



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:55 PM UTC

PDB ID : 3G XO / pdb_00003gxo
Title : Structure of the Mitomycin 7-O-methyltransferase MmcR with bound Mitomycin A
Authors : Singh, S.; Chang, A.; Bingman, C.A.; Phillips Jr., G.N.; Thorson, J.S.
Deposited on : 2009-04-02
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

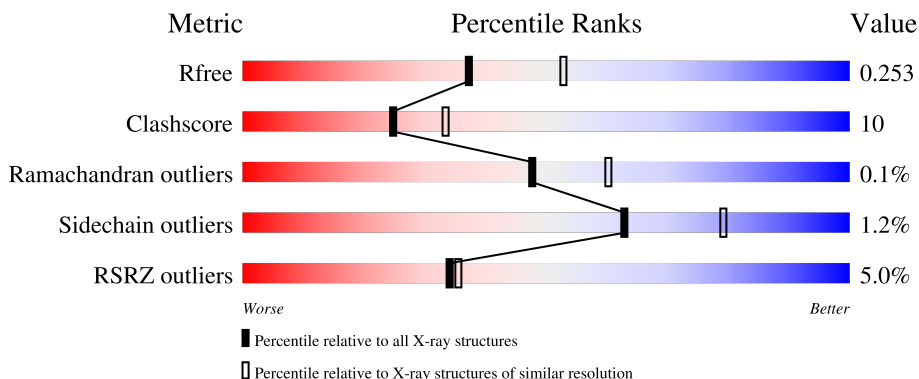
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	369	2% 79% 12% 8%
1	B	369	4% 73% 18% 8%
1	C	369	9% 69% 22% 8%
1	D	369	4% 69% 22% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10864 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 MmcR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	Se	0	0	0
			2574	1618	463	488	2	3			
1	D	339	Total	C	N	O	S	Se	0	1	0
			2585	1624	467	489	2	3			
1	C	339	Total	C	N	O	S	Se	0	1	0
			2585	1624	467	489	2	3			
1	B	339	Total	C	N	O	S	Se	0	1	0
			2585	1624	467	489	2	3			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	expression tag	UNP Q9X5T6
A	-18	GLY	-	expression tag	UNP Q9X5T6
A	-17	SER	-	expression tag	UNP Q9X5T6
A	-16	SER	-	expression tag	UNP Q9X5T6
A	-15	HIS	-	expression tag	UNP Q9X5T6
A	-14	HIS	-	expression tag	UNP Q9X5T6
A	-13	HIS	-	expression tag	UNP Q9X5T6
A	-12	HIS	-	expression tag	UNP Q9X5T6
A	-11	HIS	-	expression tag	UNP Q9X5T6
A	-10	HIS	-	expression tag	UNP Q9X5T6
A	-9	SER	-	expression tag	UNP Q9X5T6
A	-8	SER	-	expression tag	UNP Q9X5T6
A	-7	GLY	-	expression tag	UNP Q9X5T6
A	-6	LEU	-	expression tag	UNP Q9X5T6
A	-5	VAL	-	expression tag	UNP Q9X5T6
A	-4	PRO	-	expression tag	UNP Q9X5T6
A	-3	ARG	-	expression tag	UNP Q9X5T6
A	-2	GLY	-	expression tag	UNP Q9X5T6
A	-1	SER	-	expression tag	UNP Q9X5T6
A	0	HIS	-	expression tag	UNP Q9X5T6
A	1	MSE	-	expression tag	UNP Q9X5T6

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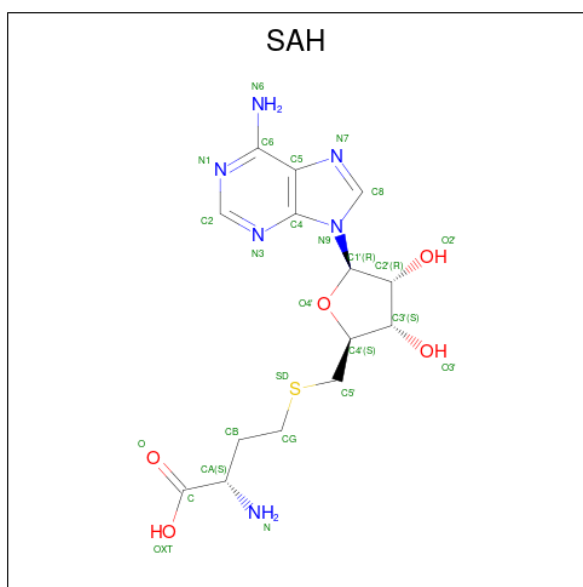
Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MSE	-	expression tag	UNP Q9X5T6
D	-18	GLY	-	expression tag	UNP Q9X5T6
D	-17	SER	-	expression tag	UNP Q9X5T6
D	-16	SER	-	expression tag	UNP Q9X5T6
D	-15	HIS	-	expression tag	UNP Q9X5T6
D	-14	HIS	-	expression tag	UNP Q9X5T6
D	-13	HIS	-	expression tag	UNP Q9X5T6
D	-12	HIS	-	expression tag	UNP Q9X5T6
D	-11	HIS	-	expression tag	UNP Q9X5T6
D	-10	HIS	-	expression tag	UNP Q9X5T6
D	-9	SER	-	expression tag	UNP Q9X5T6
D	-8	SER	-	expression tag	UNP Q9X5T6
D	-7	GLY	-	expression tag	UNP Q9X5T6
D	-6	LEU	-	expression tag	UNP Q9X5T6
D	-5	VAL	-	expression tag	UNP Q9X5T6
D	-4	PRO	-	expression tag	UNP Q9X5T6
D	-3	ARG	-	expression tag	UNP Q9X5T6
D	-2	GLY	-	expression tag	UNP Q9X5T6
D	-1	SER	-	expression tag	UNP Q9X5T6
D	0	HIS	-	expression tag	UNP Q9X5T6
D	1	MSE	-	expression tag	UNP Q9X5T6
C	-19	MSE	-	expression tag	UNP Q9X5T6
C	-18	GLY	-	expression tag	UNP Q9X5T6
C	-17	SER	-	expression tag	UNP Q9X5T6
C	-16	SER	-	expression tag	UNP Q9X5T6
C	-15	HIS	-	expression tag	UNP Q9X5T6
C	-14	HIS	-	expression tag	UNP Q9X5T6
C	-13	HIS	-	expression tag	UNP Q9X5T6
C	-12	HIS	-	expression tag	UNP Q9X5T6
C	-11	HIS	-	expression tag	UNP Q9X5T6
C	-10	HIS	-	expression tag	UNP Q9X5T6
C	-9	SER	-	expression tag	UNP Q9X5T6
C	-8	SER	-	expression tag	UNP Q9X5T6
C	-7	GLY	-	expression tag	UNP Q9X5T6
C	-6	LEU	-	expression tag	UNP Q9X5T6
C	-5	VAL	-	expression tag	UNP Q9X5T6
C	-4	PRO	-	expression tag	UNP Q9X5T6
C	-3	ARG	-	expression tag	UNP Q9X5T6
C	-2	GLY	-	expression tag	UNP Q9X5T6
C	-1	SER	-	expression tag	UNP Q9X5T6
C	0	HIS	-	expression tag	UNP Q9X5T6
C	1	MSE	-	expression tag	UNP Q9X5T6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MSE	-	expression tag	UNP Q9X5T6
B	-18	GLY	-	expression tag	UNP Q9X5T6
B	-17	SER	-	expression tag	UNP Q9X5T6
B	-16	SER	-	expression tag	UNP Q9X5T6
B	-15	HIS	-	expression tag	UNP Q9X5T6
B	-14	HIS	-	expression tag	UNP Q9X5T6
B	-13	HIS	-	expression tag	UNP Q9X5T6
B	-12	HIS	-	expression tag	UNP Q9X5T6
B	-11	HIS	-	expression tag	UNP Q9X5T6
B	-10	HIS	-	expression tag	UNP Q9X5T6
B	-9	SER	-	expression tag	UNP Q9X5T6
B	-8	SER	-	expression tag	UNP Q9X5T6
B	-7	GLY	-	expression tag	UNP Q9X5T6
B	-6	LEU	-	expression tag	UNP Q9X5T6
B	-5	VAL	-	expression tag	UNP Q9X5T6
B	-4	PRO	-	expression tag	UNP Q9X5T6
B	-3	ARG	-	expression tag	UNP Q9X5T6
B	-2	GLY	-	expression tag	UNP Q9X5T6
B	-1	SER	-	expression tag	UNP Q9X5T6
B	0	HIS	-	expression tag	UNP Q9X5T6
B	1	MSE	-	expression tag	UNP Q9X5T6

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



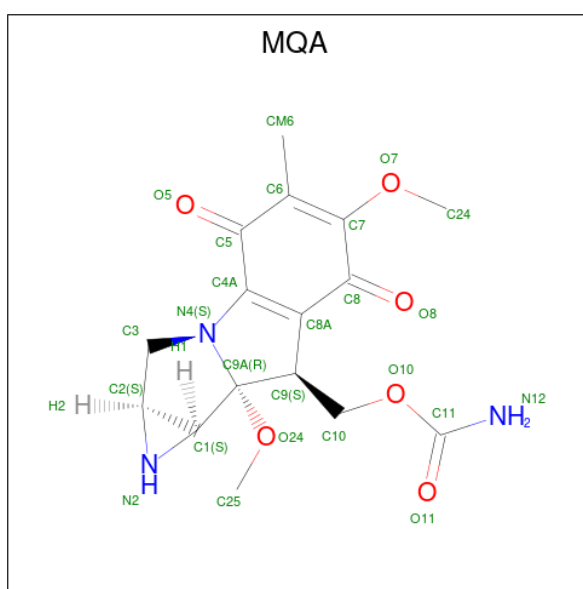
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

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

- Molecule 3 is [(1aS,8S,8aR,8bS)-6,8a-dimethoxy-5-methyl-4,7-dioxo-1,1a,2,4,7,8,8a,8b-octahydroazireno[2',3':3,4]pyrrolo[1,2-a]indol-8-yl)methyl carbamate (CCD ID: MQA) (formula: C₁₆H₁₉N₃O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			25	16	3	6		
3	D	1	Total	C	N	O	0	0
			25	16	3	6		
3	C	1	Total	C	N	O	0	0
			25	16	3	6		
3	B	1	Total	C	N	O	0	0
			25	16	3	6		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	2	Total	Ca	0	0
			2	2		

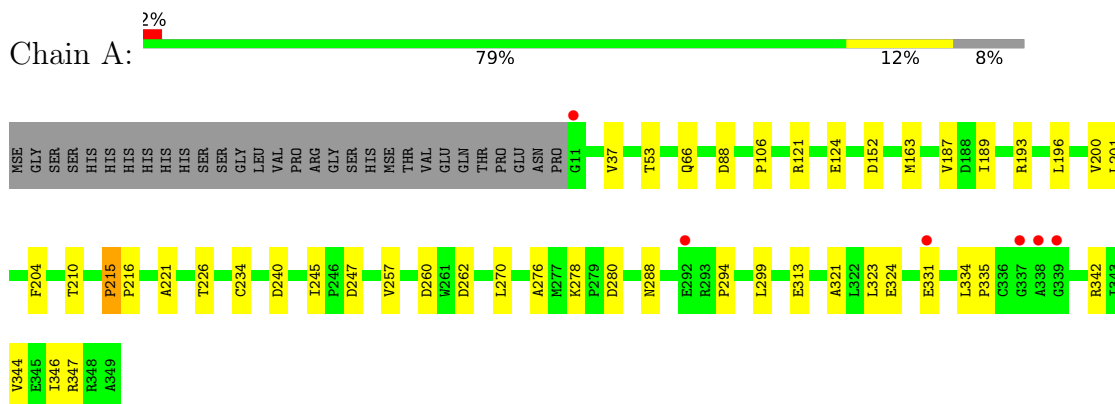
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	110	Total 110	O 110	0	0
5	D	70	Total 70	O 70	0	0
5	C	72	Total 72	O 72	0	0
5	B	77	Total 77	O 77	0	0

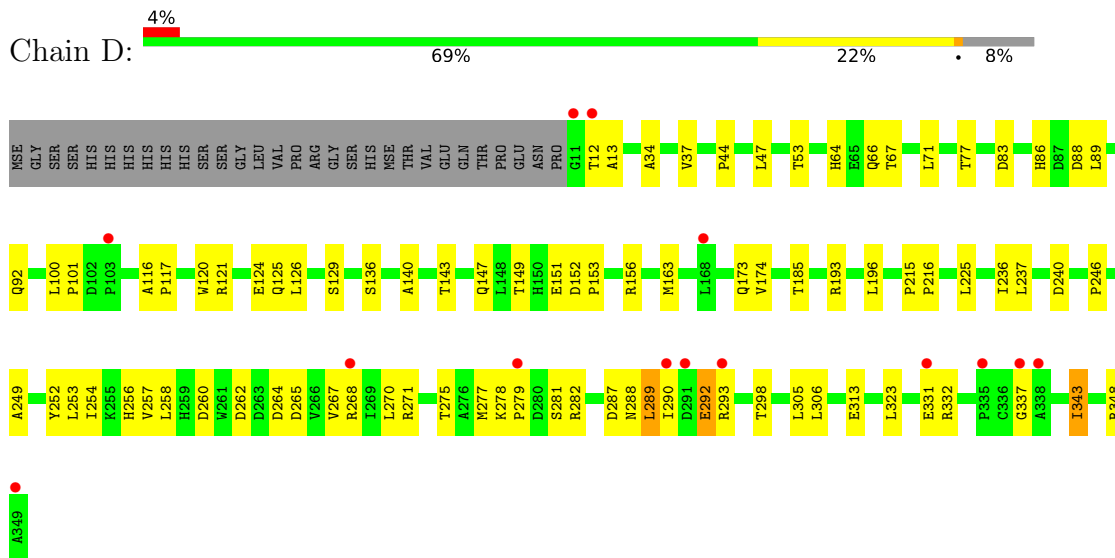
3 Residue-property plots [i](#)

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.

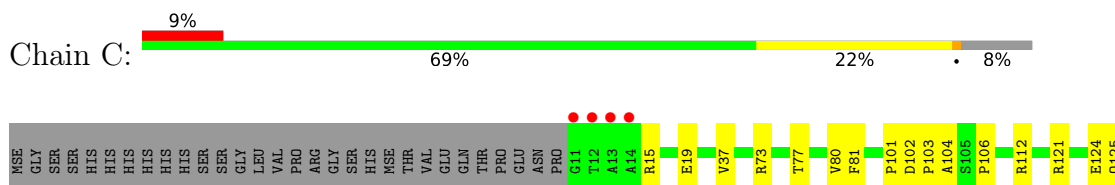
• Molecule 1: MmcR

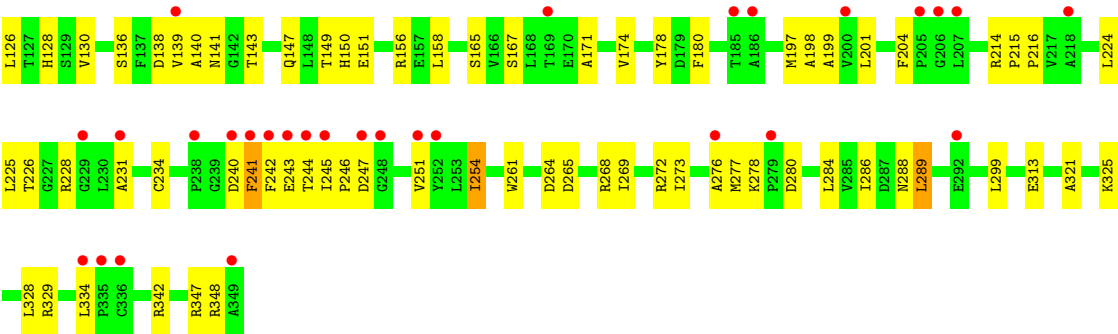


• Molecule 1: MmcR

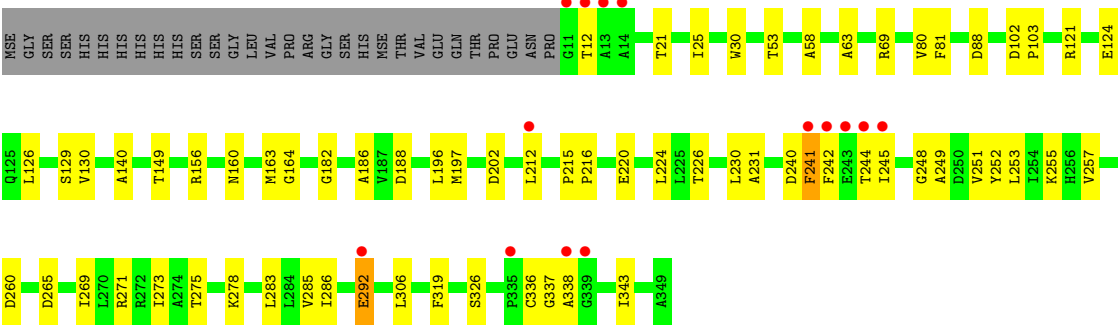


• Molecule 1: MmcR





● Molecule 1: MmcR



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.84Å 98.84Å 171.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.92 – 2.30 43.92 – 2.30	Depositor EDS
% Data completeness (in resolution range)	88.8 (43.92-2.30) 88.8 (43.92-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.55 (at 2.29Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.202 , 0.255 0.200 , 0.253	Depositor DCC
R_{free} test set	3003 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10864	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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: CA, MQA, SAH

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	0.48	0/2620	0.85	5/3563 (0.1%)
1	B	0.49	0/2631	0.80	2/3577 (0.1%)
1	C	0.46	0/2631	0.81	0/3577
1	D	0.46	0/2631	0.84	2/3577 (0.1%)
All	All	0.47	0/10513	0.82	9/14294 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	PHE	CA-C-N	6.55	127.07	119.47
1	A	204	PHE	C-N-CA	6.55	127.07	119.47
1	D	152	ASP	CA-C-N	6.28	126.02	119.05
1	D	152	ASP	C-N-CA	6.28	126.02	119.05
1	B	242	PHE	N-CA-C	-5.90	106.12	113.38
1	B	182	GLY	N-CA-C	-5.48	107.46	114.85
1	A	152	ASP	CA-C-N	5.23	124.86	119.05
1	A	152	ASP	C-N-CA	5.23	124.86	119.05
1	A	215	PRO	N-CA-C	5.18	117.02	110.70

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	2574	0	2557	32	0
1	B	2585	0	2569	46	0
1	C	2585	0	2569	71	0
1	D	2585	0	2569	64	0
2	A	26	0	19	1	0
2	B	26	0	19	1	0
2	C	26	0	19	2	0
2	D	26	0	19	2	0
3	A	25	0	19	3	0
3	B	25	0	19	3	0
3	C	25	0	19	1	0
3	D	25	0	19	2	0
4	D	2	0	0	0	0
5	A	110	0	0	1	0
5	B	77	0	0	3	0
5	C	72	0	0	1	0
5	D	70	0	0	3	0
All	All	10864	0	10416	206	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 10.

All (206) 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:292:GLU:O	1:D:293:ARG:HG2	1.68	0.93
1:C:215:PRO:HB2	1:C:216:PRO:HD3	1.62	0.81
1:D:331:GLU:O	1:D:332:ARG:HG3	1.86	0.76
1:D:47:LEU:HB3	1:D:92:GLN:HG2	1.68	0.75
1:B:292:GLU:HA	1:B:292:GLU:OE1	1.86	0.75
1:A:270:LEU:HD13	1:A:323:LEU:HD23	1.69	0.73
1:A:163:MSE:HE1	3:A:351:MQA:C8	2.19	0.72
1:B:163:MSE:HE1	3:B:351:MQA:C8	2.22	0.70
1:B:129:SER:HB3	1:B:306:LEU:HD21	1.74	0.70
1:C:243:GLU:HG2	1:C:244:THR:HG23	1.76	0.68
1:C:245:ILE:HD13	1:C:273:ILE:HG12	1.75	0.67
1:C:289:LEU:HD22	1:C:342:ARG:HB2	1.78	0.65
1:C:269:ILE:O	1:C:273:ILE:HG13	1.97	0.65
1:B:163:MSE:HE1	3:B:351:MQA:C8A	2.26	0.65
1:D:121:ARG:O	1:D:124:GLU:HB3	1.97	0.64
1:B:336:CYS:HB2	1:B:343:ILE:HD12	1.80	0.63
1:A:288:ASN:HD21	3:A:351:MQA:HN1A	1.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:ARG:O	1:B:275:THR:HG23	1.98	0.63
1:B:252:TYR:C	1:B:253:LEU:HD12	2.23	0.63
1:D:37:VAL:HG21	1:C:126:LEU:HG	1.80	0.62
1:C:121:ARG:HG2	1:C:140:ALA:HB1	1.81	0.62
1:C:167:SER:HB2	2:C:350:SAH:OXT	1.99	0.62
1:D:293:ARG:O	1:D:293:ARG:HG3	1.99	0.62
1:B:336:CYS:HB2	1:B:343:ILE:CD1	2.30	0.61
1:D:264:ASP:HB3	1:D:268[A]:ARG:HH12	1.66	0.61
1:D:44:PRO:O	1:D:92:GLN:NE2	2.32	0.61
1:D:270:LEU:HD13	1:D:323:LEU:HD23	1.82	0.60
1:A:323:LEU:HD13	1:A:346:ILE:HG12	1.82	0.60
1:C:73:ARG:O	1:C:77:THR:HG23	2.01	0.60
1:C:201:LEU:CD1	1:C:234:CYS:HB2	2.32	0.60
1:B:253:LEU:HD12	1:B:253:LEU:N	2.17	0.60
3:C:351:MQA:N12	3:C:351:MQA:H25B	2.18	0.59
1:B:336:CYS:SG	1:B:343:ILE:HD11	2.42	0.59
1:D:264:ASP:O	1:D:268[B]:ARG:HG2	2.03	0.59
1:B:265:ASP:O	1:B:269:ILE:HG13	2.04	0.58
1:B:53:THR:HA	1:B:88:ASP:O	2.04	0.58
1:A:66:GLN:HG3	5:A:402:HOH:O	2.01	0.58
1:C:198:ALA:HB2	1:C:225:LEU:HD23	1.84	0.58
1:A:187:VAL:HG22	1:A:210:THR:HB	1.86	0.57
1:B:226:THR:HA	1:B:231:ALA:HB2	1.86	0.57
1:B:102:ASP:OD1	1:B:103:PRO:HD2	2.05	0.57
1:D:163:MSE:HE1	1:D:256:HIS:CD2	2.40	0.57
1:C:174:VAL:HG21	1:C:286:ILE:HD13	1.85	0.57
1:D:121:ARG:HG2	1:D:140:ALA:HB1	1.86	0.56
1:B:188:ASP:HB2	1:B:197:MSE:HE2	1.86	0.56
1:B:249:ALA:HB3	1:B:252:TYR:CZ	2.41	0.56
1:C:104:ALA:O	1:C:106:PRO:HD3	2.06	0.56
1:C:288:ASN:HB2	1:C:313:GLU:OE1	2.06	0.55
1:C:112[B]:ARG:HG3	1:C:158:LEU:HD22	1.89	0.55
1:D:149:THR:O	1:D:156:ARG:HB2	2.07	0.54
1:C:121:ARG:O	1:C:124:GLU:HB3	2.08	0.54
1:C:149:THR:O	1:C:156:ARG:HB2	2.08	0.54
1:C:241:PHE:HD1	1:C:242:PHE:N	2.05	0.54
1:C:215:PRO:HB2	1:C:216:PRO:CD	2.37	0.53
1:A:247:ASP:HA	1:A:276:ALA:HB1	1.90	0.53
1:A:331:GLU:CD	1:A:347:ARG:HE	2.15	0.53
1:D:37:VAL:HG11	1:C:130:VAL:HG21	1.90	0.53
1:D:173:GLN:OE1	1:D:337:GLY:HA2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:193:ARG:HB2	5:D:364:HOH:O	2.09	0.53
1:D:257:VAL:O	1:D:260:ASP:HB2	2.08	0.53
1:D:125:GLN:HB2	1:D:136:SER:HB2	1.90	0.52
1:C:128:HIS:NE2	1:C:139:VAL:HG21	2.24	0.52
1:D:271:ARG:O	1:D:275:THR:HG23	2.09	0.52
1:D:281:SER:O	1:D:282:ARG:NH1	2.43	0.52
1:C:264:ASP:O	1:C:268:ARG:HG3	2.10	0.52
1:B:212:LEU:HD13	5:B:551:HOH:O	2.09	0.52
1:D:293:ARG:O	1:D:293:ARG:CG	2.58	0.51
1:C:245:ILE:HD12	1:C:272:ARG:HG2	1.92	0.51
1:B:260:ASP:OD2	3:B:351:MQA:H24	2.11	0.51
1:A:196:LEU:O	1:A:200:VAL:HG23	2.10	0.51
1:D:249:ALA:HB3	1:D:252:TYR:CZ	2.45	0.51
1:D:292:GLU:O	1:D:293:ARG:CG	2.53	0.51
1:C:201:LEU:HD11	1:C:234:CYS:HB2	1.92	0.51
1:C:280:ASP:CG	1:C:280:ASP:O	2.54	0.51
1:D:126:LEU:HG	1:C:37:VAL:HG21	1.93	0.50
1:C:215:PRO:CB	1:C:216:PRO:HD3	2.37	0.50
1:A:53:THR:HA	1:A:88:ASP:O	2.12	0.50
1:C:273:ILE:O	1:C:277:MSE:HG3	2.12	0.50
1:C:321:ALA:O	1:C:325:LYS:HG3	2.11	0.50
1:D:225:LEU:HD12	1:D:236:ILE:HD11	1.94	0.50
1:C:102:ASP:OD1	1:C:103:PRO:HD2	2.12	0.50
1:D:240:ASP:HA	2:D:350:SAH:N1	2.27	0.49
1:B:224:LEU:C	1:B:224:LEU:HD23	2.36	0.49
1:A:335:PRO:HG3	1:A:342:ARG:HH12	1.76	0.49
1:C:329:ARG:HH11	1:C:347:ARG:HH22	1.60	0.49
1:B:257:VAL:O	1:B:260:ASP:HB2	2.11	0.49
1:C:328:LEU:HD23	1:C:348:ARG:HA	1.95	0.49
1:C:197:MSE:HG2	1:C:234:CYS:SG	2.53	0.49
1:C:241:PHE:HD1	1:C:241:PHE:C	2.21	0.48
1:C:241:PHE:C	1:C:241:PHE:CD1	2.92	0.48
1:C:214:ARG:HD2	5:C:416:HOH:O	2.14	0.47
1:D:196:LEU:HD21	1:D:253:LEU:HD23	1.97	0.47
1:B:285:VAL:HG11	1:B:319:PHE:CZ	2.49	0.47
1:D:254:ILE:HG23	1:D:254:ILE:O	2.15	0.47
1:D:262:ASP:OD2	1:D:265:ASP:HB2	2.14	0.47
1:B:186:ALA:HA	1:B:251:VAL:O	2.14	0.47
1:A:321:ALA:O	1:A:324:GLU:HB3	2.15	0.46
1:D:53:THR:HA	1:D:88:ASP:O	2.15	0.46
1:D:77:THR:HG21	1:C:299:LEU:HD12	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:ALA:HB1	1:C:199:ALA:HB2	1.97	0.46
1:D:67:THR:HG21	1:C:130:VAL:HA	1.97	0.46
1:D:129:SER:HB3	1:D:306:LEU:HD21	1.96	0.46
1:D:151:GLU:O	1:D:153:PRO:HD3	2.15	0.46
1:C:101:PRO:HD3	1:C:112[A]:ARG:NH2	2.30	0.46
1:B:160:ASN:ND2	1:B:220:GLU:OE1	2.47	0.46
1:B:30:TRP:CD1	1:B:30:TRP:N	2.82	0.46
1:C:247:ASP:OD2	1:C:247:ASP:N	2.49	0.46
1:B:202:ASP:OD1	1:B:230:LEU:HD21	2.16	0.46
1:D:289:LEU:HD12	1:D:289:LEU:HA	1.67	0.46
1:A:278:LYS:C	1:A:280:ASP:H	2.24	0.45
1:B:121:ARG:O	1:B:124:GLU:HB3	2.17	0.45
1:D:86:HIS:CE1	1:D:89:LEU:HD12	2.52	0.45
1:C:15:ARG:O	1:C:19:GLU:HG3	2.15	0.45
1:D:305:LEU:HD11	1:D:313:GLU:OE2	2.15	0.45
1:C:125:GLN:HB2	1:C:136:SER:HB2	1.98	0.45
1:C:226:THR:HA	1:C:231:ALA:HB2	1.99	0.45
1:B:80:VAL:O	1:B:81:PHE:HB2	2.16	0.45
1:C:106:PRO:HA	1:C:165:SER:OG	2.15	0.45
1:D:121:ARG:HA	5:D:550:HOH:O	2.17	0.45
1:B:273:ILE:HG21	1:B:283:LEU:HD13	1.98	0.45
1:D:143:THR:OG1	1:D:147:GLN:HB3	2.17	0.45
1:B:215:PRO:HB2	1:B:216:PRO:HD3	1.99	0.45
1:D:67:THR:CG2	1:C:130:VAL:HA	2.47	0.45
1:D:288:ASN:OD1	3:D:351:MQA:N12	2.50	0.45
3:D:351:MQA:H25A	3:D:351:MQA:H1	1.87	0.45
1:A:37:VAL:HG21	1:B:126:LEU:HG	1.99	0.44
1:A:106:PRO:HD2	5:B:378:HOH:O	2.16	0.44
1:D:12:THR:HG23	1:D:13:ALA:N	2.32	0.44
1:B:58:ALA:HB1	1:B:63:ALA:O	2.17	0.44
1:B:255:LYS:HA	1:B:286:ILE:O	2.17	0.44
1:C:128:HIS:CD2	1:C:139:VAL:HG21	2.53	0.44
1:D:116:ALA:HA	1:D:117:PRO:HD3	1.89	0.44
1:A:346:ILE:CG2	1:A:347:ARG:N	2.81	0.44
1:D:254:ILE:CG1	1:D:257:VAL:HB	2.47	0.44
1:C:254:ILE:O	1:C:254:ILE:HG23	2.17	0.44
1:C:147:GLN:O	1:C:150:HIS:HB3	2.18	0.44
1:A:37:VAL:HG11	1:B:130:VAL:HG21	1.98	0.44
1:C:180:PHE:HD2	1:C:204:PHE:CE2	2.36	0.44
1:C:242:PHE:HE2	1:C:261:TRP:CH2	2.36	0.44
1:A:294:PRO:HG2	1:A:299:LEU:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:VAL:HG12	1:A:346:ILE:HD11	2.00	0.43
1:D:237:LEU:CD2	1:D:246:PRO:HG3	2.48	0.43
1:C:245:ILE:O	1:C:246:PRO:C	2.57	0.43
1:D:120:TRP:HD1	1:C:124:GLU:HB2	1.83	0.43
1:D:174:VAL:HG22	1:D:343:ILE:HD11	2.00	0.43
1:A:257:VAL:O	1:A:260:ASP:HB2	2.19	0.43
1:D:47:LEU:CB	1:D:92:GLN:HG2	2.43	0.43
1:B:241:PHE:C	1:B:241:PHE:CD1	2.96	0.43
1:D:278:LYS:HB3	1:D:279:PRO:CD	2.48	0.43
1:B:12:THR:HG22	5:B:369:HOH:O	2.19	0.43
1:A:121:ARG:O	1:A:124:GLU:HB3	2.19	0.43
1:A:189:ILE:HD13	1:A:245:ILE:HD12	2.01	0.43
1:A:240:ASP:OD1	1:A:240:ASP:C	2.62	0.43
1:D:12:THR:HG23	1:D:13:ALA:H	1.84	0.43
1:D:215:PRO:N	1:D:216:PRO:HD2	2.33	0.43
1:C:278:LYS:C	1:C:280:ASP:H	2.26	0.43
1:A:262:ASP:OD1	1:A:262:ASP:C	2.60	0.43
1:B:196:LEU:HD21	1:B:253:LEU:HD23	2.01	0.43
1:B:240:ASP:HA	2:B:350:SAH:N1	2.34	0.43
1:B:248:GLY:HA2	1:B:278:LYS:HG3	2.01	0.43
1:D:185:THR:OG1	1:D:249:ALA:HA	2.19	0.42
1:C:247:ASP:HB3	1:C:276:ALA:HA	2.00	0.42
1:B:69:ARG:HH21	1:B:88:ASP:CG	2.26	0.42
1:D:64:HIS:CE1	1:D:66:GLN:HB3	2.54	0.42
1:D:264:ASP:HB3	1:D:268[B]:ARG:NH2	2.35	0.42
1:A:288:ASN:HB2	1:A:313:GLU:OE1	2.19	0.42
1:C:240:ASP:HB3	1:C:243:GLU:HB3	2.01	0.42
1:C:141:ASN:O	1:C:143:THR:HG22	2.20	0.42
1:C:278:LYS:C	1:C:280:ASP:N	2.77	0.42
1:A:344:VAL:O	1:A:346:ILE:HD12	2.20	0.42
1:D:277:MSE:O	1:D:348:ARG:NH1	2.52	0.42
2:D:350:SAH:H4'	2:D:350:SAH:HB1	2.01	0.42
1:B:121:ARG:HG2	1:B:140:ALA:HB1	2.02	0.42
1:B:244:THR:C	1:B:245:ILE:HG12	2.44	0.42
1:A:215:PRO:HB2	1:A:216:PRO:HD3	2.02	0.42
1:A:226:THR:HG22	5:D:546:HOH:O	2.20	0.42
1:A:240:ASP:HA	2:A:350:SAH:N1	2.35	0.41
3:A:351:MQA:H25B	3:A:351:MQA:H9	1.81	0.41
1:B:336:CYS:HB2	1:B:343:ILE:HD11	2.02	0.41
1:A:193:ARG:O	1:A:221:ALA:HA	2.20	0.41
1:A:278:LYS:C	1:A:280:ASP:N	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:PHE:CD1	1:C:242:PHE:N	2.87	0.41
1:C:102:ASP:HA	1:C:103:PRO:HD3	1.84	0.41
1:D:34:ALA:HB1	1:D:71:LEU:HD11	2.03	0.41
1:D:267:VAL:HG12	1:D:268[B]:ARG:NH1	2.35	0.41
1:D:290:ILE:HD13	1:D:298:THR:HG21	2.01	0.41
1:C:224:LEU:O	1:C:228:ARG:HG2	2.20	0.41
1:C:240:ASP:OD1	2:C:350:SAH:N6	2.53	0.41
1:B:149:THR:O	1:B:156:ARG:HB2	2.21	0.41
1:B:337:GLY:O	1:B:338:ALA:C	2.63	0.41
1:D:100:LEU:HA	1:D:101:PRO:HD3	1.83	0.41
1:D:254:ILE:HD13	1:D:258:LEU:HD21	2.03	0.41
1:C:80:VAL:O	1:C:81:PHE:HB2	2.20	0.41
1:C:247:ASP:HA	1:C:276:ALA:HB1	2.03	0.41
1:A:201:LEU:HD11	1:A:234:CYS:HB2	2.02	0.41
1:C:178:TYR:CD2	1:C:284:LEU:HD11	2.55	0.41
1:C:245:ILE:CD1	1:C:272:ARG:HG2	2.50	0.41
1:C:265:ASP:OD1	1:C:268:ARG:NH1	2.54	0.41
1:D:120:TRP:CD1	1:C:124:GLU:HB2	2.56	0.40
1:D:83:ASP:OD1	1:D:83:ASP:C	2.64	0.40
1:C:138:ASP:HA	1:C:143:THR:O	2.21	0.40
1:B:160:ASN:O	1:B:164:GLY:N	2.54	0.40
1:D:37:VAL:HG21	1:C:126:LEU:CG	2.51	0.40
1:D:163:MSE:HE1	1:D:256:HIS:HD2	1.84	0.40
1:C:102:ASP:OD1	1:C:103:PRO:CD	2.70	0.40
1:B:21:THR:O	1:B:25:ILE:HG13	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	337/369 (91%)	324 (96%)	13 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	338/369 (92%)	324 (96%)	14 (4%)	0	100	100
1	C	338/369 (92%)	322 (95%)	15 (4%)	1 (0%)	36	46
1	D	338/369 (92%)	331 (98%)	7 (2%)	0	100	100
All	All	1351/1476 (92%)	1301 (96%)	49 (4%)	1 (0%)	48	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	254	ILE

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	261/283 (92%)	260 (100%)	1 (0%)	84	92
1	B	262/283 (93%)	259 (99%)	3 (1%)	65	81
1	C	262/283 (93%)	257 (98%)	5 (2%)	50	69
1	D	262/283 (93%)	258 (98%)	4 (2%)	57	75
All	All	1047/1132 (92%)	1034 (99%)	13 (1%)	63	79

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	334	LEU
1	D	287	ASP
1	D	289	LEU
1	D	292	GLU
1	D	343	ILE
1	C	151	GLU
1	C	241	PHE
1	C	251	VAL
1	C	289	LEU
1	C	334	LEU

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Mol	Chain	Res	Type
1	B	241	PHE
1	B	292	GLU
1	B	326	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	92	GLN
1	A	288	ASN
1	D	48	GLN
1	D	259	HIS
1	C	150	HIS
1	B	128	HIS
1	B	147	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MQA	D	351	-	25,28,28	2.48	6 (24%)	24,45,45	2.41	6 (25%)
2	SAH	D	350	-	27,28,28	1.47	5 (18%)	36,40,40	2.00	9 (25%)
2	SAH	B	350	-	27,28,28	1.45	5 (18%)	36,40,40	1.96	10 (27%)
3	MQA	A	351	-	25,28,28	2.35	6 (24%)	24,45,45	2.75	9 (37%)
2	SAH	C	350	-	27,28,28	1.50	6 (22%)	36,40,40	1.97	10 (27%)
3	MQA	C	351	-	25,28,28	2.23	6 (24%)	24,45,45	2.99	6 (25%)
2	SAH	A	350	-	27,28,28	1.51	6 (22%)	36,40,40	2.13	11 (30%)
3	MQA	B	351	-	25,28,28	2.34	6 (24%)	24,45,45	2.53	5 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MQA	D	351	-	-	3/10/69/69	0/4/4/4
2	SAH	D	350	-	-	2/15/31/31	0/3/3/3
2	SAH	B	350	-	-	0/15/31/31	0/3/3/3
3	MQA	A	351	-	-	3/10/69/69	0/4/4/4
2	SAH	C	350	-	-	4/15/31/31	0/3/3/3
3	MQA	C	351	-	-	5/10/69/69	0/4/4/4
2	SAH	A	350	-	-	0/15/31/31	0/3/3/3
3	MQA	B	351	-	-	4/10/69/69	0/4/4/4

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	351	MQA	O10-C11	7.24	1.46	1.35
3	B	351	MQA	O10-C11	7.06	1.45	1.35
3	C	351	MQA	O10-C11	6.72	1.45	1.35
3	A	351	MQA	O10-C11	6.49	1.44	1.35
3	D	351	MQA	C4A-N4	6.16	1.41	1.35
3	B	351	MQA	C7-C6	5.77	1.50	1.36
3	D	351	MQA	C7-C6	5.76	1.50	1.36
3	A	351	MQA	C4A-N4	5.47	1.41	1.35
3	C	351	MQA	C7-C6	5.42	1.49	1.36
3	A	351	MQA	C7-C6	5.24	1.48	1.36
2	C	350	SAH	C5-C4	4.98	1.48	1.39
2	D	350	SAH	C5-C4	4.87	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	350	SAH	C5-C4	4.84	1.47	1.39
3	B	351	MQA	C4A-N4	4.67	1.40	1.35
2	B	350	SAH	C5-C4	4.67	1.47	1.39
3	C	351	MQA	C4A-N4	4.21	1.39	1.35
3	A	351	MQA	C9-C8A	-4.07	1.46	1.51
3	C	351	MQA	C9-C8A	-3.30	1.47	1.51
3	B	351	MQA	C9-C8A	-3.24	1.47	1.51
3	B	351	MQA	C1-C2	2.84	1.53	1.48
2	D	350	SAH	C5-C6	2.77	1.48	1.41
2	A	350	SAH	C5-C6	2.77	1.48	1.41
3	A	351	MQA	C1-C2	2.74	1.53	1.48
3	D	351	MQA	C9-C8A	-2.69	1.48	1.51
3	C	351	MQA	C1-C2	2.67	1.53	1.48
2	B	350	SAH	C5-C6	2.66	1.48	1.41
2	B	350	SAH	C8-N7	2.64	1.36	1.31
2	A	350	SAH	C8-N7	2.58	1.36	1.31
3	D	351	MQA	C1-C2	2.55	1.53	1.48
2	C	350	SAH	C5-N7	-2.53	1.34	1.39
3	D	351	MQA	C4A-C8A	2.43	1.46	1.38
2	D	350	SAH	C8-N7	2.37	1.36	1.31
2	C	350	SAH	C8-N7	2.31	1.36	1.31
3	B	351	MQA	C4A-C8A	2.26	1.46	1.38
2	C	350	SAH	C5-C6	2.26	1.47	1.41
3	A	351	MQA	C4A-C8A	2.23	1.46	1.38
2	A	350	SAH	C4-N9	-2.23	1.33	1.37
3	C	351	MQA	C4A-C8A	2.21	1.46	1.38
2	A	350	SAH	C5-N7	-2.20	1.35	1.39
2	C	350	SAH	OXT-C	-2.20	1.23	1.30
2	D	350	SAH	OXT-C	-2.14	1.23	1.30
2	C	350	SAH	C4-N9	-2.12	1.33	1.37
2	D	350	SAH	C5-N7	-2.10	1.35	1.39
2	B	350	SAH	C5-N7	-2.06	1.35	1.39
2	B	350	SAH	OXT-C	-2.05	1.24	1.30
2	A	350	SAH	OXT-C	-2.05	1.24	1.30

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	351	MQA	O10-C11-N12	7.63	120.60	111.11
3	C	351	MQA	O10-C11-O11	-7.37	116.28	123.08
3	B	351	MQA	O10-C11-N12	6.83	119.60	111.11
3	A	351	MQA	O10-C11-N12	6.25	118.89	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	351	MQA	O10-C11-O11	-6.13	117.43	123.08
3	D	351	MQA	C3-N4-C4A	-5.97	112.43	126.45
3	A	351	MQA	O10-C11-O11	-5.96	117.58	123.08
2	C	350	SAH	C5-C4-N3	-5.91	118.58	126.72
3	C	351	MQA	C3-N4-C4A	-5.87	112.65	126.45
3	D	351	MQA	O10-C11-N12	5.85	118.39	111.11
2	D	350	SAH	C5-C4-N3	-5.71	118.85	126.72
2	B	350	SAH	C5-C4-N3	-5.61	118.99	126.72
3	A	351	MQA	C3-N4-C4A	-5.36	113.85	126.45
2	A	350	SAH	C5-C4-N3	-5.34	119.36	126.72
3	C	351	MQA	C9-C9A-N4	5.27	109.59	104.34
3	B	351	MQA	C3-N4-C4A	-5.02	114.66	126.45
3	A	351	MQA	C9-C9A-N4	5.02	109.34	104.34
2	C	350	SAH	N3-C4-N9	4.88	135.47	127.17
2	A	350	SAH	N3-C4-N9	4.75	135.25	127.17
2	D	350	SAH	N3-C4-N9	4.75	135.25	127.17
3	B	351	MQA	C9-C9A-N4	4.61	108.93	104.34
3	D	351	MQA	O10-C11-O11	-4.44	118.98	123.08
2	B	350	SAH	N3-C4-N9	4.44	134.72	127.17
2	A	350	SAH	C4-N9-C8	4.22	110.17	105.74
3	A	351	MQA	C5-C4A-N4	3.95	128.56	123.85
3	D	351	MQA	C9-C9A-N4	3.73	108.05	104.34
2	A	350	SAH	C2-N3-C4	3.71	120.90	111.83
2	B	350	SAH	C2-N3-C4	3.71	120.90	111.83
2	A	350	SAH	N3-C2-N1	-3.60	123.14	128.58
2	D	350	SAH	C2-N3-C4	3.57	120.54	111.83
2	C	350	SAH	C2-N3-C4	3.50	120.38	111.83
2	B	350	SAH	N3-C2-N1	-3.44	123.38	128.58
3	D	351	MQA	C5-C4A-N4	3.35	127.85	123.85
3	C	351	MQA	O10-C10-C9	-3.34	100.62	107.48
2	B	350	SAH	C4-C5-N7	-3.26	106.85	110.58
2	A	350	SAH	C4-C5-N7	-3.14	106.99	110.58
2	D	350	SAH	N3-C2-N1	-3.10	123.89	128.58
3	A	351	MQA	C10-C9-C8A	-3.08	105.33	112.00
2	A	350	SAH	CB-CG-SD	-3.04	106.67	113.45
2	D	350	SAH	C4-C5-N7	-2.98	107.18	110.58
2	A	350	SAH	N9-C8-N7	-2.95	109.75	113.94
2	D	350	SAH	C4-N9-C8	2.82	108.70	105.74
2	B	350	SAH	C4-N9-C8	2.79	108.67	105.74
2	C	350	SAH	N3-C2-N1	-2.77	124.38	128.58
2	A	350	SAH	C5-N7-C8	2.72	107.72	103.45
2	A	350	SAH	OXT-C-O	-2.68	118.00	124.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	351	MQA	C10-O10-C11	2.62	119.95	116.26
2	C	350	SAH	OXT-C-O	-2.59	118.20	124.08
2	D	350	SAH	OXT-C-O	-2.55	118.30	124.08
2	B	350	SAH	OXT-C-O	-2.53	118.35	124.08
3	A	351	MQA	CM6-C6-C7	-2.52	117.78	122.45
3	C	351	MQA	C10-O10-C11	2.48	119.75	116.26
2	D	350	SAH	CB-CG-SD	-2.45	107.98	113.45
3	B	351	MQA	C5-C4A-N4	2.45	126.77	123.85
2	B	350	SAH	C5-N7-C8	2.40	107.22	103.45
3	A	351	MQA	C9-C8A-C8	-2.32	126.52	128.65
2	C	350	SAH	C4-C5-N7	-2.31	107.94	110.58
3	A	351	MQA	C10-O10-C11	2.29	119.48	116.26
2	B	350	SAH	C6-C5-N7	2.19	136.32	132.09
2	A	350	SAH	C6-C5-N7	2.15	136.24	132.09
2	C	350	SAH	CB-CG-SD	-2.15	108.65	113.45
2	D	350	SAH	C5-N7-C8	2.12	106.78	103.45
2	B	350	SAH	N9-C8-N7	-2.09	110.97	113.94
2	C	350	SAH	O4'-C1'-N9	2.06	112.04	108.09
2	C	350	SAH	C1'-N9-C8	-2.05	122.54	127.09
2	C	350	SAH	C4-N9-C8	2.04	107.88	105.74

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	350	SAH	N-CA-CB-CG
2	C	350	SAH	C-CA-CB-CG
3	A	351	MQA	O11-C11-O10-C10
3	A	351	MQA	N12-C11-O10-C10
3	D	351	MQA	O10-C10-C9-C8A
3	C	351	MQA	O10-C10-C9-C8A
3	C	351	MQA	O10-C10-C9-C9A
3	C	351	MQA	O11-C11-O10-C10
3	C	351	MQA	N12-C11-O10-C10
3	B	351	MQA	O11-C11-O10-C10
3	B	351	MQA	N12-C11-O10-C10
3	A	351	MQA	C9-C10-O10-C11
3	C	351	MQA	C1-C9A-O24-C25
3	B	351	MQA	C1-C9A-O24-C25
3	D	351	MQA	O10-C10-C9-C9A
2	C	350	SAH	CB-CG-SD-C5'
2	D	350	SAH	O-C-CA-CB

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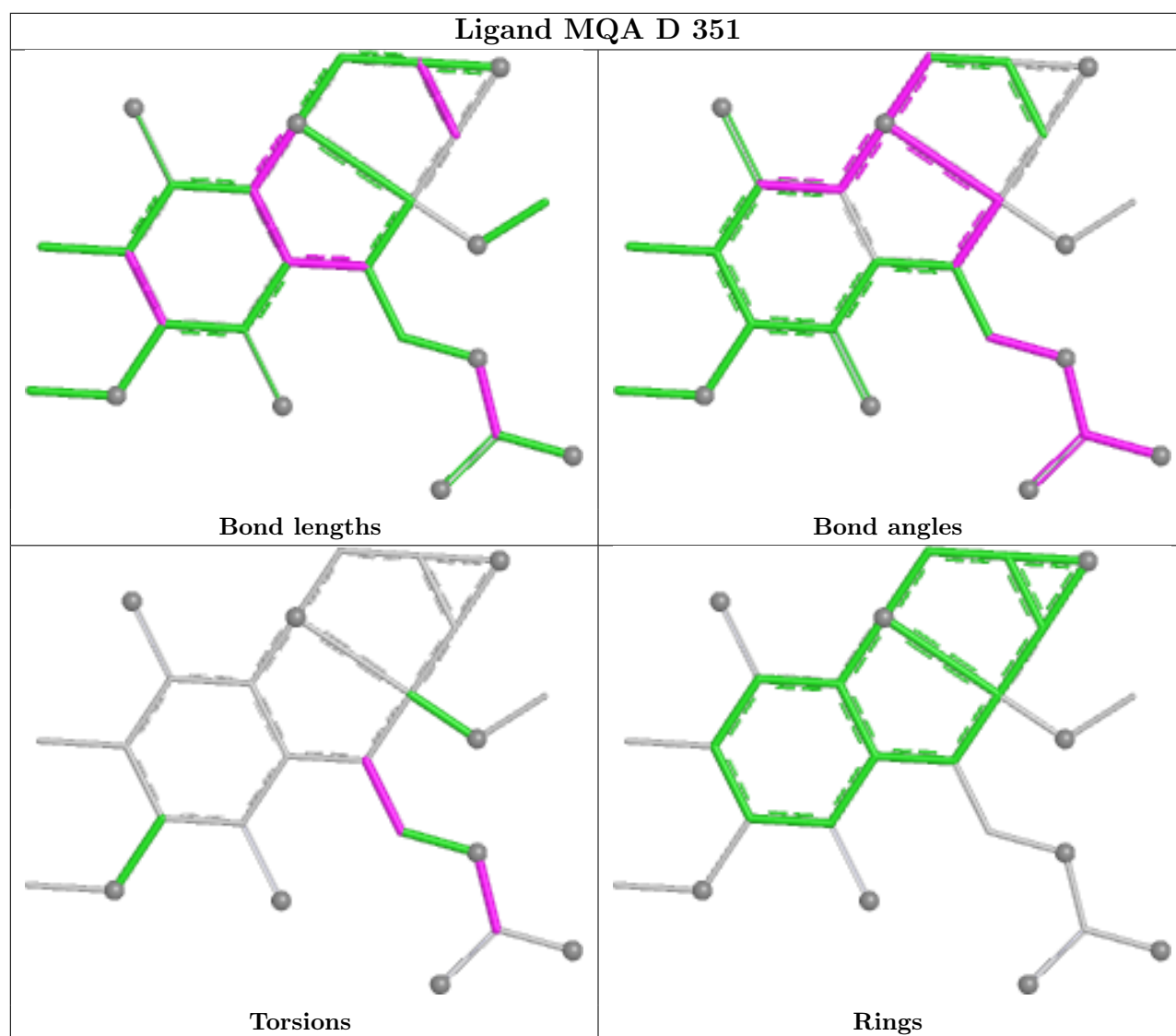
Mol	Chain	Res	Type	Atoms
2	D	350	SAH	OXT-C-CA-CB
3	D	351	MQA	N12-C11-O10-C10
3	B	351	MQA	N4-C9A-O24-C25
2	C	350	SAH	O4'-C1'-N9-C8

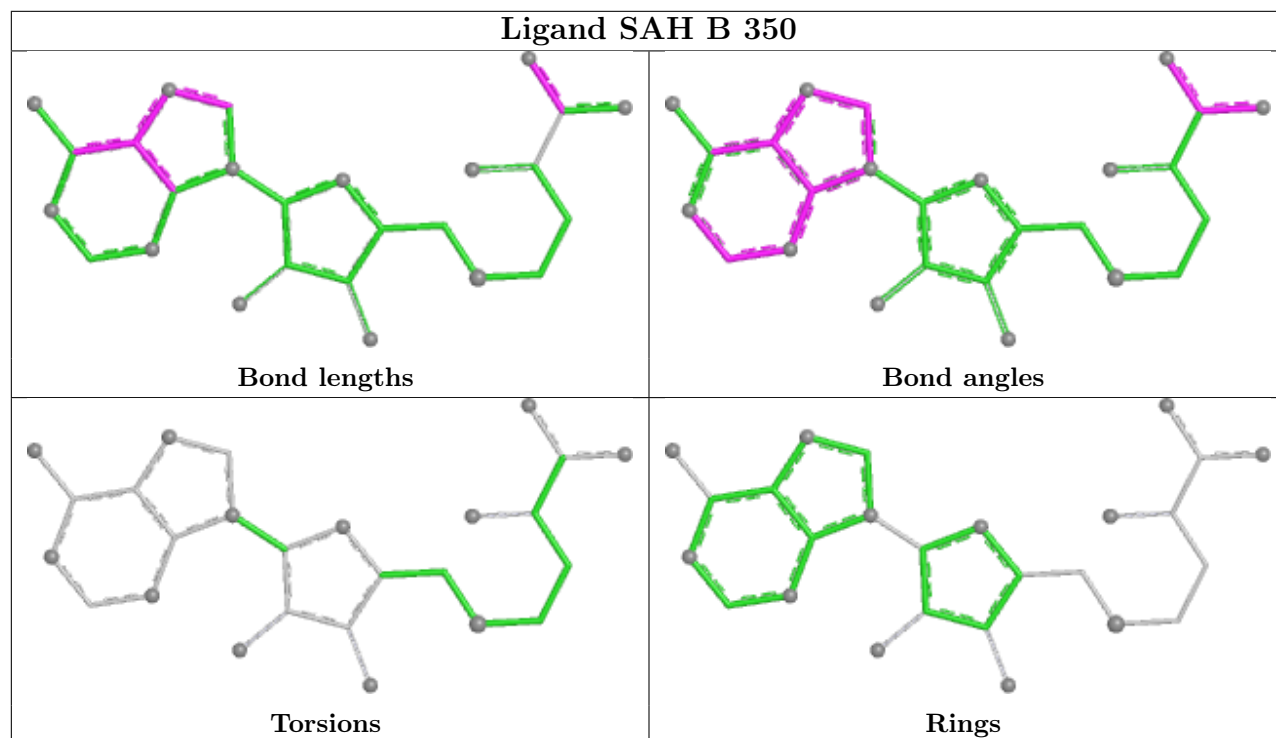
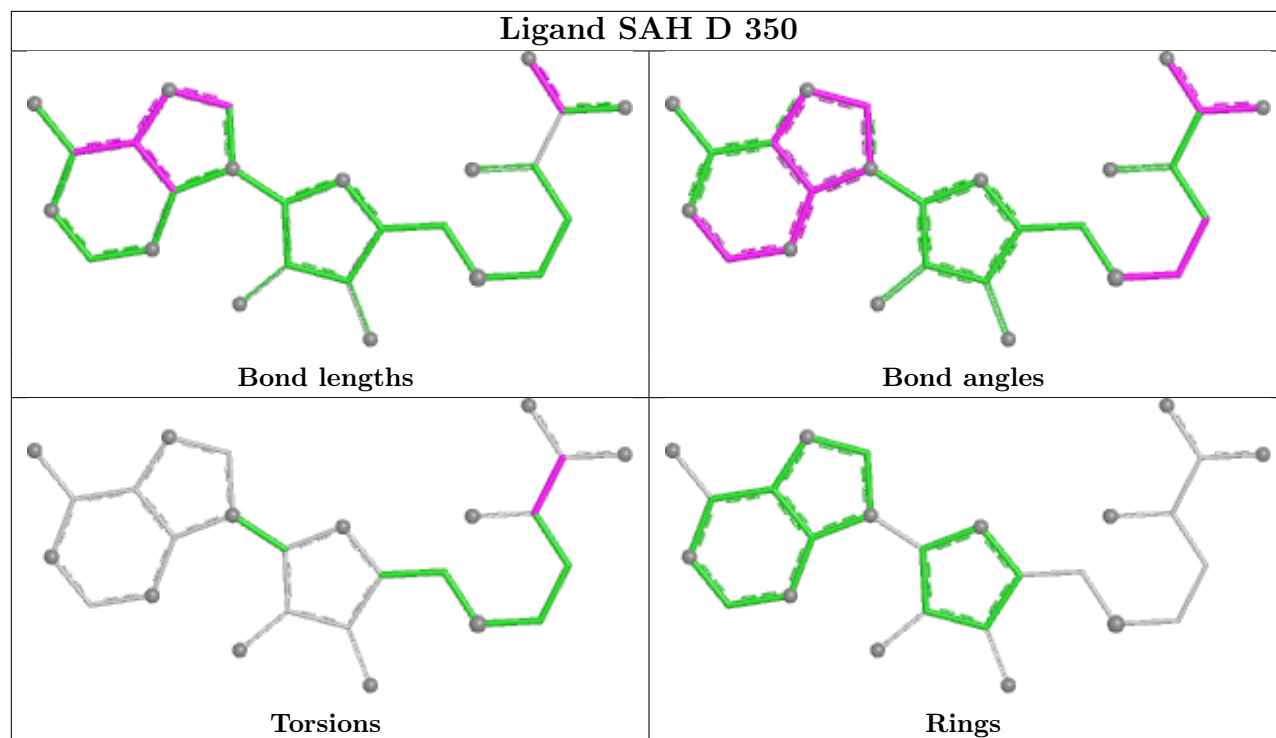
There are no ring outliers.

8 monomers are involved in 15 short contacts:

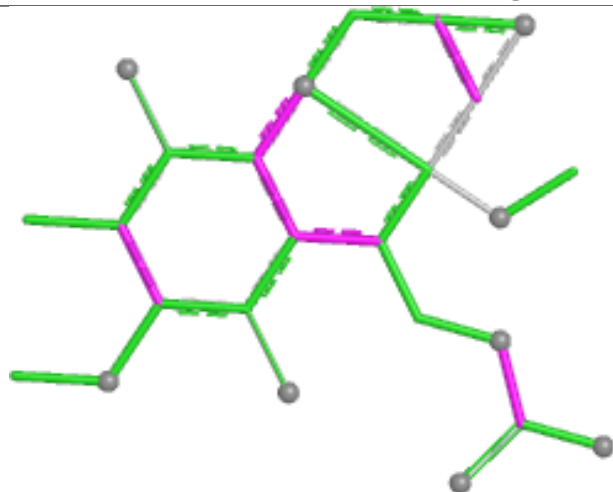
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	351	MQA	2	0
2	D	350	SAH	2	0
2	B	350	SAH	1	0
3	A	351	MQA	3	0
2	C	350	SAH	2	0
3	C	351	MQA	1	0
2	A	350	SAH	1	0
3	B	351	MQA	3	0

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.

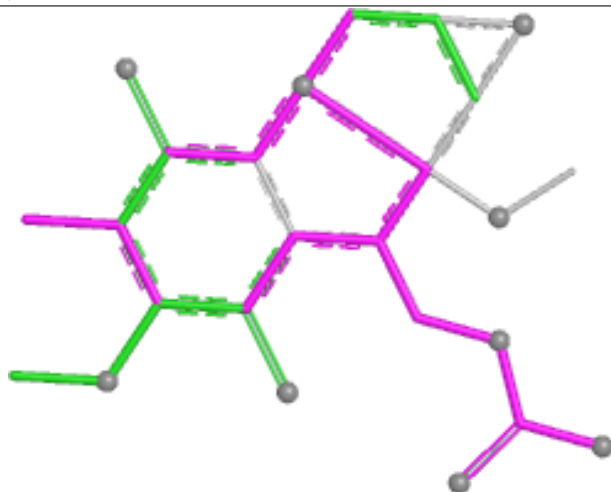




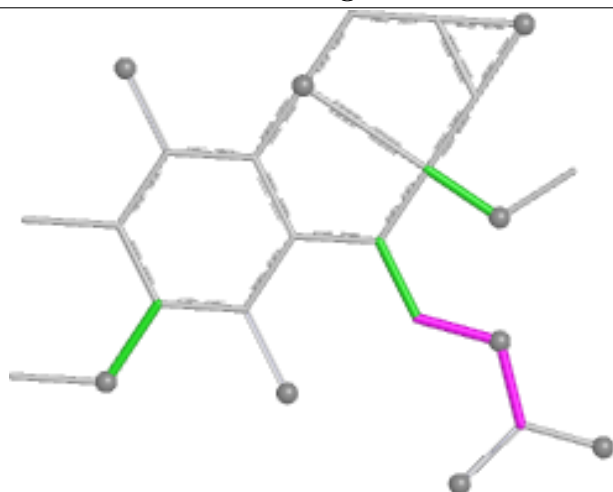
Ligand MQA A 351



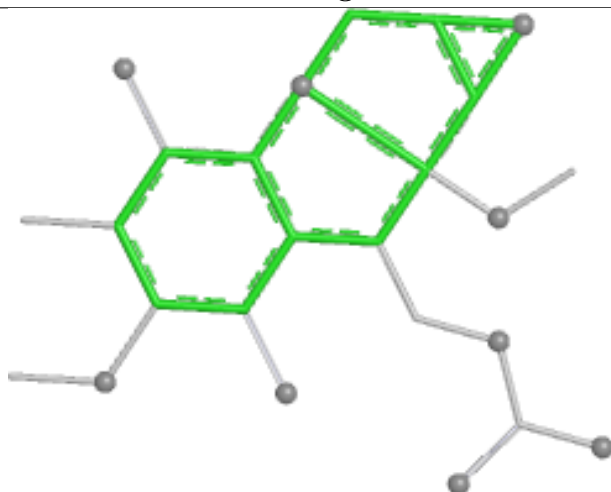
Bond lengths



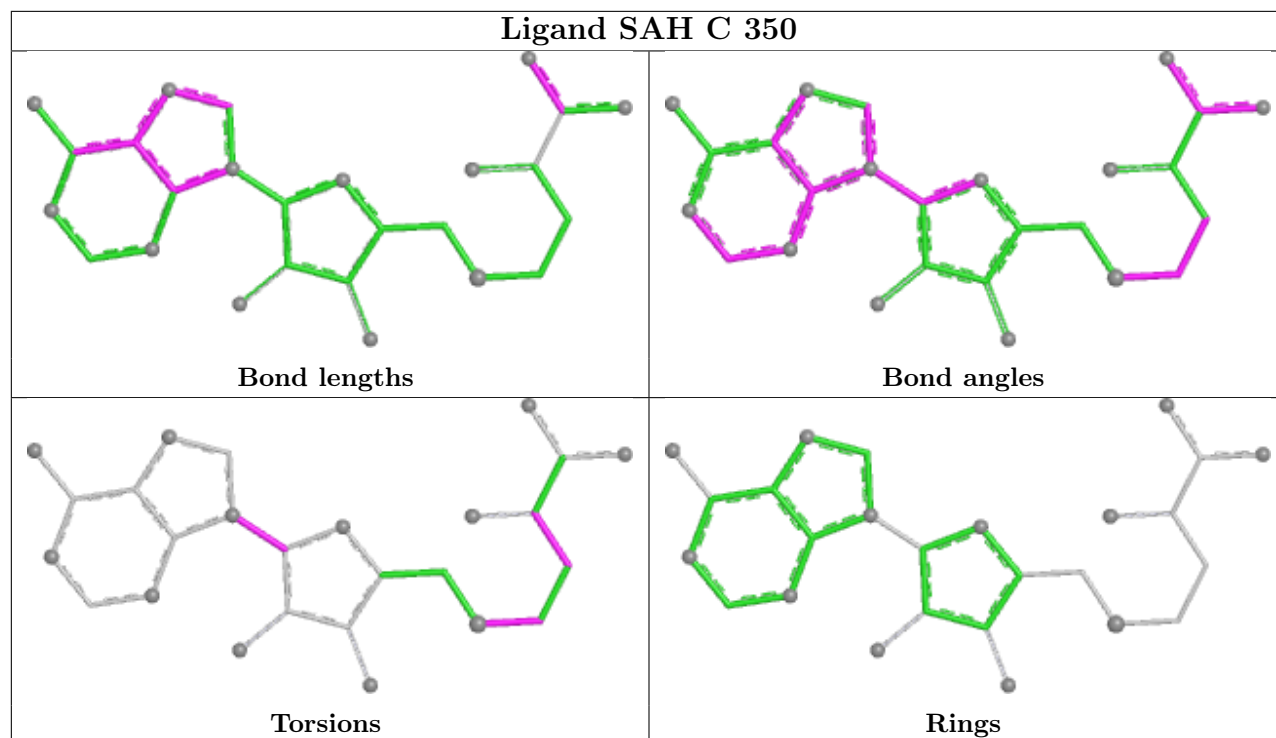
Bond angles

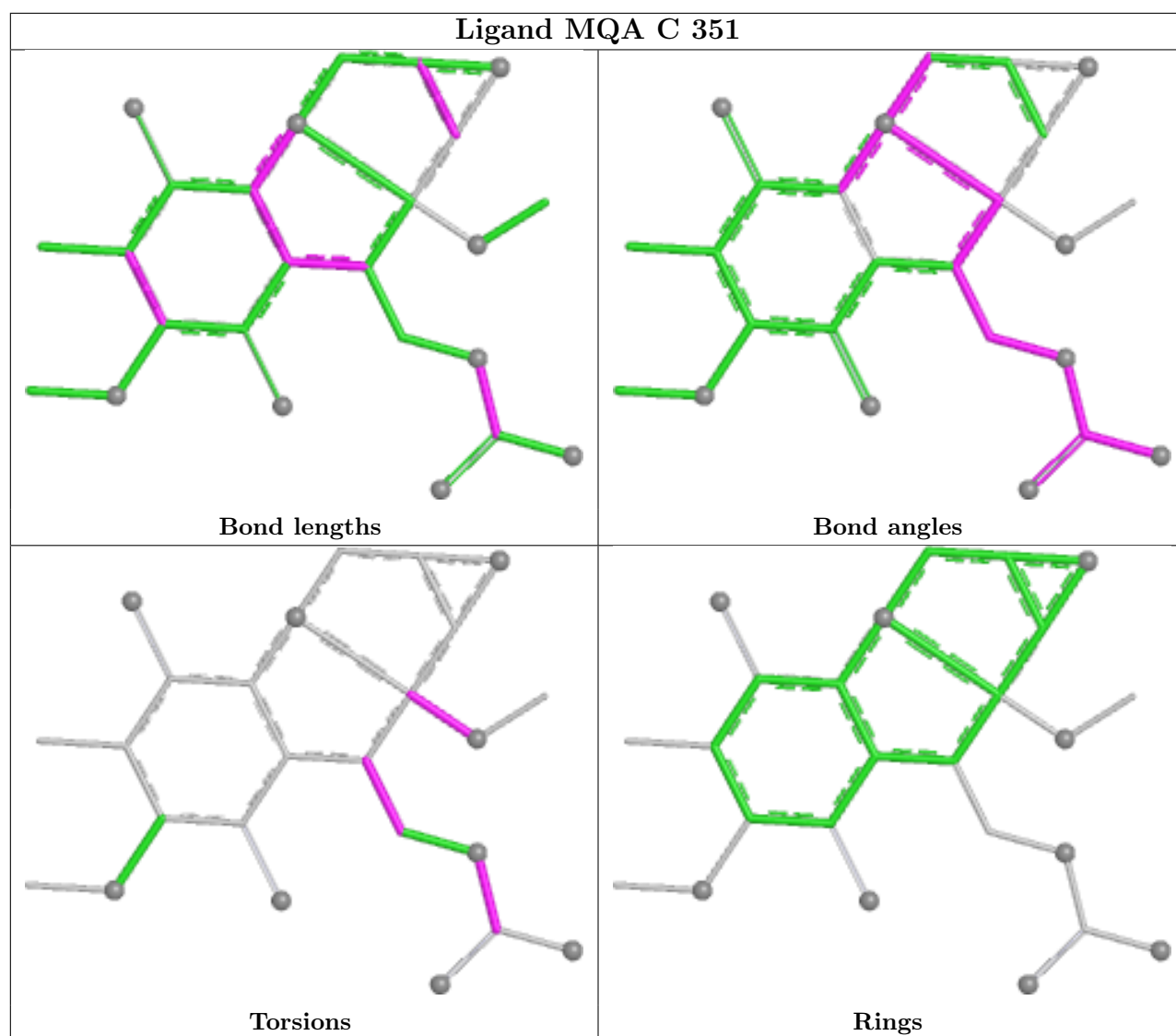


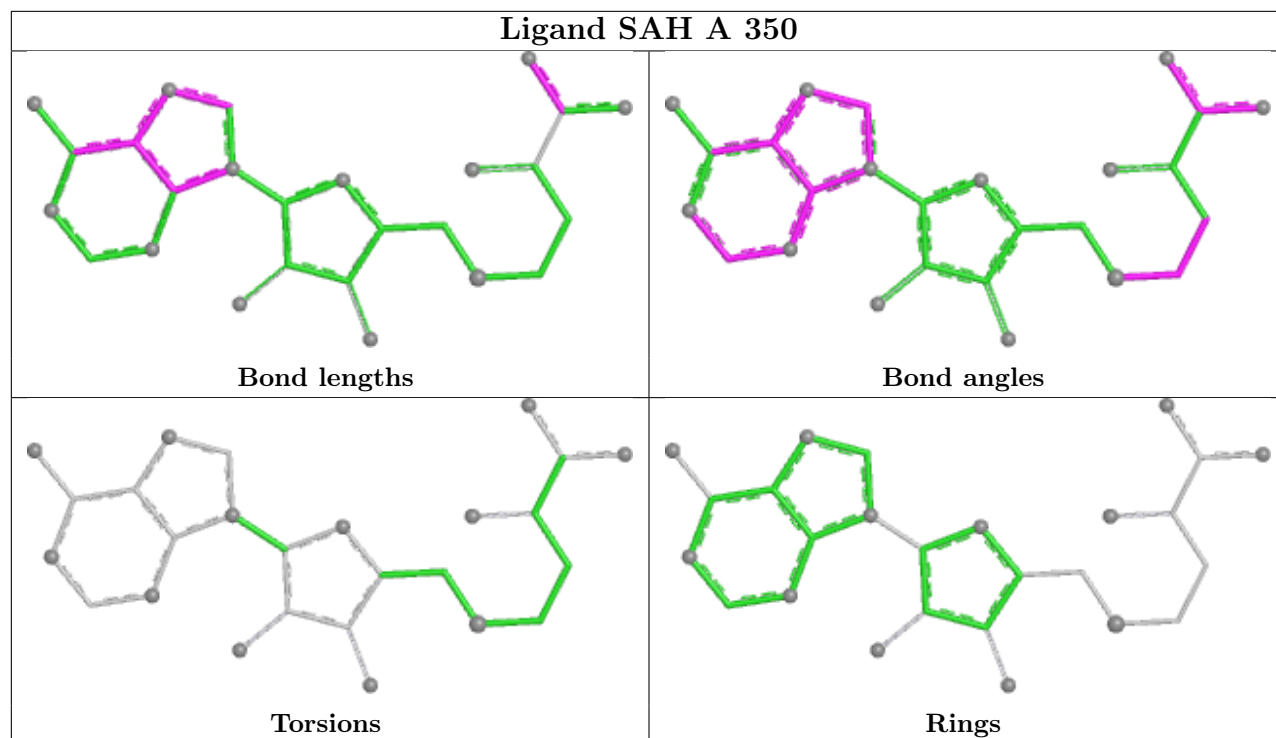
Torsions

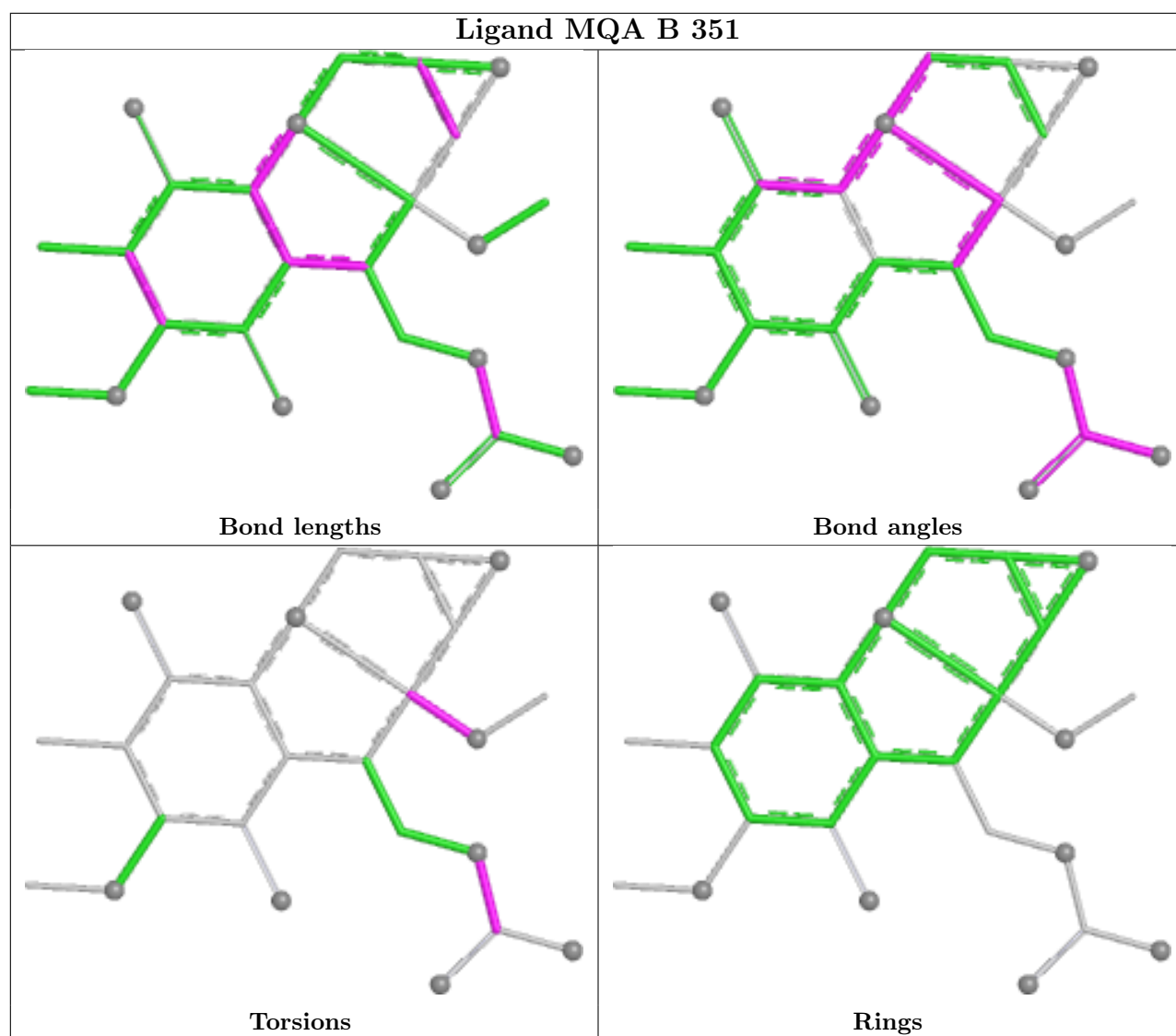


Rings









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, 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	336/369 (91%)	-0.06	6 (1%) 67 69	13, 29, 49, 72	4 (1%)
1	B	336/369 (91%)	0.21	14 (4%) 40 42	15, 34, 57, 99	3 (0%)
1	C	336/369 (91%)	0.57	33 (9%) 13 14	12, 39, 67, 89	2 (0%)
1	D	336/369 (91%)	0.46	14 (4%) 40 42	17, 39, 59, 77	3 (0%)
All	All	1344/1476 (91%)	0.29	67 (4%) 34 35	12, 35, 61, 99	12 (0%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	12	THR	5.1
1	B	241	PHE	4.8
1	D	349	ALA	4.7
1	B	13	ALA	4.4
1	C	335	PRO	4.2
1	C	11	GLY	4.1
1	B	11	GLY	4.0
1	C	12	THR	3.7
1	D	338	ALA	3.7
1	C	186	ALA	3.6
1	B	338	ALA	3.4
1	C	14	ALA	3.3
1	B	243	GLU	3.3
1	C	241	PHE	3.2
1	C	139	VAL	3.2
1	C	244	THR	3.1
1	D	331	GLU	3.1
1	D	291	ASP	3.1
1	D	290	ILE	3.0
1	B	244	THR	2.9
1	B	335	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	13	ALA	2.8
1	D	168	LEU	2.8
1	A	337	GLY	2.7
1	C	242	PHE	2.7
1	A	339	GLY	2.6
1	B	339	GLY	2.6
1	C	207	LEU	2.6
1	C	240	ASP	2.6
1	C	251	VAL	2.5
1	A	292	GLU	2.5
1	A	338	ALA	2.5
1	C	205	PRO	2.5
1	C	336	CYS	2.5
1	B	212	LEU	2.5
1	C	229	GLY	2.5
1	A	331	GLU	2.4
1	D	268[A]	ARG	2.4
1	C	247	ASP	2.4
1	D	337	GLY	2.4
1	C	276	ALA	2.4
1	D	279	PRO	2.3
1	C	231	ALA	2.3
1	C	169	THR	2.3
1	C	334	LEU	2.3
1	C	248	GLY	2.3
1	D	12	THR	2.3
1	C	238	PRO	2.3
1	C	279	PRO	2.3
1	D	11	GLY	2.3
1	D	293	ARG	2.3
1	C	185	THR	2.3
1	B	245	ILE	2.3
1	C	243	GLU	2.2
1	C	252	TYR	2.2
1	C	218	ALA	2.2
1	C	349	ALA	2.2
1	B	14	ALA	2.1
1	C	200	VAL	2.1
1	B	242	PHE	2.1
1	C	292	GLU	2.1
1	A	11	GLY	2.1
1	C	206	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	103	PRO	2.0
1	B	292	GLU	2.0
1	D	335	PRO	2.0
1	C	245	ILE	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](#)

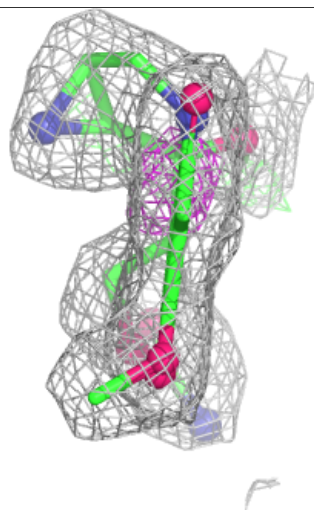
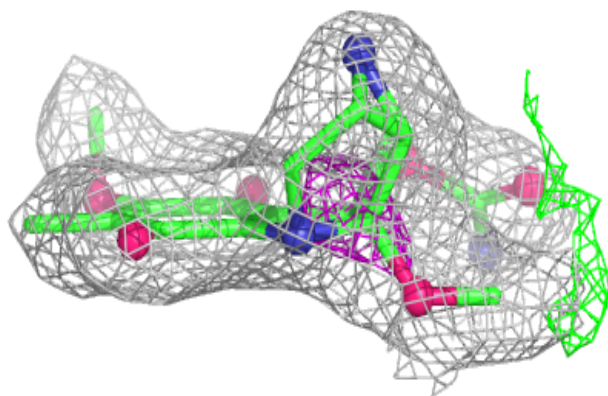
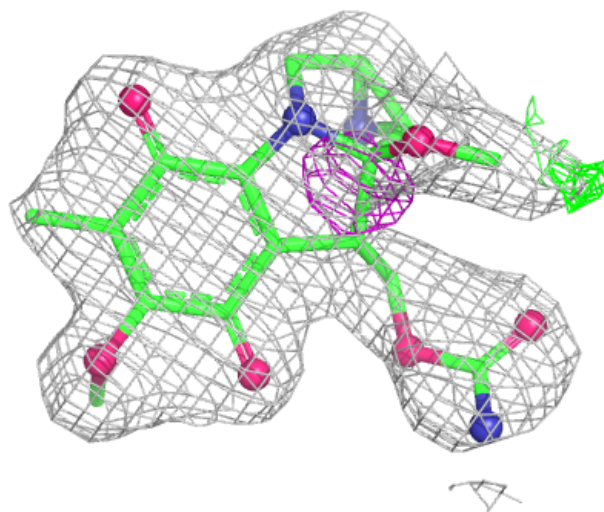
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MQA	D	351	25/25	0.86	0.10	33,38,44,51	0
4	CA	D	353	1/1	0.89	0.08	30,30,30,30	1
2	SAH	C	350	26/26	0.91	0.11	30,40,48,50	0
4	CA	D	352	1/1	0.93	0.06	45,45,45,45	0
3	MQA	B	351	25/25	0.93	0.07	23,27,32,32	0
3	MQA	C	351	25/25	0.94	0.08	24,28,36,44	0
2	SAH	A	350	26/26	0.95	0.07	16,21,30,34	0
2	SAH	B	350	26/26	0.95	0.07	23,33,42,47	0
3	MQA	A	351	25/25	0.95	0.07	15,23,29,33	0
2	SAH	D	350	26/26	0.95	0.08	26,34,38,48	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.

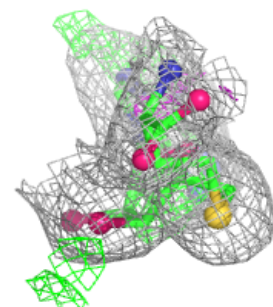
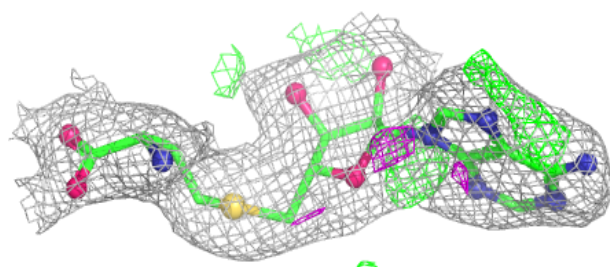
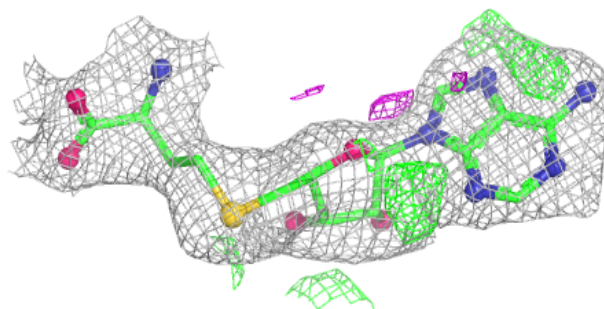
Electron density around MQA D 351:

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

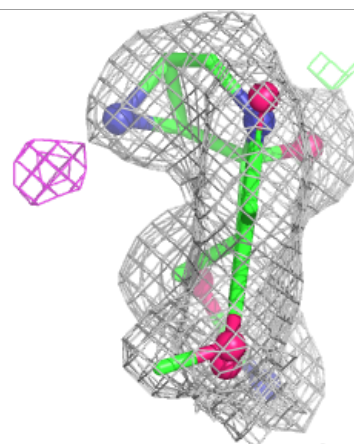
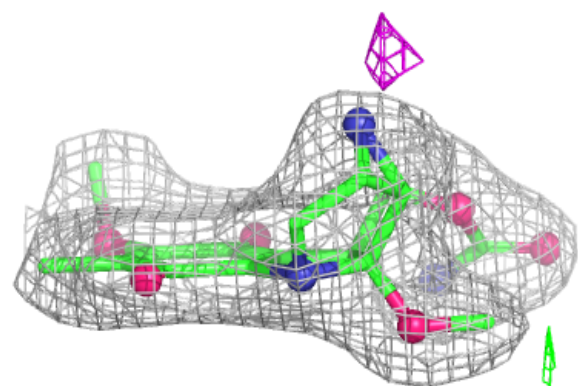
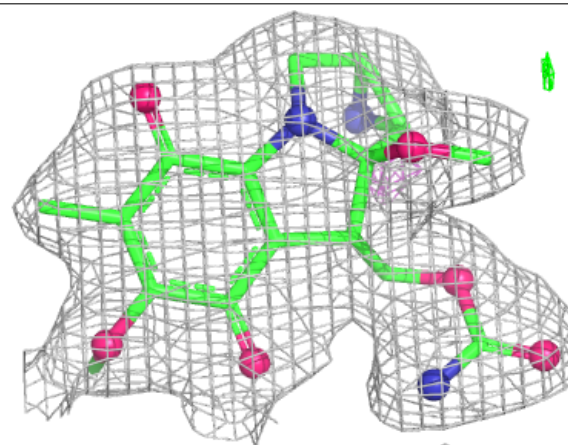


Electron density around SAH C 350:

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

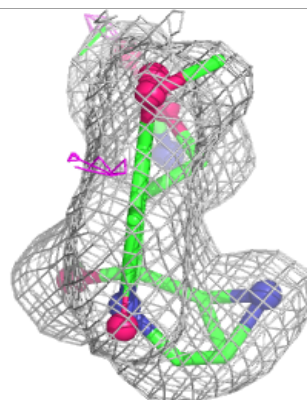
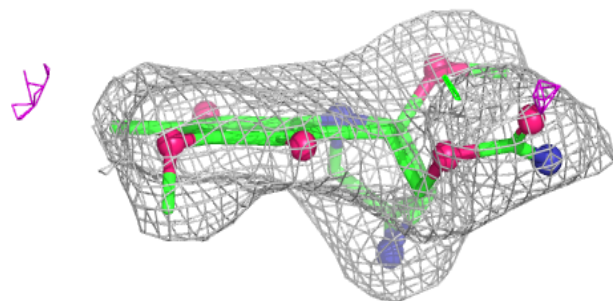
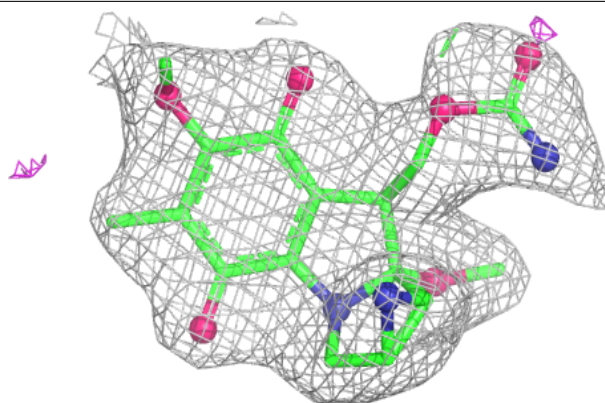
**Electron density around MQA B 351:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

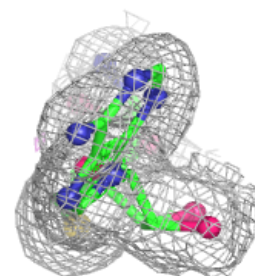
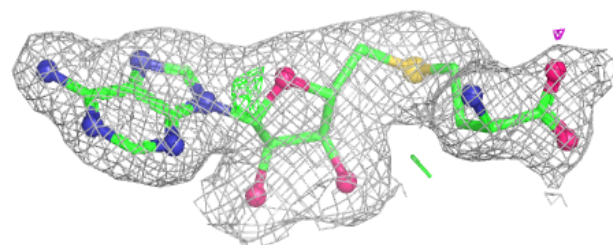
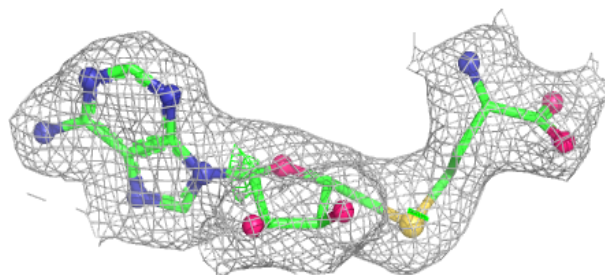


Electron density around MQA C 351:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

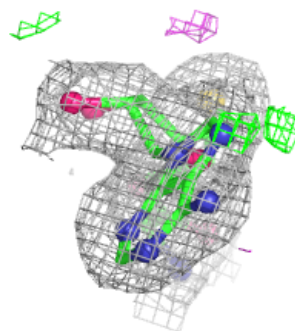
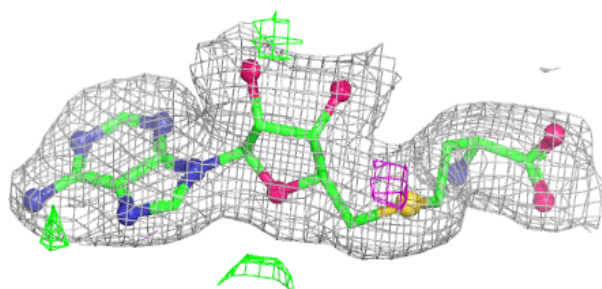
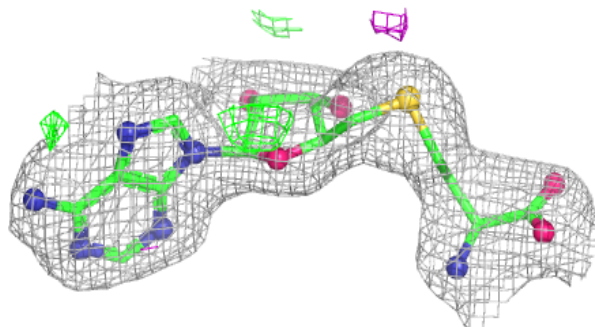
**Electron density around SAH A 350:**

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

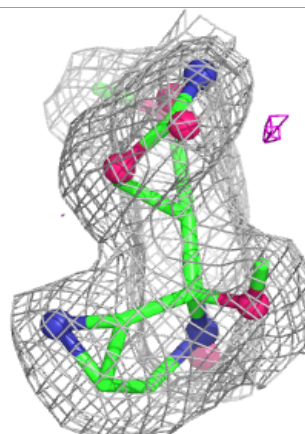
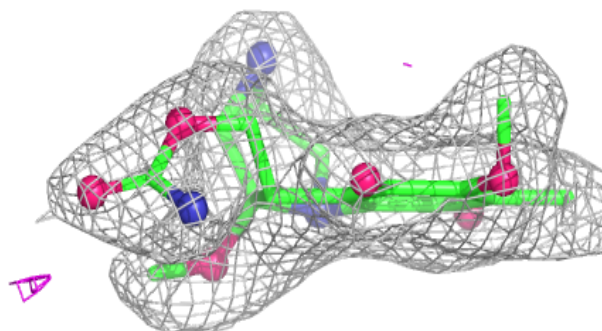
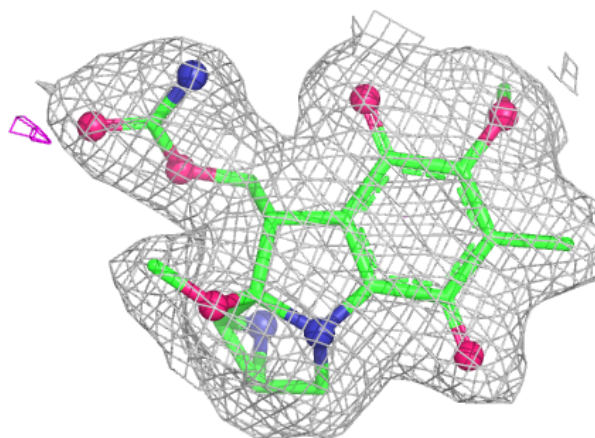


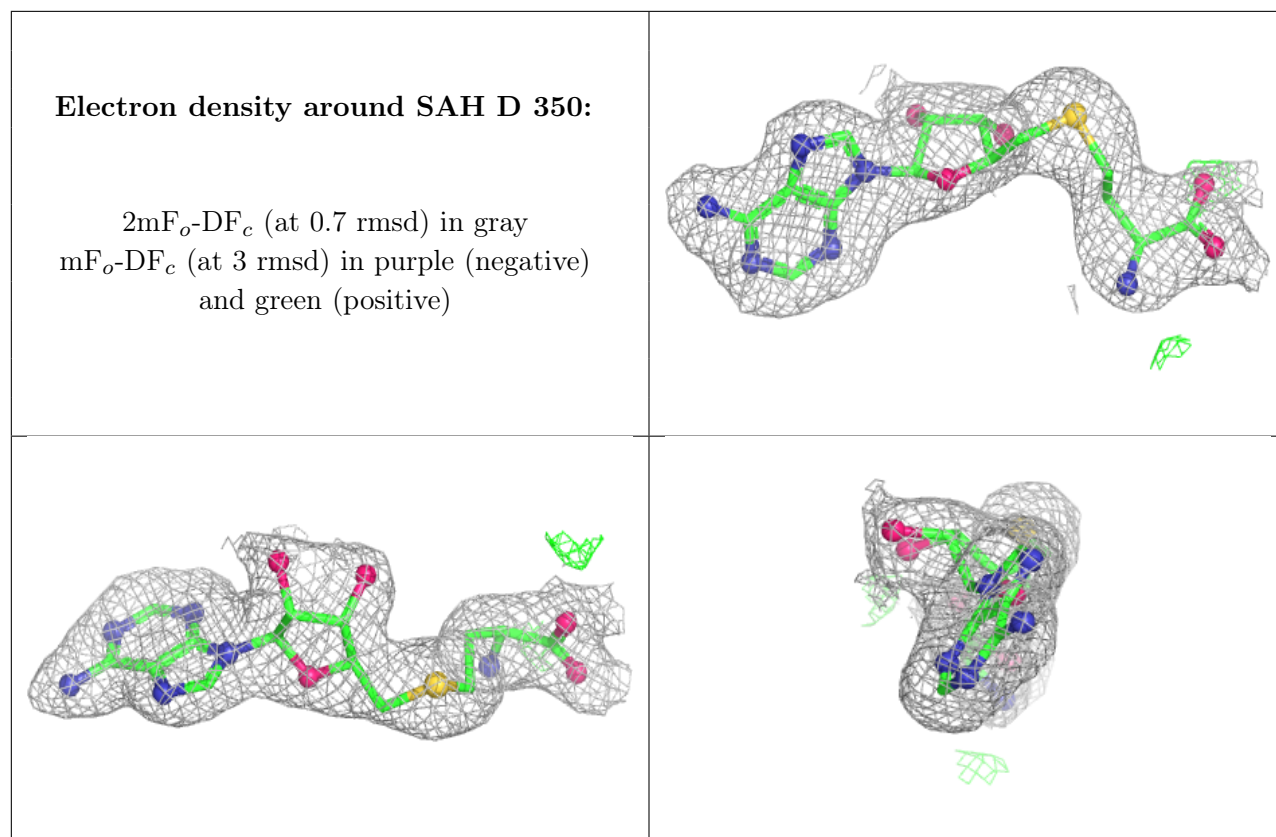
Electron density around SAH B 350:

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

**Electron density around MQA A 351:**

$2mF_o-DF_c$ (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.