	1923	509	564	13			

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: 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		

Continued on next page...

Continued from previous page...

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		

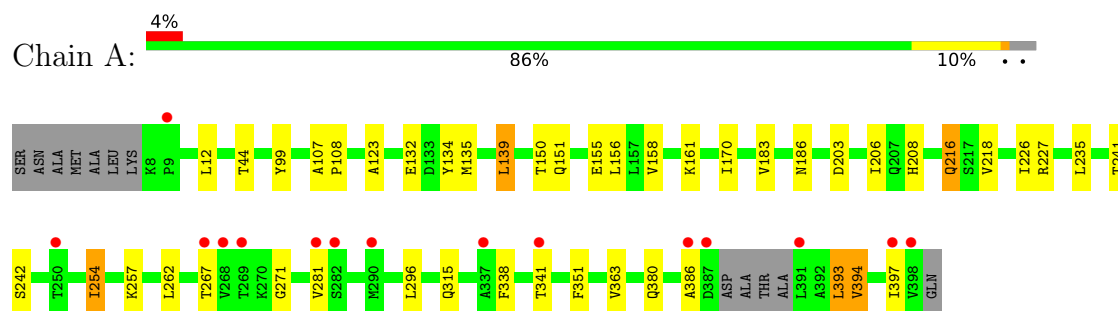
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	224	Total	O	0	0
			224	224		
3	B	236	Total	O	0	0
			236	236		
3	C	194	Total	O	0	0
			194	194		
3	D	161	Total	O	0	0
			161	161		

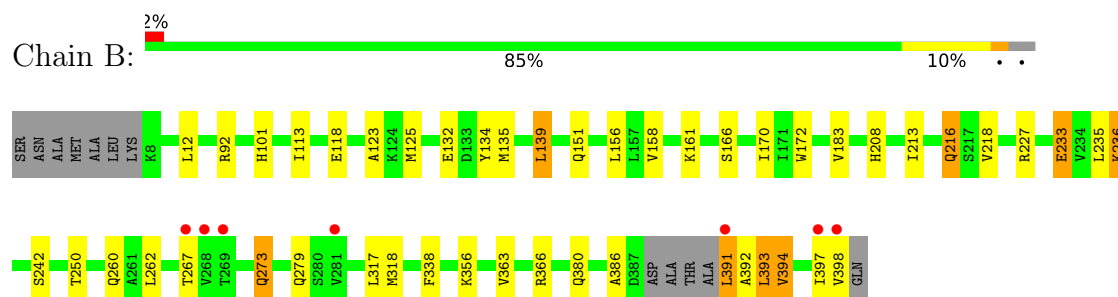
3 Residue-property plots [i](#)

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.

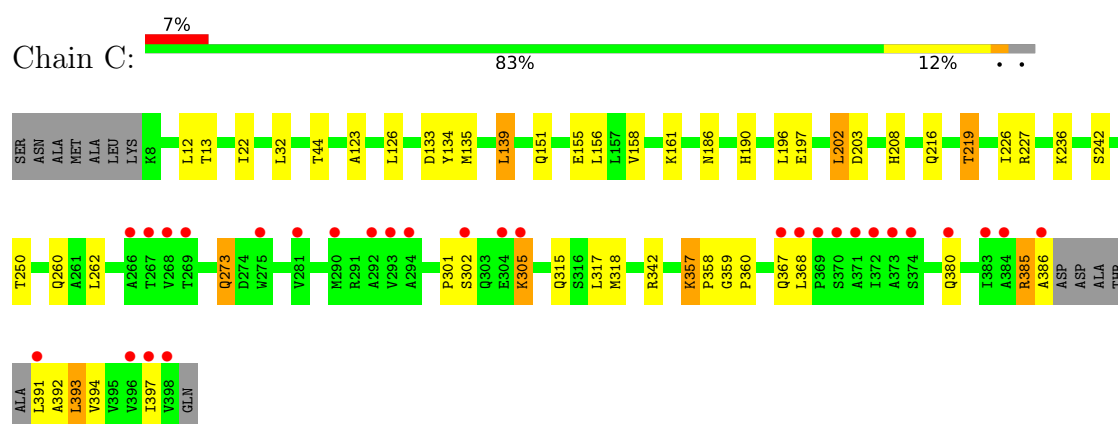
• Molecule 1: MroMA2



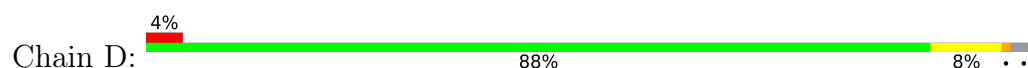
• Molecule 1: MroMA2

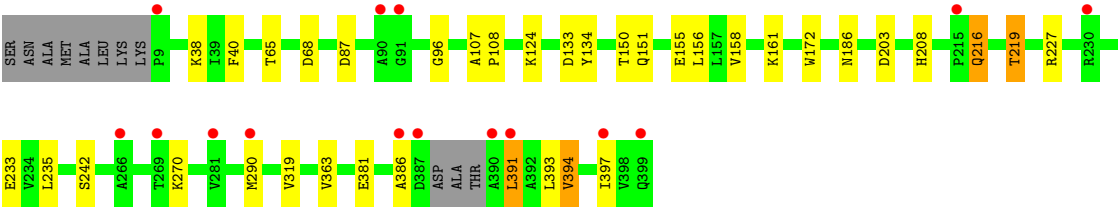


• Molecule 1: MroMA2



• Molecule 1: MroMA2





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.11Å 125.23Å 203.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.86 25.00 – 1.86	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.00-1.86) 99.9 (25.00-1.86)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.188 , 0.223 0.191 , 0.225	Depositor DCC
R_{free} test set	7291 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12984	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 2.96% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, MVA, 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	0.51	0/3068	0.93	0/4162
1	B	0.51	1/3088 (0.0%)	0.91	0/4186
1	C	0.49	0/3077	0.93	2/4173 (0.0%)
1	D	0.49	0/3062	0.90	0/4154
All	All	0.50	1/12295 (0.0%)	0.92	2/16675 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	101	HIS	CE1-NE2	5.43	1.38	1.32

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	219	THR	CB-CA-C	6.10	119.41	109.90
1	C	357	LYS	CB-CA-C	5.46	117.65	109.63

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3012	0	3029	32	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3029	0	3057	38	0
1	C	3015	0	3037	46	0
1	D	3009	0	3018	31	0
2	A	26	0	19	0	0
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	2	0
3	B	236	0	0	8	0
3	C	194	0	0	5	0
3	D	161	0	0	6	0
All	All	12984	0	12217	123	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 (123) 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:B:273:GLN:HG3	3:B:778:HOH:O	1.47	1.11
1:C:273:GLN:HG3	3:C:676:HOH:O	1.52	1.06
1:C:357:LYS:HD2	1:C:358:PRO:HD2	1.38	1.01
1:B:250:THR:HB	3:B:743:HOH:O	1.65	0.95
1:B:213:ILE:HG23	3:B:611:HOH:O	1.79	0.81
1:D:203:ASP:OD1	1:D:227:ARG:NH1	2.14	0.80
1:B:135:MET:HG3	1:B:139:LEU:HD22	1.66	0.78
1:C:135:MET:HG3	1:C:139:LEU:HD22	1.69	0.75
1:D:38:LYS:HD3	1:D:87:ASP:OD2	1.88	0.74
1:B:92[B]:ARG:NH2	3:B:601:HOH:O	2.20	0.73
1:B:156:LEU:HD12	1:B:161:LYS:HB2	1.74	0.70
1:C:32[B]:LEU:HD12	3:C:765:HOH:O	1.90	0.69
1:C:305:LYS:HD3	1:D:65:THR:HG22	1.73	0.68
1:B:208:HIS:HD2	3:B:635:HOH:O	1.75	0.68
1:C:161:LYS:HE3	3:D:613:HOH:O	1.92	0.68
1:C:357:LYS:HG3	1:C:360:PRO:HD2	1.77	0.67
1:C:367:GLN:HE21	1:C:368:LEU:H	1.42	0.66
1:C:317:LEU:HD12	1:C:342:ARG:HG3	1.77	0.66
1:C:385:ARG:HG3	1:C:386:ALA:N	2.11	0.65
1:C:397:ILE:HG12	1:D:155:GLU:HB2	1.77	0.65
1:A:156:LEU:HD12	1:A:161:LYS:HB2	1.78	0.64
1:D:219:THR:HG22	3:D:614:HOH:O	1.98	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:MET:HG3	1:A:139:LEU:HD22	1.78	0.63
1:C:203:ASP:OD1	1:C:227:ARG:NH2	2.32	0.63
1:C:301:PRO:HA	1:D:68:ASP:OD2	1.99	0.63
1:C:208:HIS:HE1	1:C:242:SER:OG	1.82	0.62
1:C:13:THR:HG21	1:C:32[B]:LEU:HD21	1.81	0.62
1:C:208:HIS:HD2	3:C:696:HOH:O	1.82	0.62
1:B:366[A]:ARG:HD3	3:B:787:HOH:O	2.00	0.61
1:A:132:GLU:HG2	1:A:170:ILE:HD13	1.85	0.59
1:D:208:HIS:HD2	3:D:603:HOH:O	1.85	0.59
1:A:271:GLY:HA2	1:A:397:ILE:O	2.02	0.59
1:A:44:THR:HG22	1:B:391:LEU:HD23	1.85	0.58
1:A:155:GLU:HB2	1:B:397:ILE:HG21	1.84	0.58
1:A:208:HIS:HD2	3:A:684:HOH:O	1.87	0.57
1:A:208:HIS:HE1	1:A:242:SER:OG	1.88	0.57
1:B:397:ILE:HD12	1:B:398:VAL:HG13	1.86	0.57
1:C:32[A]:LEU:HD11	1:C:126:LEU:HD11	1.87	0.56
1:A:158:VAL:HG12	1:B:262:LEU:HD13	1.87	0.55
1:D:156:LEU:HD12	1:D:161:LYS:HB2	1.88	0.55
1:C:197:GLU:HG2	1:C:202:LEU:HD22	1.89	0.55
1:C:385:ARG:HG3	1:C:386:ALA:H	1.71	0.55
1:D:208:HIS:HE1	1:D:242:SER:OG	1.89	0.55
1:C:305:LYS:CD	1:D:65:THR:HG22	2.37	0.54
1:C:393:MLE:HN2	1:C:393:MLE:HG	1.88	0.54
1:C:156:LEU:HD12	1:C:161:LYS:HB2	1.89	0.54
1:A:44:THR:HG22	1:B:391:LEU:CD2	2.39	0.53
1:C:357:LYS:HG3	1:C:360:PRO:CD	2.38	0.53
1:A:158:VAL:CG1	1:B:262:LEU:HD13	2.40	0.52
1:C:155:GLU:HB2	1:D:397:ILE:HG12	1.90	0.52
1:B:317:LEU:HD11	1:B:338:PHE:HE2	1.75	0.51
1:D:363:VAL:HG21	1:D:386:ALA:HB2	1.91	0.51
1:B:132:GLU:HG3	1:B:172:TRP:CZ2	2.45	0.51
1:C:196:LEU:HB3	1:C:226:ILE:HD12	1.93	0.51
1:C:394:MVA:HN2	1:C:394:MVA:HG22	1.92	0.51
1:A:158:VAL:HG12	1:B:262:LEU:CD1	2.41	0.51
1:A:206:ILE:CG2	1:A:226:ILE:HD11	2.41	0.50
1:A:241:THR:HA	1:B:391:LEU:HD12	1.94	0.50
1:B:213:ILE:CG2	3:B:611:HOH:O	2.48	0.49
1:B:233:GLU:HA	1:B:236:LYS:HE2	1.93	0.49
1:B:132:GLU:HG2	1:B:170:ILE:HD13	1.93	0.49
3:A:605:HOH:O	1:B:161:LYS:HE3	2.12	0.49
1:B:279:GLN:NE2	3:B:602:HOH:O	2.38	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:13:THR:HG21	1:C:32[B]:LEU:CD2	2.44	0.48
1:A:206:ILE:HG23	1:A:226:ILE:HD11	1.94	0.48
1:C:397:ILE:HG12	1:D:155:GLU:CB	2.41	0.48
1:A:338:PHE:O	1:A:341:THR:HB	2.14	0.48
1:A:351:PHE:CE2	1:A:380:GLN:HG3	2.50	0.47
1:C:392:ALA:HA	1:C:393:MLE:HN1	1.59	0.47
1:B:397:ILE:HD12	1:B:397:ILE:C	2.39	0.47
1:D:150:THR:HG23	1:D:172:TRP:NE1	2.30	0.47
1:D:216:GLN:NE2	1:D:216:GLN:H	2.13	0.47
1:B:208:HIS:HE1	1:B:242:SER:OG	1.97	0.47
1:B:235:LEU:C	1:B:235:LEU:HD23	2.40	0.47
1:C:318:MET:HE1	1:D:216:GLN:HE22	1.80	0.46
3:C:643:HOH:O	1:D:161:LYS:HE3	2.15	0.46
1:C:155:GLU:CB	1:D:397:ILE:HG12	2.46	0.45
1:B:393:MLE:HA	1:B:394:MVA:HN1	1.81	0.45
1:C:357:LYS:HE3	1:C:359:GLY:H	1.82	0.45
1:C:32[A]:LEU:CD1	1:C:126:LEU:HD11	2.45	0.45
1:A:262:LEU:CD1	1:B:158:VAL:HG12	2.47	0.45
1:A:186:ASN:HD22	1:A:186:ASN:HA	1.63	0.44
1:A:393:MLE:HA	1:A:394:MVA:HN1	1.76	0.44
1:B:392:ALA:HA	1:B:393:MLE:HN1	1.67	0.43
1:C:190:HIS:HE1	3:C:647:HOH:O	2.01	0.43
1:D:107:ALA:N	1:D:108:PRO:HD2	2.34	0.43
1:C:12:LEU:O	1:C:123:ALA:HA	2.19	0.43
1:B:317:LEU:CD1	1:B:338:PHE:HE2	2.31	0.43
1:B:363:VAL:HG21	1:B:386:ALA:HB2	2.00	0.43
1:A:12:LEU:O	1:A:123:ALA:HA	2.19	0.42
1:B:216:GLN:H	1:B:216:GLN:HE21	1.67	0.42
1:C:155:GLU:HA	1:C:158:VAL:HG22	2.00	0.42
1:D:219:THR:HG23	3:D:737:HOH:O	2.18	0.42
1:D:270:LYS:HE2	3:D:685:HOH:O	2.19	0.42
1:C:391:LEU:CD2	1:C:393:MLE:HD22	2.49	0.42
1:C:315:GLN:HE21	1:C:315:GLN:HA	1.85	0.42
1:A:161:LYS:NZ	1:B:166:SER:OG	2.52	0.42
1:C:202:LEU:HB3	1:C:227:ARG:HB3	2.01	0.42
1:A:254:ILE:H	1:A:254:ILE:HG12	1.43	0.42
1:D:216:GLN:H	1:D:216:GLN:HE21	1.68	0.42
1:A:296:LEU:C	1:A:296:LEU:HD23	2.43	0.41
1:B:113:ILE:HD12	1:B:125:MET:HE3	2.02	0.41
1:A:363:VAL:HG21	1:A:386:ALA:HB2	2.01	0.41
1:A:394:MVA:HN2	1:A:394:MVA:HG22	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:394:MVA:HN2	1:B:394:MVA:HG22	2.03	0.41
1:B:12:LEU:O	1:B:123:ALA:HA	2.20	0.41
1:D:219:THR:CG2	3:D:614:HOH:O	2.61	0.41
1:A:99:TYR:CZ	1:B:391:LEU:HD21	2.56	0.41
1:C:133:ASP:OD2	1:D:133:ASP:OD2	2.37	0.41
1:C:22:ILE:HD13	1:D:319:VAL:HG22	2.02	0.41
1:C:208:HIS:CE1	1:C:242:SER:OG	2.70	0.41
1:A:315:GLN:NE2	1:A:315:GLN:HA	2.36	0.41
1:C:262:LEU:CD1	1:D:158:VAL:HG12	2.51	0.41
1:D:186:ASN:HD22	1:D:186:ASN:HA	1.67	0.41
1:A:132:GLU:OE2	1:A:150:THR:OG1	2.21	0.40
1:A:107:ALA:N	1:A:108:PRO:HD2	2.36	0.40
1:A:216:GLN:HE22	1:B:318:MET:HE1	1.87	0.40
1:C:44:THR:HG22	1:D:391:LEU:CD2	2.51	0.40
1:D:394:MVA:HG22	1:D:394:MVA:HN2	2.03	0.40
1:A:203:ASP:OD1	1:A:227:ARG:NH1	2.45	0.40
1:D:40:PHE:O	1:D:96:GLY:HA2	2.21	0.40
1:C:44:THR:CG2	1:D:391:LEU:CD2	2.99	0.40
1:C:186:ASN:HD22	1:C:186:ASN:HA	1.72	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	385/400 (96%)	377 (98%)	8 (2%)	0	100	100
1	B	386/400 (96%)	379 (98%)	7 (2%)	0	100	100
1	C	386/400 (96%)	378 (98%)	8 (2%)	0	100	100
1	D	385/400 (96%)	376 (98%)	9 (2%)	0	100	100
All	All	1542/1600 (96%)	1510 (98%)	32 (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	321/327 (98%)	310 (97%)	11 (3%)	32	17
1	B	323/327 (99%)	307 (95%)	16 (5%)	22	8
1	C	321/327 (98%)	307 (96%)	14 (4%)	25	10
1	D	320/327 (98%)	310 (97%)	10 (3%)	35	20
All	All	1285/1308 (98%)	1234 (96%)	51 (4%)	28	13

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	TYR
1	A	139	LEU
1	A	151	GLN
1	A	183	VAL
1	A	216	GLN
1	A	218	VAL
1	A	235	LEU
1	A	254	ILE
1	A	257	LYS
1	A	267	THR
1	A	281	VAL
1	B	118	GLU
1	B	134	TYR
1	B	139	LEU
1	B	151	GLN
1	B	183	VAL
1	B	216	GLN
1	B	218	VAL
1	B	227	ARG
1	B	233	GLU
1	B	236	LYS
1	B	260	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	267	THR
1	B	273	GLN
1	B	356	LYS
1	B	380	GLN
1	B	391	LEU
1	C	134	TYR
1	C	139	LEU
1	C	151	GLN
1	C	202	LEU
1	C	216	GLN
1	C	219	THR
1	C	236	LYS
1	C	250	THR
1	C	260	GLN
1	C	273	GLN
1	C	302	SER
1	C	305	LYS
1	C	380	GLN
1	C	385	ARG
1	D	124	LYS
1	D	134	TYR
1	D	151	GLN
1	D	216	GLN
1	D	219	THR
1	D	233	GLU
1	D	235	LEU
1	D	290	MET
1	D	381	GLU
1	D	391	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	186	ASN
1	A	190	HIS
1	A	208	HIS
1	A	216	GLN
1	A	303	GLN
1	A	309	HIS
1	A	315	GLN
1	A	343	ASN
1	A	367	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	186	ASN
1	B	208	HIS
1	B	216	GLN
1	B	273	GLN
1	B	279	GLN
1	B	315	GLN
1	B	343	ASN
1	B	380	GLN
1	C	186	ASN
1	C	190	HIS
1	C	208	HIS
1	C	216	GLN
1	C	273	GLN
1	C	279	GLN
1	C	309	HIS
1	C	315	GLN
1	C	367	GLN
1	C	380	GLN
1	D	186	ASN
1	D	208	HIS
1	D	216	GLN
1	D	260	GLN
1	D	279	GLN
1	D	340	ASN
1	D	343	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	393	1	7,8,9	0.52	0	7,9,11	1.52	2 (28%)
1	MLE	C	393	1	7,8,9	0.63	0	7,9,11	1.61	1 (14%)
1	MVA	C	394	1	6,7,8	0.71	0	6,8,10	1.09	0
1	MVA	D	394	1	6,7,8	0.64	0	6,8,10	1.13	1 (16%)
1	MLE	A	393	1	7,8,9	0.53	0	7,9,11	1.85	1 (14%)
1	MLE	B	393	1	7,8,9	0.54	0	7,9,11	1.41	2 (28%)
1	MVA	B	394	1	6,7,8	0.57	0	6,8,10	1.44	1 (16%)
1	MVA	A	394	1	6,7,8	0.72	0	6,8,10	1.49	1 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLE	D	393	1	-	0/5/8/10	-
1	MLE	C	393	1	-	0/5/8/10	-
1	MVA	C	394	1	-	4/6/8/10	-
1	MVA	D	394	1	-	5/6/8/10	-
1	MLE	A	393	1	-	0/5/8/10	-
1	MLE	B	393	1	-	0/5/8/10	-
1	MVA	B	394	1	-	5/6/8/10	-
1	MVA	A	394	1	-	5/6/8/10	-

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	MLE	CB-CA-N	4.31	117.14	110.59
1	C	393	MLE	CB-CA-N	3.44	115.81	110.59
1	A	394	MVA	CB-CA-N	3.05	115.14	111.17
1	B	394	MVA	CB-CA-N	2.61	114.57	111.17
1	B	393	MLE	CB-CA-N	2.55	114.47	110.59
1	D	393	MLE	CB-CA-N	2.44	114.30	110.59
1	B	393	MLE	O-C-CA	-2.23	119.03	124.77
1	D	394	MVA	CB-CA-N	2.18	114.01	111.17
1	D	393	MLE	O-C-CA	-2.16	119.21	124.77

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	394	MVA	N-CA-CB-CG1
1	A	394	MVA	N-CA-CB-CG2
1	A	394	MVA	C-CA-CB-CG1
1	A	394	MVA	C-CA-CB-CG2
1	B	394	MVA	N-CA-CB-CG1
1	B	394	MVA	N-CA-CB-CG2
1	B	394	MVA	C-CA-CB-CG1
1	B	394	MVA	C-CA-CB-CG2
1	C	394	MVA	N-CA-CB-CG1
1	C	394	MVA	N-CA-CB-CG2
1	C	394	MVA	C-CA-CB-CG1
1	C	394	MVA	C-CA-CB-CG2
1	D	394	MVA	N-CA-CB-CG1
1	D	394	MVA	N-CA-CB-CG2
1	D	394	MVA	C-CA-CB-CG1
1	D	394	MVA	C-CA-CB-CG2
1	A	394	MVA	O-C-CA-CB
1	B	394	MVA	O-C-CA-CB
1	D	394	MVA	O-C-CA-CB

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	393	MLE	3	0
1	C	394	MVA	1	0
1	D	394	MVA	1	0
1	A	393	MLE	1	0
1	B	393	MLE	2	0
1	B	394	MVA	2	0
1	A	394	MVA	2	0

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	$\# Z > 2$
2	SAH	A	500	-	27,28,28	0.48	0	36,40,40	0.67	1 (2%)
2	SAH	C	500	-	27,28,28	0.45	0	36,40,40	0.59	1 (2%)
2	SAH	D	500	-	27,28,28	0.49	1 (3%)	36,40,40	0.64	1 (2%)
2	SAH	B	500	-	27,28,28	0.47	0	36,40,40	0.61	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SAH	A	500	-	-	2/15/31/31	0/3/3/3
2	SAH	C	500	-	-	2/15/31/31	0/3/3/3
2	SAH	D	500	-	-	3/15/31/31	0/3/3/3
2	SAH	B	500	-	-	2/15/31/31	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	SAH	OXT-C	-2.16	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	SAH	OXT-C-O	-2.71	117.93	124.08
2	D	500	SAH	OXT-C-O	-2.41	118.61	124.08
2	C	500	SAH	OXT-C-O	-2.25	118.97	124.08
2	B	500	SAH	OXT-C-O	-2.04	119.45	124.08

There are no chirality outliers.

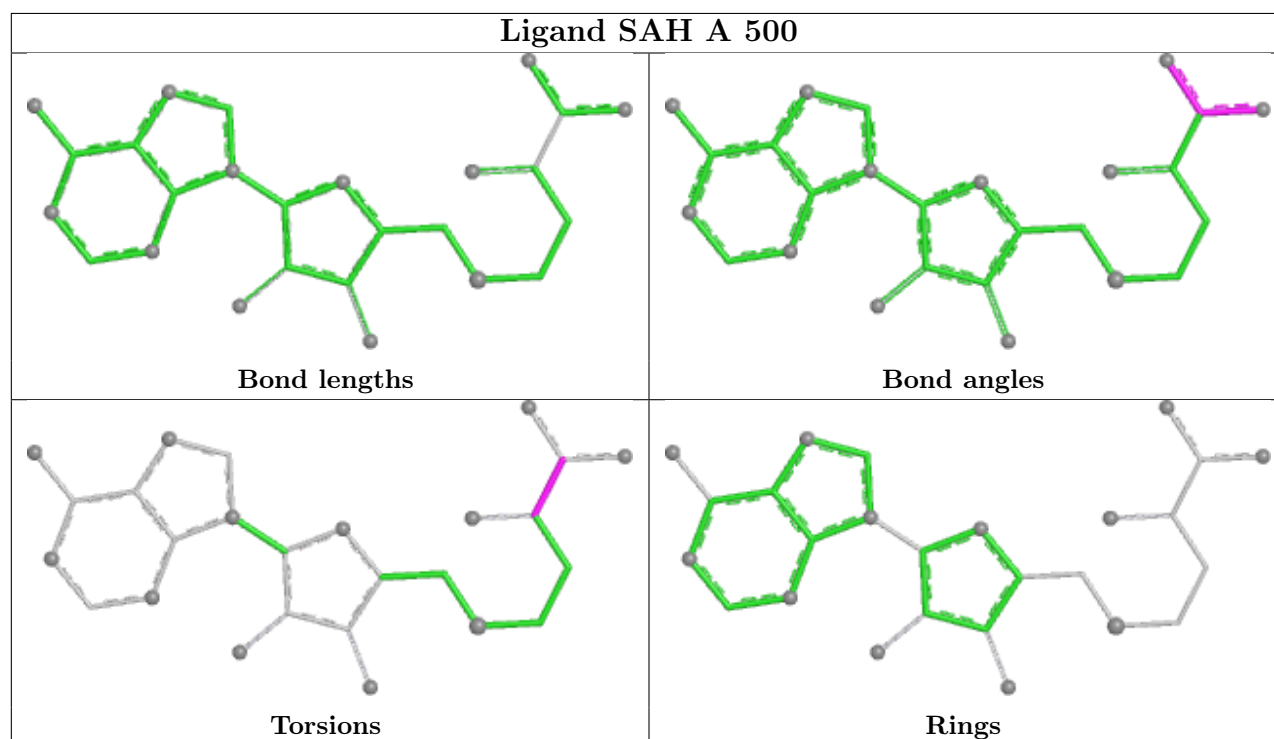
All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	500	SAH	C3'-C4'-C5'-SD
2	D	500	SAH	O-C-CA-CB
2	B	500	SAH	OXT-C-CA-CB
2	D	500	SAH	OXT-C-CA-CB
2	B	500	SAH	O-C-CA-CB
2	A	500	SAH	O-C-CA-CB
2	A	500	SAH	OXT-C-CA-CB
2	C	500	SAH	OXT-C-CA-CB
2	C	500	SAH	O-C-CA-CB

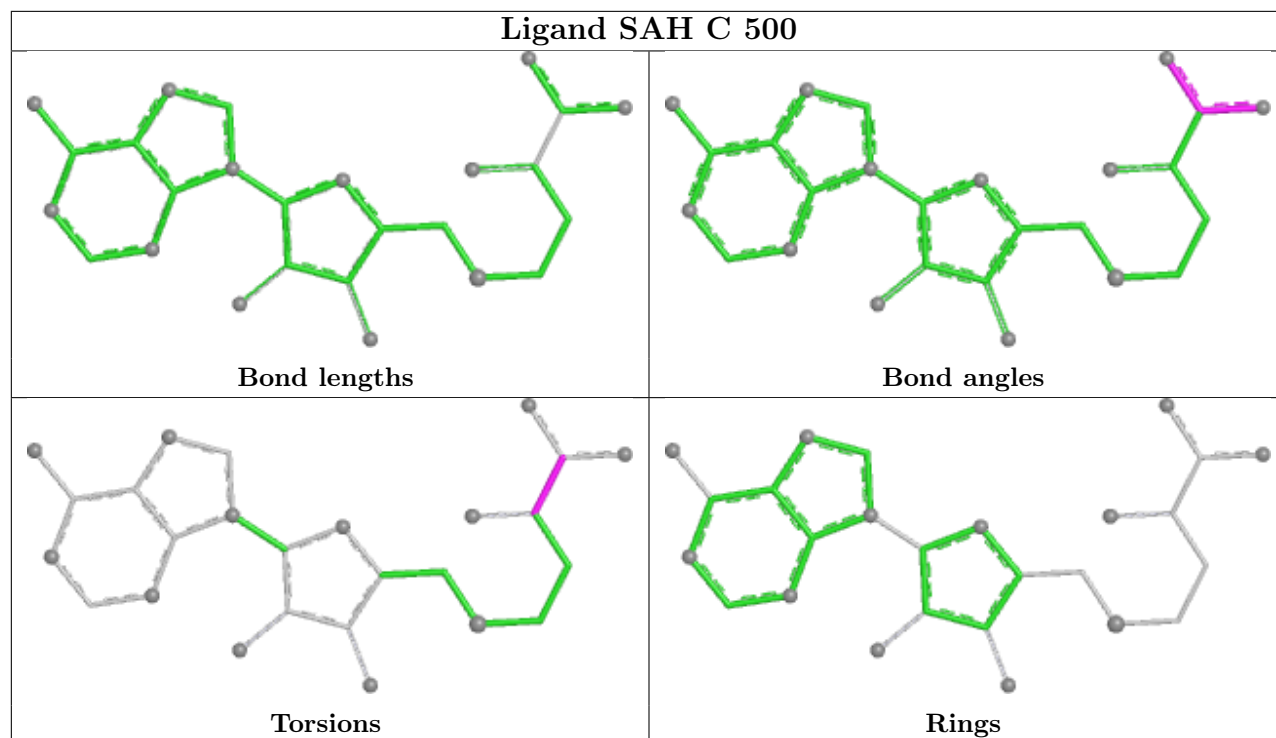
There are no ring outliers.

No monomer is involved in short contacts.

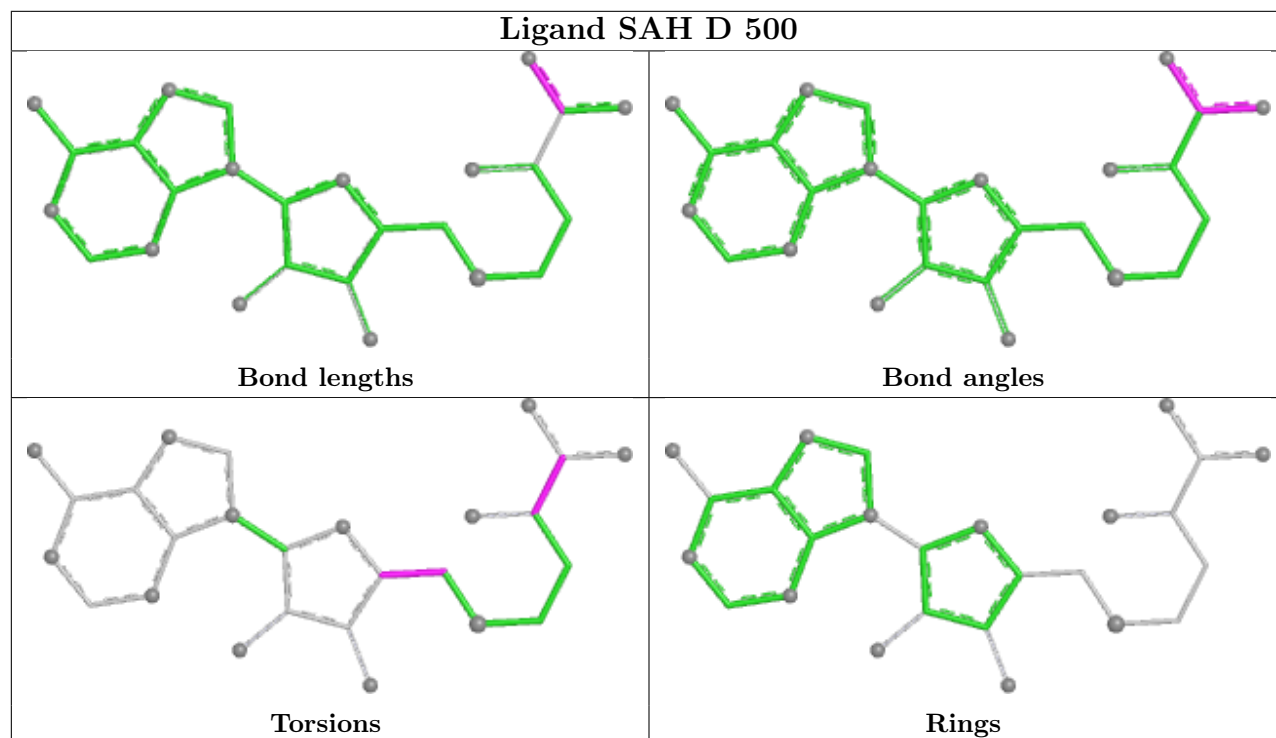
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

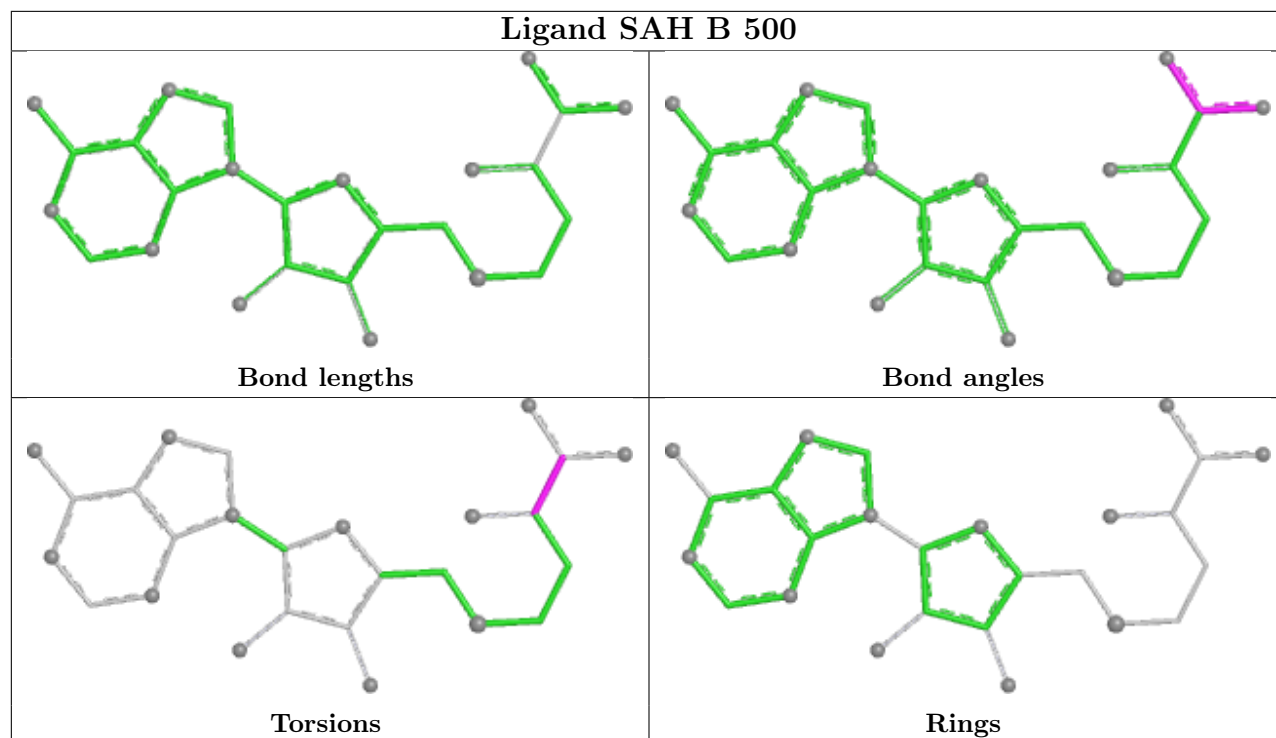


Ligand SAH C 500



Ligand SAH D 500





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	386/400 (96%)	0.04	15 (3%) 43 47	14, 30, 56, 95	3 (0%)
1	B	386/400 (96%)	-0.15	7 (1%) 67 71	15, 28, 46, 75	4 (1%)
1	C	385/400 (96%)	0.23	29 (7%) 20 22	15, 31, 66, 117	5 (1%)
1	D	387/400 (96%)	0.21	15 (3%) 43 47	18, 35, 54, 104	2 (0%)
All	All	1544/1600 (96%)	0.08	66 (4%) 40 43	14, 31, 58, 117	14 (0%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	268	VAL	6.2
1	A	391	LEU	5.0
1	A	281	VAL	4.5
1	C	281	VAL	4.4
1	A	268	VAL	4.4
1	C	391	LEU	4.4
1	B	268	VAL	4.0
1	D	390	ALA	4.0
1	D	281	VAL	3.9
1	B	391	LEU	3.7
1	C	269	THR	3.7
1	B	397	ILE	3.7
1	C	397	ILE	3.6
1	B	281	VAL	3.6
1	C	398	VAL	3.6
1	D	9	PRO	3.6
1	B	398	VAL	3.5
1	A	267	THR	3.4
1	D	386	ALA	3.4
1	C	383	ILE	3.1
1	A	397	ILE	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	90	ALA	2.8
1	C	368	LEU	2.8
1	B	269	THR	2.8
1	A	398	VAL	2.8
1	C	371	ALA	2.8
1	A	341	THR	2.8
1	C	384	ALA	2.7
1	C	305	LYS	2.7
1	D	387	ASP	2.7
1	C	396	VAL	2.7
1	C	292	ALA	2.7
1	B	267	THR	2.7
1	C	374	SER	2.6
1	C	369	PRO	2.6
1	C	373	ALA	2.6
1	C	372	ILE	2.6
1	C	386	ALA	2.5
1	C	380	GLN	2.5
1	D	266	ALA	2.5
1	D	391	LEU	2.5
1	C	370	SER	2.5
1	A	269	THR	2.5
1	A	386	ALA	2.4
1	C	266	ALA	2.4
1	C	293	VAL	2.4
1	C	304	GLU	2.3
1	A	282	SER	2.3
1	C	290	MET	2.3
1	C	267	THR	2.2
1	D	269	THR	2.2
1	D	397	ILE	2.1
1	A	250	THR	2.1
1	C	275	TRP	2.1
1	A	290	MET	2.1
1	D	230	ARG	2.1
1	D	91	GLY	2.1
1	D	215	PRO	2.1
1	D	399	GLN	2.1
1	A	337	ALA	2.1
1	C	302	SER	2.0
1	D	290	MET	2.0
1	A	9	PRO	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	294	ALA	2.0
1	A	387	ASP	2.0
1	C	367	GLN	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	MVA	C	394	8/9	0.91	0.12	34,37,39,39	0
1	MVA	B	394	8/9	0.92	0.10	21,25,26,29	0
1	MLE	C	393	9/10	0.92	0.11	35,40,42,44	0
1	MLE	D	393	9/10	0.93	0.09	26,28,31,32	0
1	MVA	A	394	8/9	0.93	0.08	25,26,28,29	0
1	MLE	B	393	9/10	0.94	0.09	26,29,36,38	0
1	MLE	A	393	9/10	0.94	0.10	27,30,38,40	0
1	MVA	D	394	8/9	0.97	0.04	23,25,27,27	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

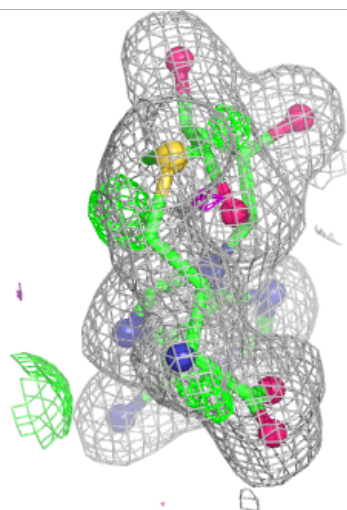
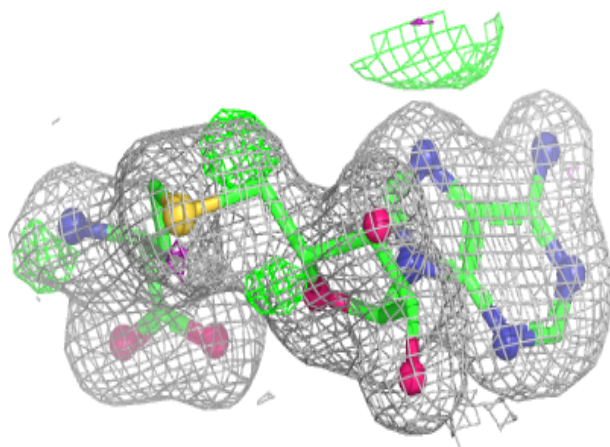
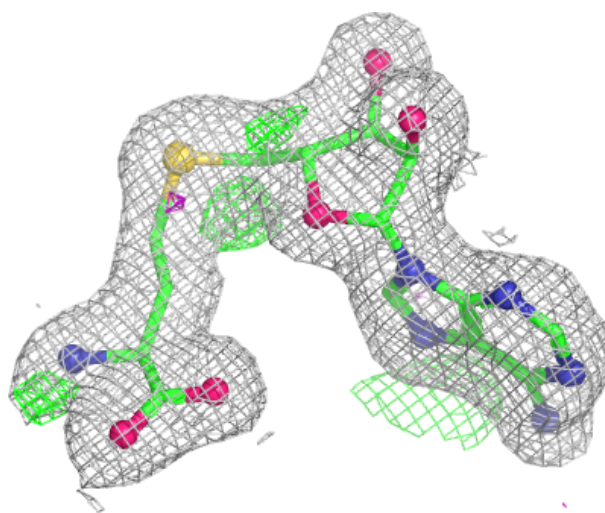
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SAH	D	500	26/26	0.95	0.06	23,26,32,35	0
2	SAH	B	500	26/26	0.97	0.06	19,20,22,25	0
2	SAH	C	500	26/26	0.98	0.05	20,23,24,25	0
2	SAH	A	500	26/26	0.98	0.04	18,20,21,22	0

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.

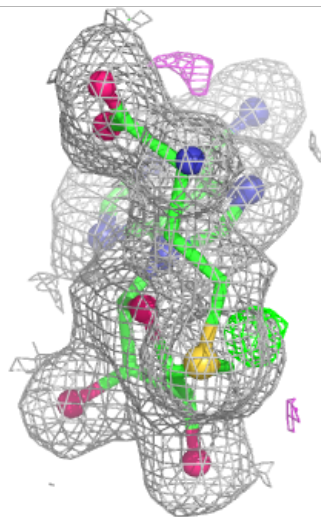
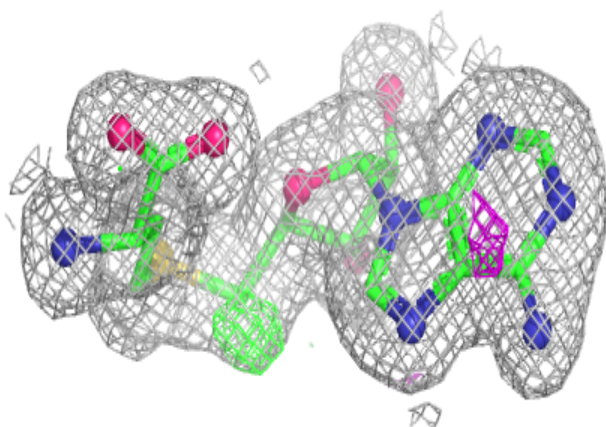
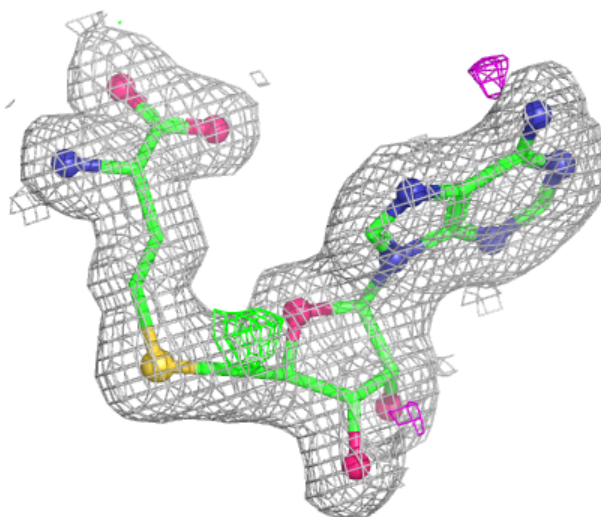
Electron density around SAH D 500:

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



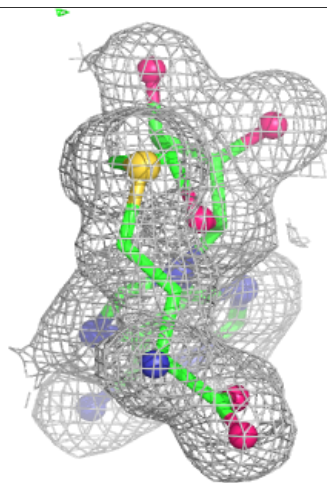
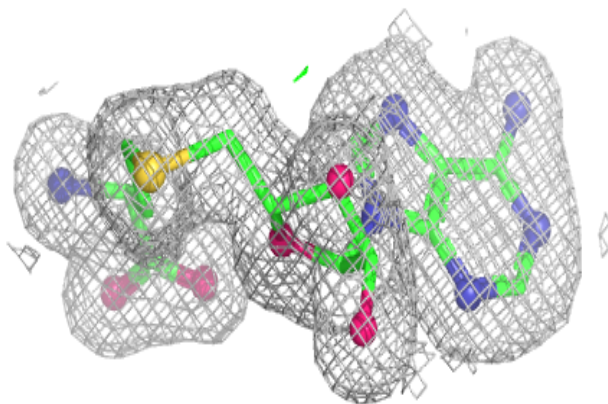
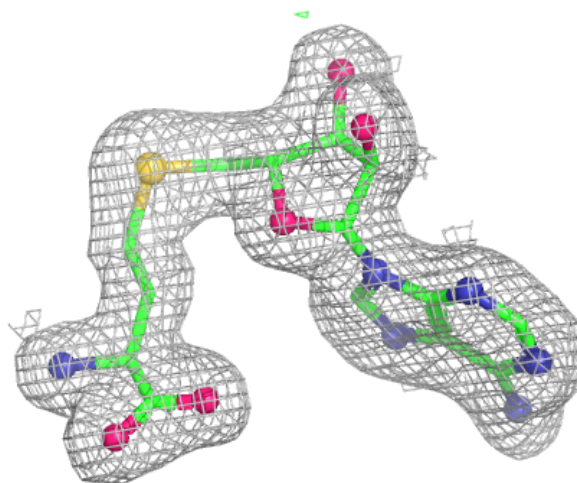
Electron density around SAH B 500:

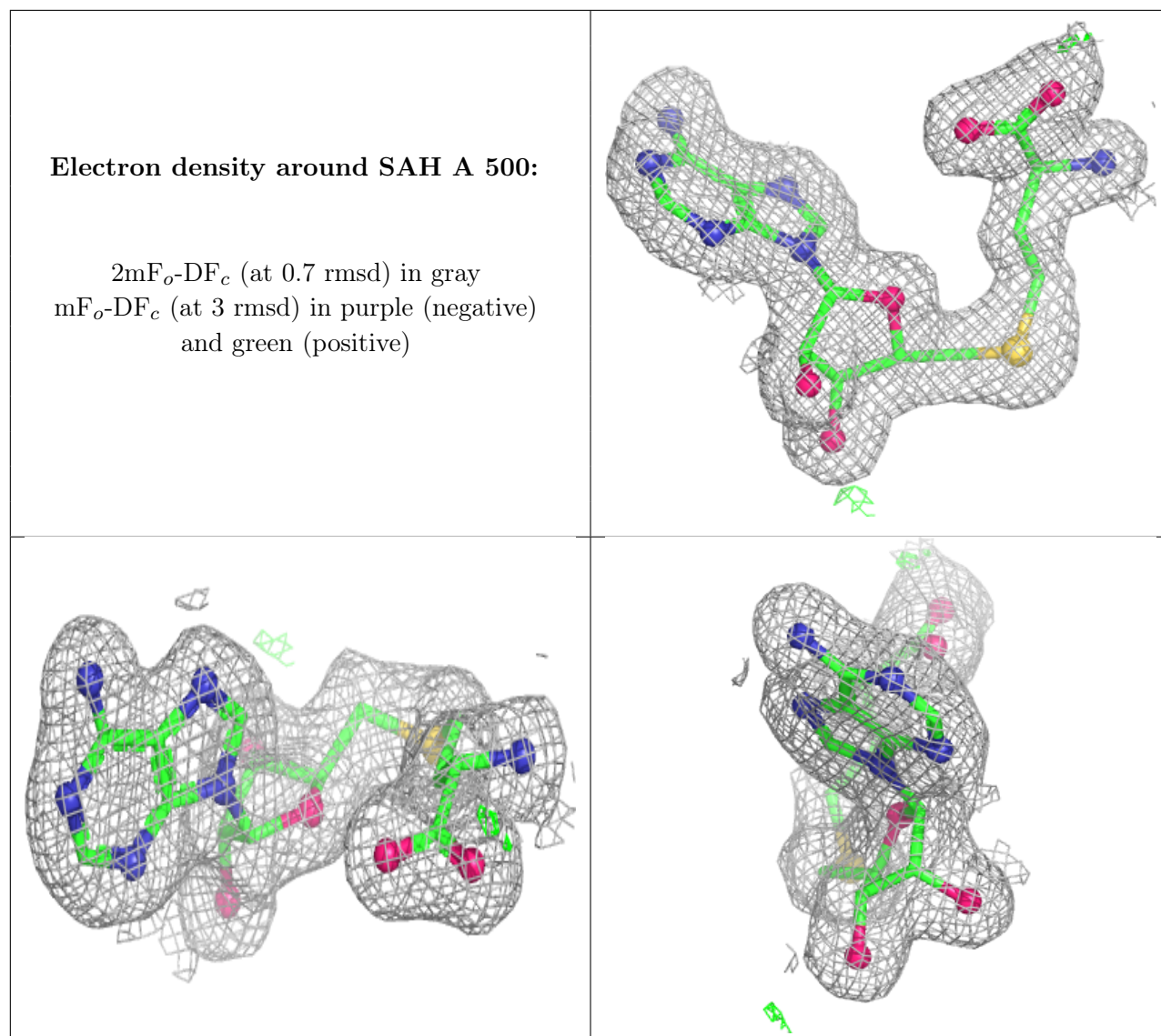
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.5 Other polymers [i](#)

There are no such residues in this entry.