



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:56 PM UTC

PDB ID : 3WVG / pdb_00003wvg
Title : Crystal structure of an inward-facing eukaryotic ABC multidrug transporter G277V/A278V/A279V mutant in complex with an cyclic peptide inhibitor, aCAP
Authors : Kodan, A.; Yamaguchi, T.; Nakatsu, T.; Sakiyama, K.; Hipolito, C.J.; Fujioka, A.; Hirokane, R.; Ikeguchi, K.; Watanabe, B.; Hirtake, J.; Kimura, Y.; Suga, H.; Ueda, K.; Kato, H.
Deposited on : 2013-11-18
Resolution : 2.40 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)

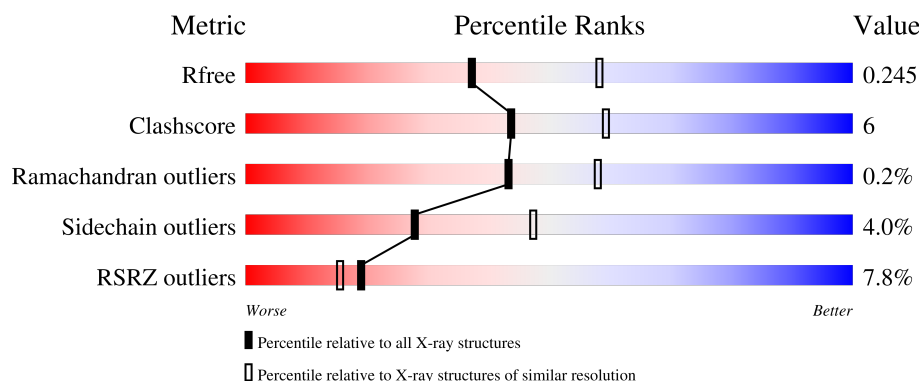
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	621	
2	B	19	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4747 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 ATP-binding cassette, sub-family B, member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	589	4401	2830	750	805	16	0	1	0

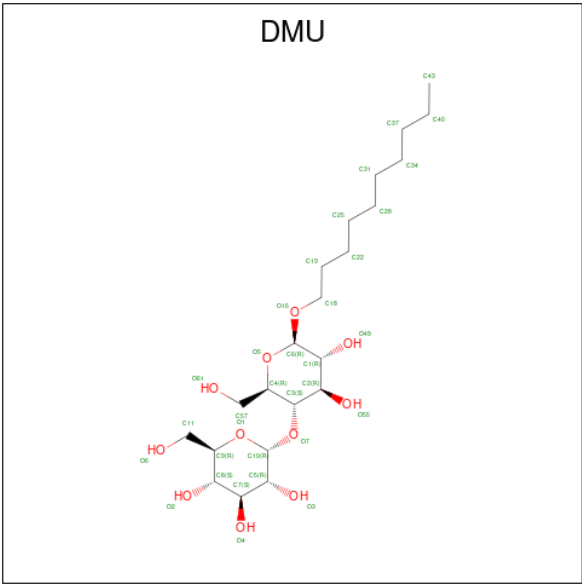
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	277	VAL	GLY	engineered mutation	UNP M1VAN7
A	278	VAL	ALA	engineered mutation	UNP M1VAN7
A	279	VAL	ALA	engineered mutation	UNP M1VAN7
A	697	SER	-	expression tag	UNP M1VAN7
A	698	GLY	-	expression tag	UNP M1VAN7
A	699	ARG	-	expression tag	UNP M1VAN7
A	700	ASP	-	expression tag	UNP M1VAN7
A	701	TYR	-	expression tag	UNP M1VAN7
A	702	LYS	-	expression tag	UNP M1VAN7
A	703	ASP	-	expression tag	UNP M1VAN7
A	704	ASP	-	expression tag	UNP M1VAN7
A	705	ASP	-	expression tag	UNP M1VAN7
A	706	ASP	-	expression tag	UNP M1VAN7
A	707	LYS	-	expression tag	UNP M1VAN7
A	708	HIS	-	expression tag	UNP M1VAN7
A	709	HIS	-	expression tag	UNP M1VAN7
A	710	HIS	-	expression tag	UNP M1VAN7
A	711	HIS	-	expression tag	UNP M1VAN7
A	712	HIS	-	expression tag	UNP M1VAN7
A	713	HIS	-	expression tag	UNP M1VAN7

- Molecule 2 is a protein called anti-CmABCB1 peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	18	146	98	23	24	1	0	0	0

- Molecule 3 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: $C_{22}H_{42}O_{11}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 26 15 11	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C O 23 13 10	0	0
3	B	1	Total C O 28 17 11	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		

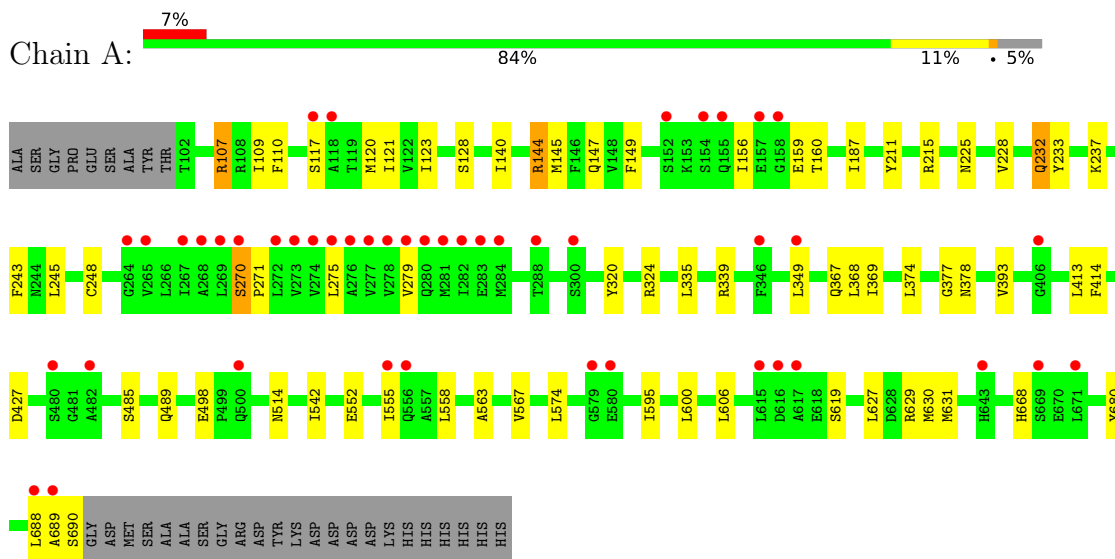
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		

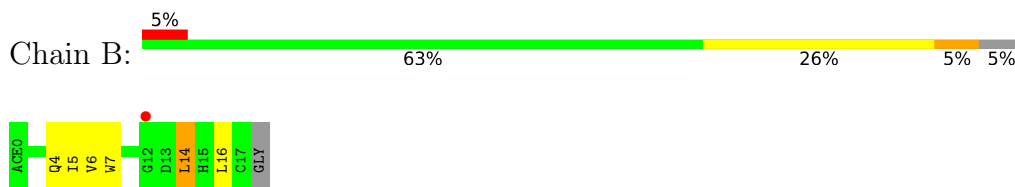
3 Residue-property plots [i](#)

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: ATP-binding cassette, sub-family B, member 1



- Molecule 2: anti-CmABCB1 peptide



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	180.49Å 180.49Å 153.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.47 – 2.40 36.47 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (36.47-2.40) 98.5 (36.47-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.38 (at 2.39Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.219 , 0.246 0.218 , 0.245	Depositor DCC
R_{free} test set	1839 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	57.2	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.2	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	0.95	EDS
Total number of atoms	4747	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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: DTR, DMU, TRS, ACE

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	0.54	0/4487	0.87	2/6089 (0.0%)
2	B	0.85	0/133	0.64	0/182
All	All	0.55	0/4620	0.86	2/6271 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	498	GLU	CA-C-N	5.62	125.09	119.24
1	A	498	GLU	C-N-CA	5.62	125.09	119.24

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	4401	0	4353	45	0
2	B	146	0	132	6	0
3	A	63	0	67	2	0
3	B	28	0	29	6	0
4	A	8	0	12	1	0
5	A	101	0	0	0	0
All	All	4747	0	4593	56	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 6.

All (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ARG:HG2	1:A:144:ARG:HH11	1.13	1.07
1:A:228:VAL:HG22	1:A:413:LEU:HD11	1.52	0.91
1:A:144:ARG:HG2	1:A:144:ARG:NH1	1.83	0.90
3:B:101:DMU:O49	3:B:101:DMU:H6	1.74	0.87
1:A:228:VAL:CG2	1:A:413:LEU:HD11	2.15	0.76
2:B:7:TRP:HA	2:B:14:LEU:HD22	1.66	0.76
1:A:144:ARG:HH11	1:A:144:ARG:CG	1.97	0.72
1:A:689:ALA:O	1:A:690:SER:CB	2.40	0.69
1:A:107:ARG:HH21	1:A:110:PHE:HD2	1.40	0.69
1:A:320:TYR:CE2	1:A:324:ARG:HD2	2.31	0.66
1:A:595:ILE:HG23	1:A:630:MET:HE2	1.77	0.66
1:A:427:ASP:H	1:A:514:ASN:HD21	1.47	0.62
1:A:563:ALA:O	1:A:567:VAL:HG12	1.98	0.62
1:A:147:GLN:HE21	1:A:377:GLY:H	1.48	0.61
1:A:225:ASN:C	1:A:225:ASN:HD22	2.09	0.60
3:B:101:DMU:O1	3:B:101:DMU:C2	2.50	0.60
3:B:101:DMU:O49	3:B:101:DMU:C18	2.50	0.59
1:A:147:GLN:NE2	1:A:377:GLY:H	2.01	0.59
1:A:668:HIS:HD2	1:A:680:TYR:OH	1.87	0.58
3:B:101:DMU:O55	3:B:101:DMU:C9	2.52	0.58
1:A:689:ALA:O	1:A:690:SER:HB2	2.04	0.57
3:B:101:DMU:O1	3:B:101:DMU:H2	2.04	0.57
1:A:144:ARG:NH2	1:A:378:ASN:OD1	2.35	0.57
1:A:631:MET:O	4:A:805:TRS:H32	2.04	0.56
1:A:320:TYR:CZ	1:A:324:ARG:HD2	2.39	0.56
1:A:369:ILE:HA	1:A:374:LEU:O	2.08	0.52
1:A:225:ASN:C	1:A:225:ASN:ND2	2.67	0.52
1:A:228:VAL:HG22	1:A:413:LEU:CD1	2.32	0.49
1:A:542:ILE:HG22	1:A:600:LEU:HD22	1.94	0.49
1:A:156:ILE:O	1:A:160:THR:HG23	2.13	0.49
1:A:232:GLN:HG3	1:A:233:TYR:N	2.28	0.49
1:A:270:SER:N	1:A:271:PRO:CD	2.76	0.49
1:A:627:LEU:HD23	1:A:630:MET:HE3	1.95	0.48
1:A:144:ARG:HD2	2:B:7:TRP:O	2.13	0.48
1:A:144:ARG:NH1	1:A:144:ARG:CG	2.62	0.48
2:B:7:TRP:CA	2:B:14:LEU:HD22	2.42	0.48
1:A:117:SER:O	1:A:121:ILE:HD12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:SER:O	1:A:489:GLN:HG2	2.14	0.46
2:B:4:GLN:O	2:B:7:TRP:CD1	2.68	0.46
1:A:689:ALA:O	1:A:690:SER:OG	2.32	0.46
3:B:101:DMU:O55	3:B:101:DMU:H35	2.16	0.45
1:A:211:TYR:O	1:A:215:ARG:HG2	2.18	0.44
1:A:552:GLU:O	1:A:555:ILE:HG13	2.18	0.43
1:A:140:ILE:O	1:A:144:ARG:NH1	2.52	0.43
1:A:123:ILE:HD12	3:A:803:DMU:H12	2.00	0.42
1:A:248:CYS:SG	1:A:393:VAL:HG22	2.60	0.42
1:A:144:ARG:HD3	2:B:7:TRP:CD2	2.55	0.42
1:A:145:MET:HE3	1:A:149:PHE:CE2	2.55	0.42
1:A:237:LYS:HA	1:A:237:LYS:HD2	1.92	0.42
2:B:5:ILE:HG13	2:B:6:VAL:HG23	2.01	0.42
1:A:275:LEU:O	1:A:279:VAL:HG22	2.19	0.41
1:A:413:LEU:HD23	1:A:413:LEU:HA	1.91	0.41
1:A:120:MET:HE1	1:A:187:ILE:HG21	2.03	0.41
1:A:558:LEU:HD11	1:A:574:LEU:HD21	2.03	0.41
3:A:804:DMU:O6	3:A:804:DMU:H30	2.21	0.41
1:A:109:ILE:HG13	1:A:414:PHE:HE2	1.85	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	588/621 (95%)	573 (97%)	14 (2%)	1 (0%)	43	58
2	B	15/19 (79%)	12 (80%)	3 (20%)	0	100	100
All	All	603/640 (94%)	585 (97%)	17 (3%)	1 (0%)	43	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	270	SER

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	435/494 (88%)	419 (96%)	16 (4%)	30	51
2	B	14/14 (100%)	12 (86%)	2 (14%)	3	4
All	All	449/508 (88%)	431 (96%)	18 (4%)	28	47

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	ARG
1	A	128	SER
1	A	144	ARG
1	A	159	GLU
1	A	232	GLN
1	A	243	PHE
1	A	245	LEU
1	A	335	LEU
1	A	339	ARG
1	A	349	LEU
1	A	367	GLN
1	A	368	LEU
1	A	606	LEU
1	A	619	SER
1	A	629	ARG
1	A	688	LEU
2	B	14	LEU
2	B	16	LEU

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	147	GLN
1	A	155	GLN
1	A	225	ASN
1	A	470	ASN
1	A	514	ASN
1	A	591	GLN
1	A	665	GLN
1	A	668	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DMU	B	101	-	29,29,34	0.54	1 (3%)	40,40,45	0.87	0
3	DMU	A	802	-	7,7,34	0.29	0	6,6,45	0.39	0
3	DMU	A	804	-	24,24,34	0.67	0	30,34,45	1.35	3 (10%)
3	DMU	A	801	-	27,27,34	0.52	0	38,38,45	0.73	1 (2%)
3	DMU	A	803	-	5,5,34	0.31	0	4,4,45	0.37	0
4	TRS	A	805	-	7,7,7	0.33	0	9,9,9	0.63	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMU	B	101	-	-	9/14/54/59	0/2/2/2
3	DMU	A	802	-	-	5/5/5/59	-
3	DMU	A	804	-	-	2/10/46/59	0/2/2/2
3	DMU	A	801	-	-	5/12/52/59	0/2/2/2
3	DMU	A	803	-	-	2/3/3/59	-
4	TRS	A	805	-	-	9/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	101	DMU	O16-C6	2.12	1.43	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	804	DMU	C2-C3-C4	4.34	116.75	110.76
3	A	801	DMU	C10-O7-C3	-3.33	110.09	117.98
3	A	804	DMU	O5-C4-C3	2.69	113.82	109.90
3	A	804	DMU	C8-C7-C5	2.19	114.67	110.83

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	101	DMU	C1-C6-O16-C18
3	B	101	DMU	O5-C6-O16-C18

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Mol	Chain	Res	Type	Atoms
3	A	804	DMU	O5-C4-C57-O61
3	A	801	DMU	C3-C4-C57-O61
3	A	801	DMU	O6-C11-C9-O1
3	B	101	DMU	C2-C3-O7-C10
3	A	804	DMU	C3-C4-C57-O61
3	A	801	DMU	O5-C4-C57-O61
3	A	801	DMU	O6-C11-C9-C8
3	B	101	DMU	O6-C11-C9-O1
3	A	801	DMU	O16-C18-C19-C22
3	A	803	DMU	C25-C28-C31-C34
4	A	805	TRS	C3-C-C1-O1
3	A	802	DMU	C25-C28-C31-C34
3	B	101	DMU	O16-C18-C19-C22
3	B	101	DMU	C4-C3-O7-C10
3	A	802	DMU	C28-C31-C34-C37
3	A	802	DMU	C31-C34-C37-C40
3	A	802	DMU	C34-C37-C40-C43
4	A	805	TRS	N-C-C1-O1
4	A	805	TRS	C1-C-C2-O2
4	A	805	TRS	N-C-C2-O2
4	A	805	TRS	C1-C-C3-O3
4	A	805	TRS	C2-C-C3-O3
3	A	803	DMU	C22-C25-C28-C31
3	A	802	DMU	C22-C25-C28-C31
4	A	805	TRS	C2-C-C1-O1
4	A	805	TRS	C3-C-C2-O2
3	B	101	DMU	O6-C11-C9-C8
3	B	101	DMU	O1-C10-O7-C3
4	A	805	TRS	N-C-C3-O3
3	B	101	DMU	C5-C10-O7-C3

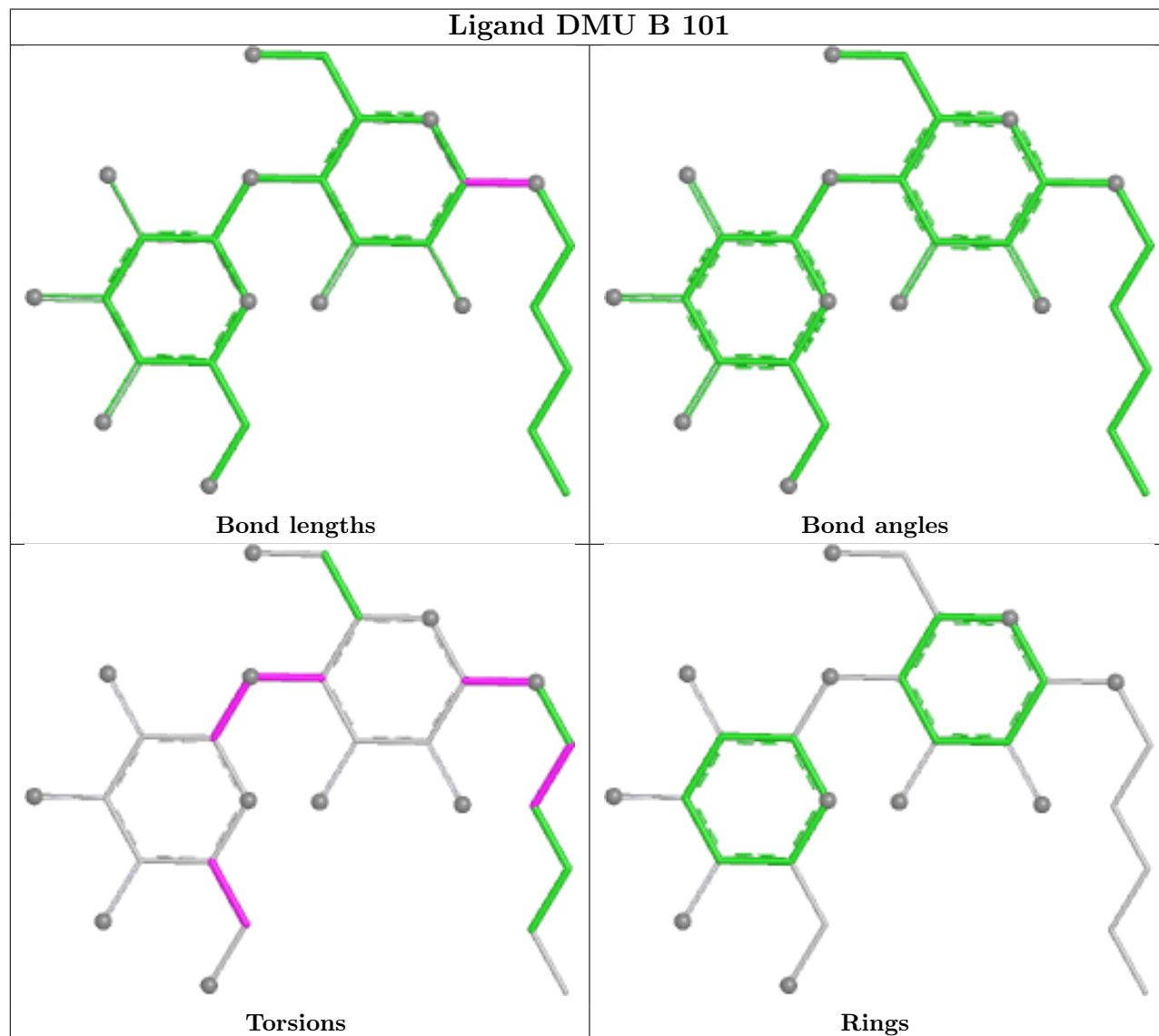
There are no ring outliers.

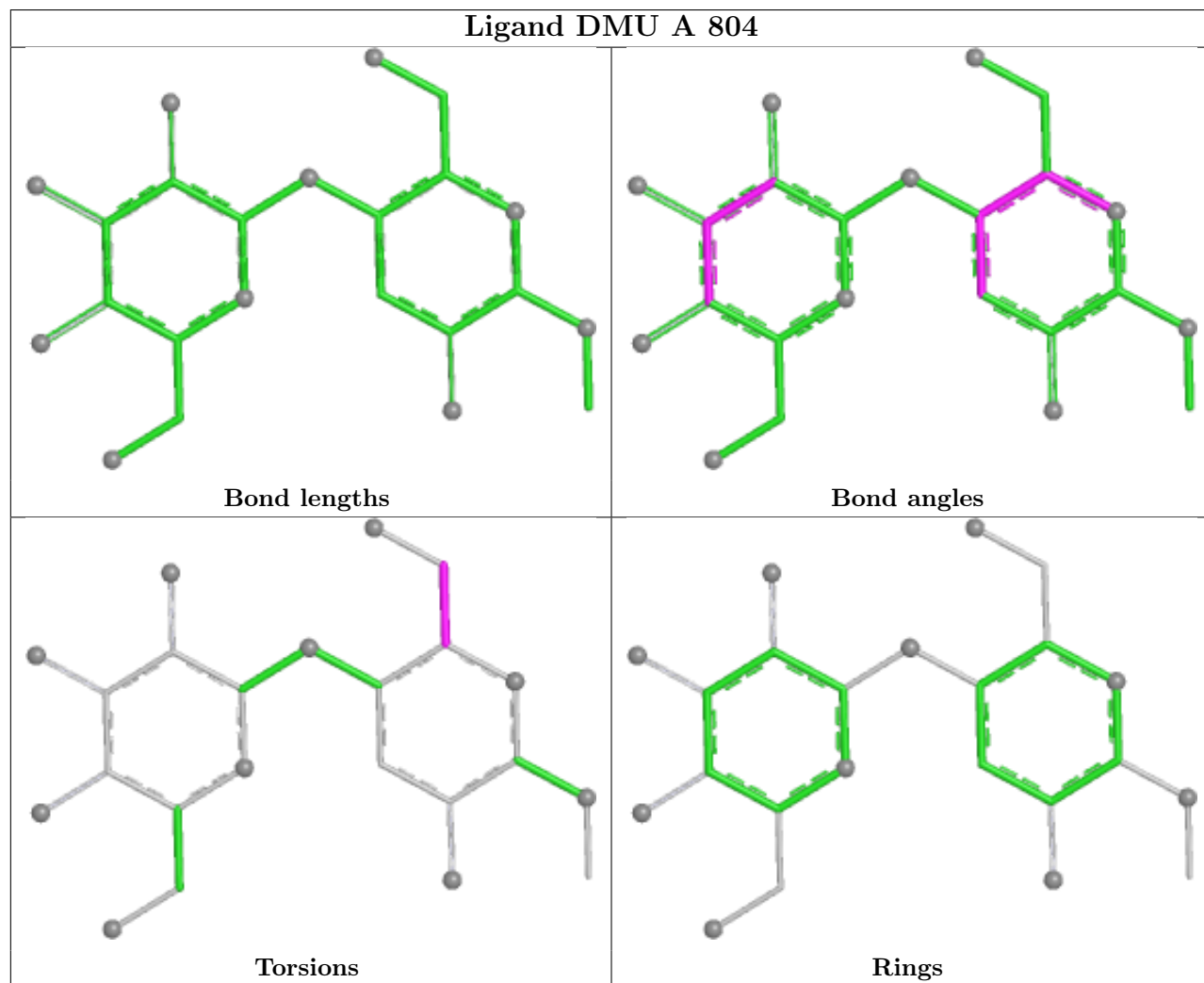
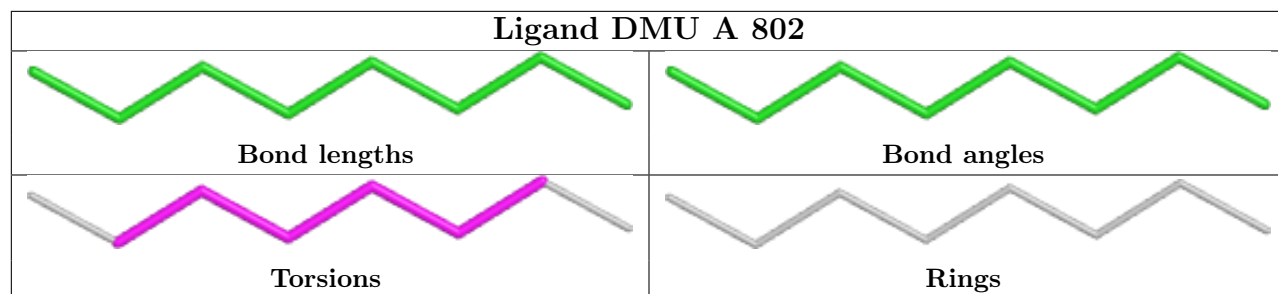
4 monomers are involved in 9 short contacts:

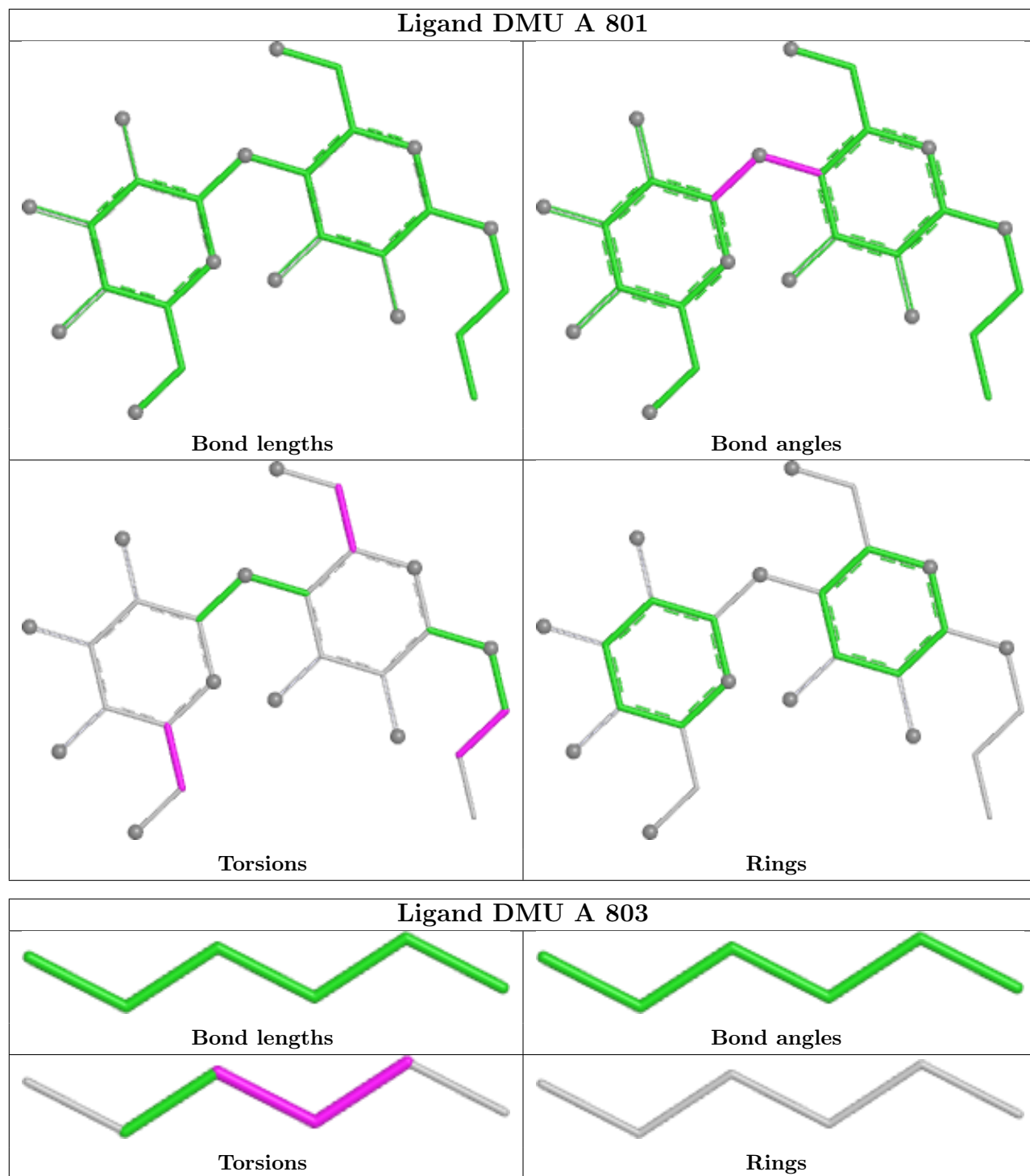
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	101	DMU	6	0
3	A	804	DMU	1	0
3	A	803	DMU	1	0
4	A	805	TRS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	589/621 (94%)	0.52	46 (7%) 19 15	36, 59, 98, 124	1 (0%)
2	B	16/19 (84%)	1.15	1 (6%) 26 22	60, 76, 96, 110	0
All	All	605/640 (94%)	0.53	47 (7%) 19 15	36, 59, 98, 124	1 (0%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	283	GLU	7.8
1	A	269	LEU	6.9
1	A	282	ILE	6.3
1	A	270	SER	6.1
1	A	280	GLN	5.1
1	A	274	VAL	4.9
1	A	284	MET	4.9
1	A	689	ALA	4.3
1	A	279	VAL	4.1
1	A	265	VAL	3.9
1	A	616	ASP	3.8
1	A	267	ILE	3.7
1	A	273	VAL	3.7
1	A	154	SER	3.5
1	A	480	SER	3.5
1	A	580	GLU	3.3
1	A	264	GLY	3.3
1	A	406	GLY	3.2
1	A	643[A]	HIS	3.1
1	A	281	MET	3.1
1	A	272	LEU	3.0
1	A	158	GLY	2.9
1	A	300	SER	2.7
1	A	278	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	346	PHE	2.7
1	A	157	GLU	2.7
1	A	556	GLN	2.6
1	A	688	LEU	2.5
1	A	669	SER	2.5
1	A	555	ILE	2.4
1	A	275	LEU	2.4
1	A	277	VAL	2.4
1	A	288	THR	2.3
1	A	152	SER	2.3
1	A	617	ALA	2.3
1	A	155	GLN	2.3
1	A	500	GLN	2.3
1	A	117	SER	2.2
1	A	276	ALA	2.2
2	B	12	GLY	2.2
1	A	482	ALA	2.2
1	A	349	LEU	2.2
1	A	615	LEU	2.1
1	A	579	GLY	2.1
1	A	118	ALA	2.1
1	A	268	ALA	2.0
1	A	671	LEU	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
2	DTR	B	1	14/15	0.81	0.18	97,115,117,118	0

6.3 Carbohydrates [i](#)

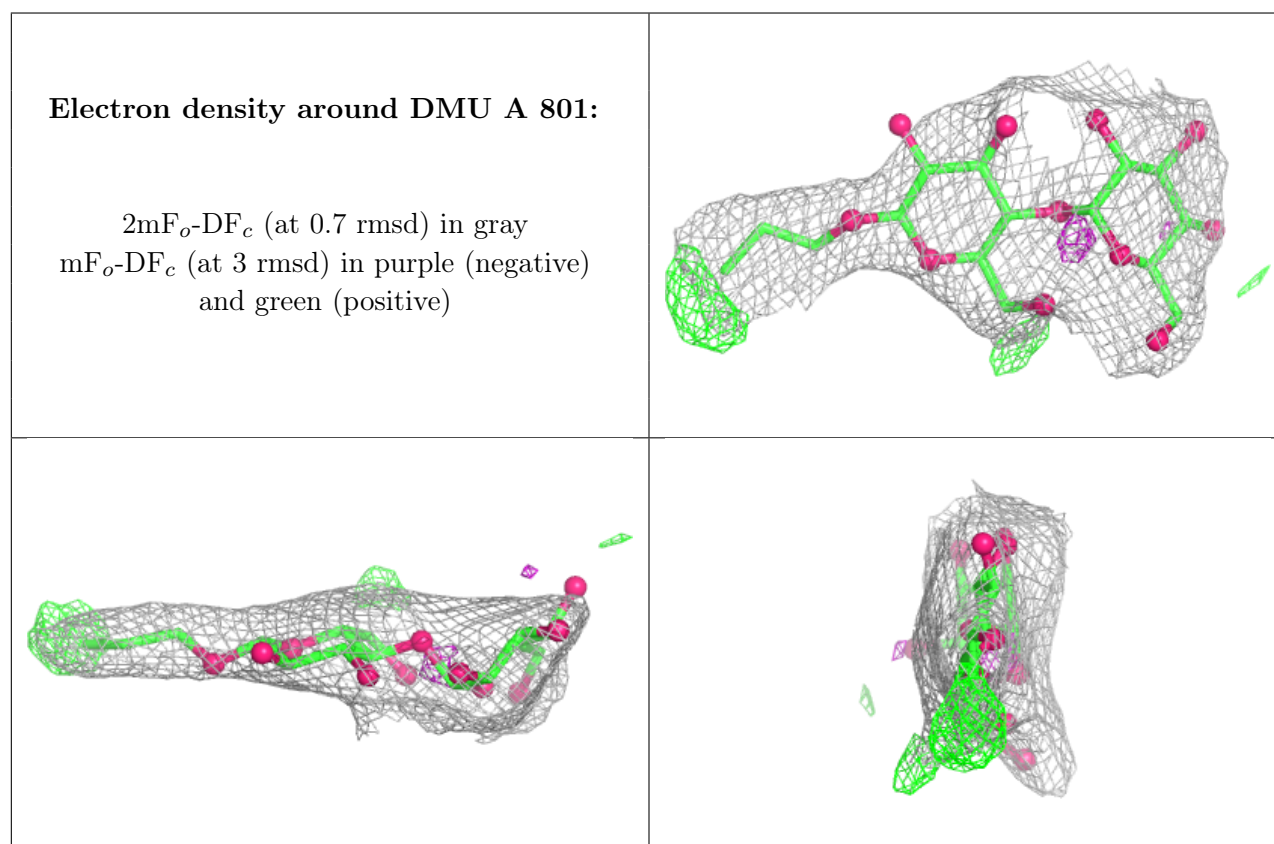
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

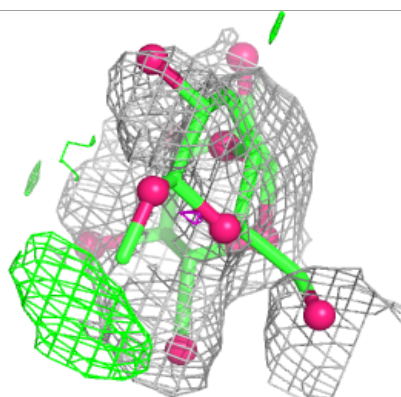
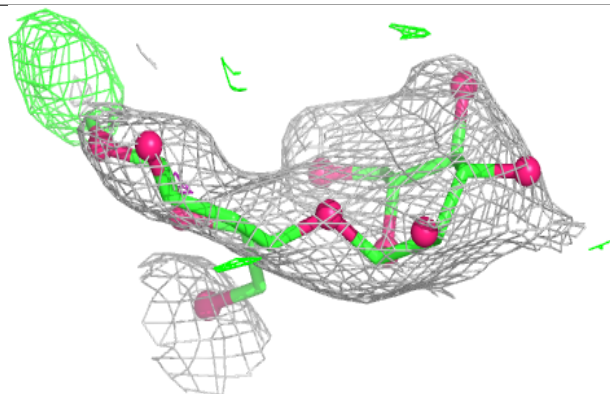
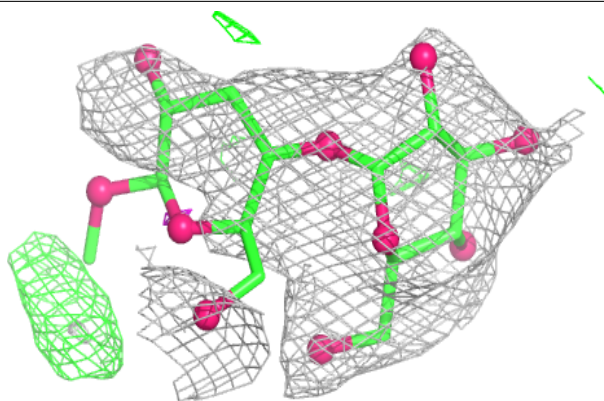
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	DMU	A	801	26/33	0.69	0.17	96,108,113,114	0
3	DMU	A	804	23/33	0.69	0.20	116,123,126,127	0
3	DMU	B	101	28/33	0.71	0.19	96,115,119,121	0
3	DMU	A	802	8/33	0.83	0.17	81,82,84,84	0
4	TRS	A	805	8/8	0.84	0.14	70,72,72,73	7
3	DMU	A	803	6/33	0.85	0.15	72,77,78,80	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.

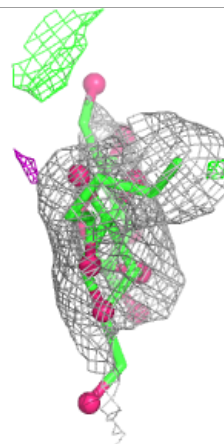
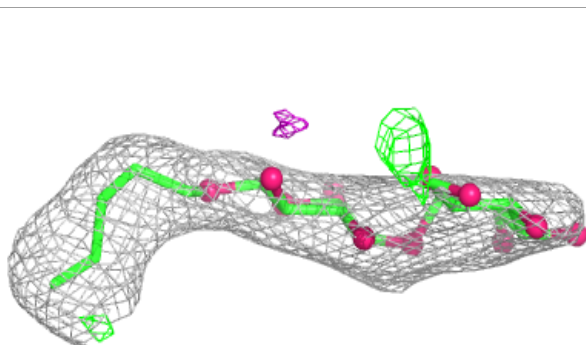
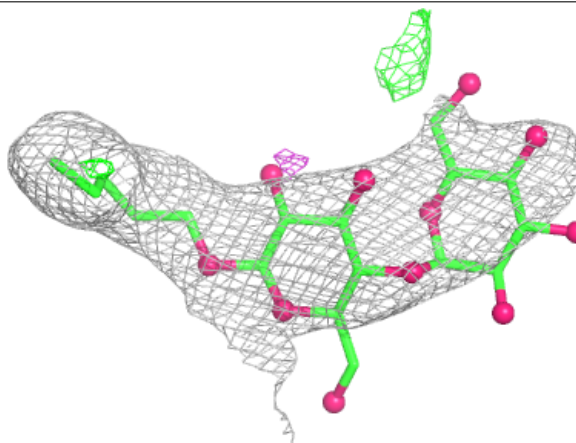


Electron density around DMU A 804:

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

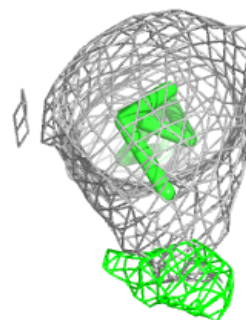
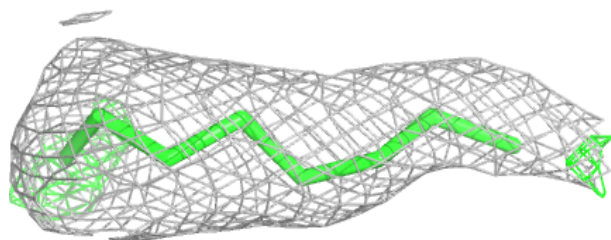
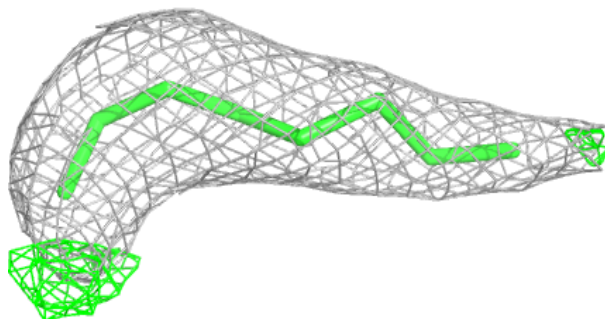
**Electron density around DMU B 101:**

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

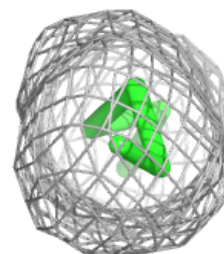
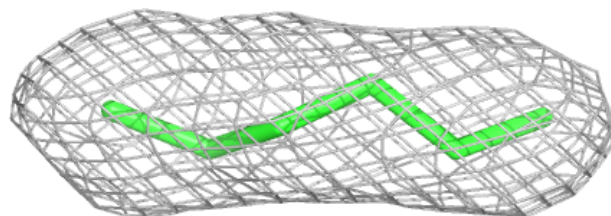
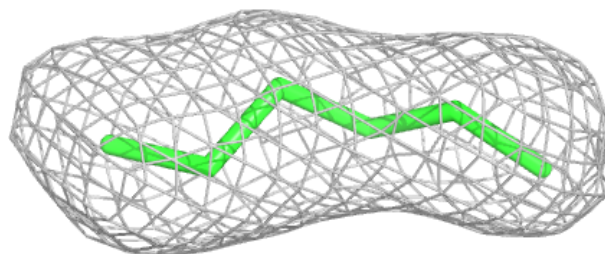


Electron density around DMU A 802:

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

**Electron density around DMU A 803:**

$2mF_o-DF_c$ (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.