



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:45 AM UTC

PDB ID : 6ZLH / pdb_00006zlh
Title : the structure of glutamate transporter homologue GltTk in complex with the photo switchable compound (trans)
Authors : Arkhipova, V.; Slotboom, D.J.; Guskov, A.
Deposited on : 2020-06-30
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

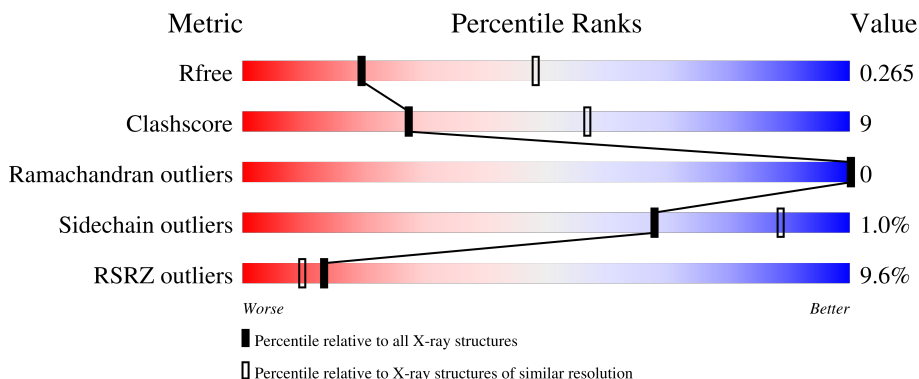
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	438	9% 77% 20% .
1	B	438	10% 78% 18% .
1	C	438	9% 73% 23% .

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 9881 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 Proton/glutamate symporter, SDF family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3161	2085	511	549	16			
1	B	423	Total	C	N	O	S	0	1	0
			3159	2084	511	548	16			
1	C	423	Total	C	N	O	S	0	1	0
			3159	2084	511	548	16			

There are 24 discrepancies between the modelled and reference sequences:

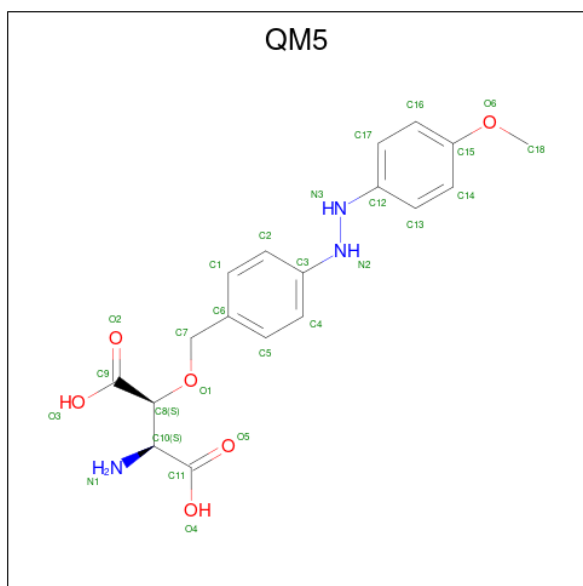
Chain	Residue	Modelled	Actual	Comment	Reference
A	431	HIS	-	expression tag	UNP Q5JID0
A	432	HIS	-	expression tag	UNP Q5JID0
A	433	HIS	-	expression tag	UNP Q5JID0
A	434	HIS	-	expression tag	UNP Q5JID0
A	435	HIS	-	expression tag	UNP Q5JID0
A	436	HIS	-	expression tag	UNP Q5JID0
A	437	HIS	-	expression tag	UNP Q5JID0
A	438	HIS	-	expression tag	UNP Q5JID0
B	431	HIS	-	expression tag	UNP Q5JID0
B	432	HIS	-	expression tag	UNP Q5JID0
B	433	HIS	-	expression tag	UNP Q5JID0
B	434	HIS	-	expression tag	UNP Q5JID0
B	435	HIS	-	expression tag	UNP Q5JID0
B	436	HIS	-	expression tag	UNP Q5JID0
B	437	HIS	-	expression tag	UNP Q5JID0
B	438	HIS	-	expression tag	UNP Q5JID0
C	431	HIS	-	expression tag	UNP Q5JID0
C	432	HIS	-	expression tag	UNP Q5JID0
C	433	HIS	-	expression tag	UNP Q5JID0
C	434	HIS	-	expression tag	UNP Q5JID0
C	435	HIS	-	expression tag	UNP Q5JID0
C	436	HIS	-	expression tag	UNP Q5JID0
C	437	HIS	-	expression tag	UNP Q5JID0

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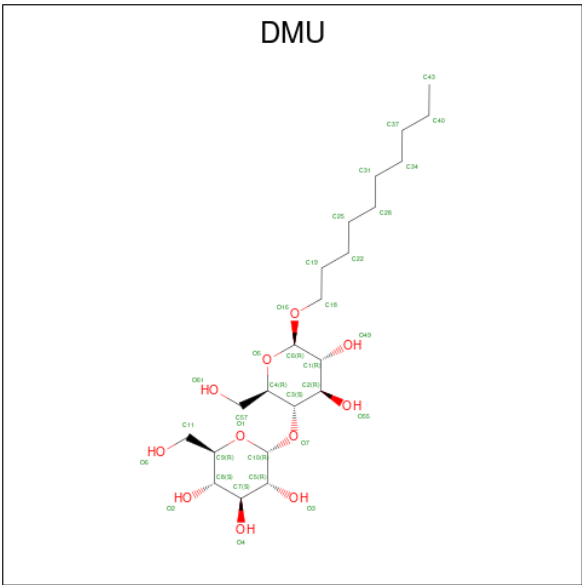
Chain	Residue	Modelled	Actual	Comment	Reference
C	438	HIS	-	expression tag	UNP Q5JID0

- Molecule 2 is (2 {S},3 {S})-2-azanyl-3-[[4-[2-(4-methoxyphenyl)hydrazinyl]phenyl]methoxy]butanedioic acid (CCD ID: QM5) (formula: C₁₈H₂₁N₃O₆).



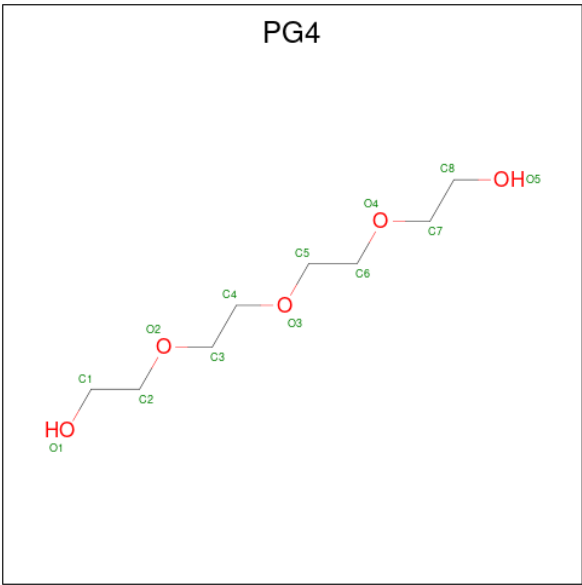
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			27	18	3	6		
2	B	1	Total	C	N	O	0	0
			27	18	3	6		
2	C	1	Total	C	N	O	0	0
			27	18	3	6		

- Molecule 3 is DECYL-BETA-D-MALTOPYRANOSIDE (CCD ID: DMU) (formula: C₂₂H₄₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			33	22	11		
3	B	1	Total	C	O	0	0
			33	22	11		
3	C	1	Total	C	O	0	0
			33	22	11		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



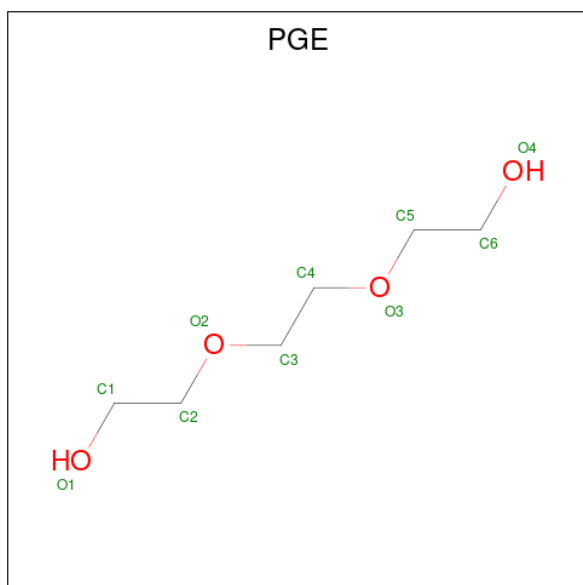
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		
5	A	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		
5	B	1	Total	C	O	0	0
			10	6	4		
5	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

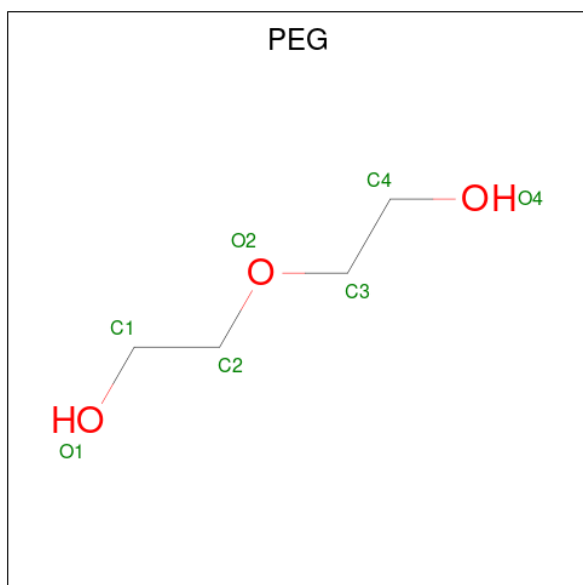
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	Na	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	3	Total 3	Na 3	0	0
6	C	3	Total 3	Na 3	0	0

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



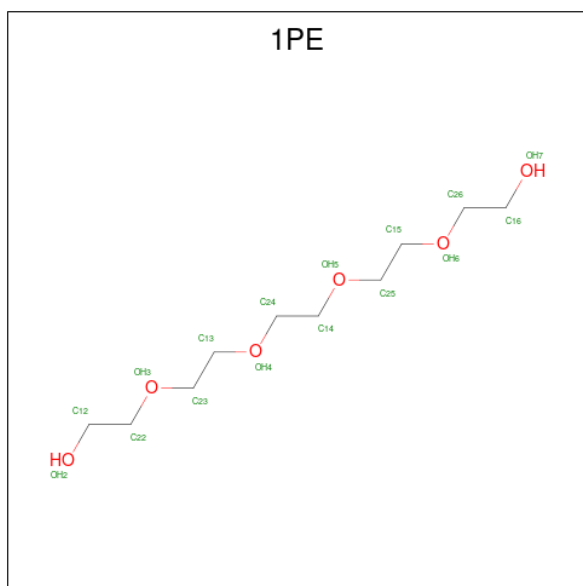
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 7	C 4	O 3	0	0
7	A	1	Total 7	C 4	O 3	0	0
7	B	1	Total 7	C 4	O 3	0	0
7	B	1	Total 7	C 4	O 3	0	0
7	B	1	Total 7	C 4	O 3	0	0
7	B	1	Total 7	C 4	O 3	0	0
7	B	1	Total 7	C 4	O 3	0	0
7	C	1	Total 7	C 4	O 3	0	0
7	C	1	Total 7	C 4	O 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			7	4	3		
7	C	1	Total	C	O	0	0
			7	4	3		
7	C	1	Total	C	O	0	0
			7	4	3		
7	C	1	Total	C	O	0	0
			7	4	3		
7	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).

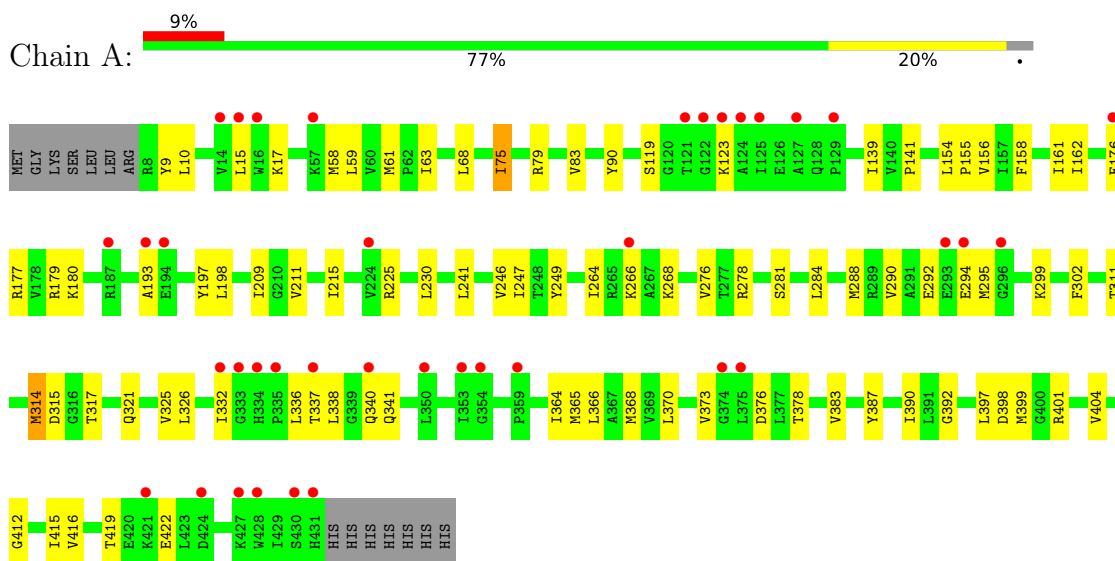


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			16	10	6		

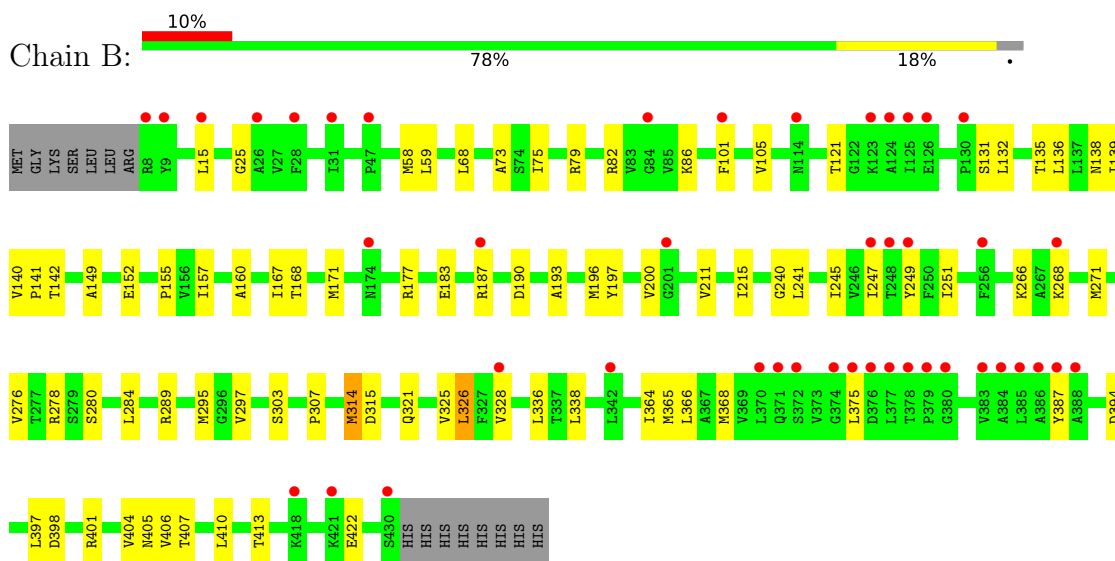
3 Residue-property plots [i](#)

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.

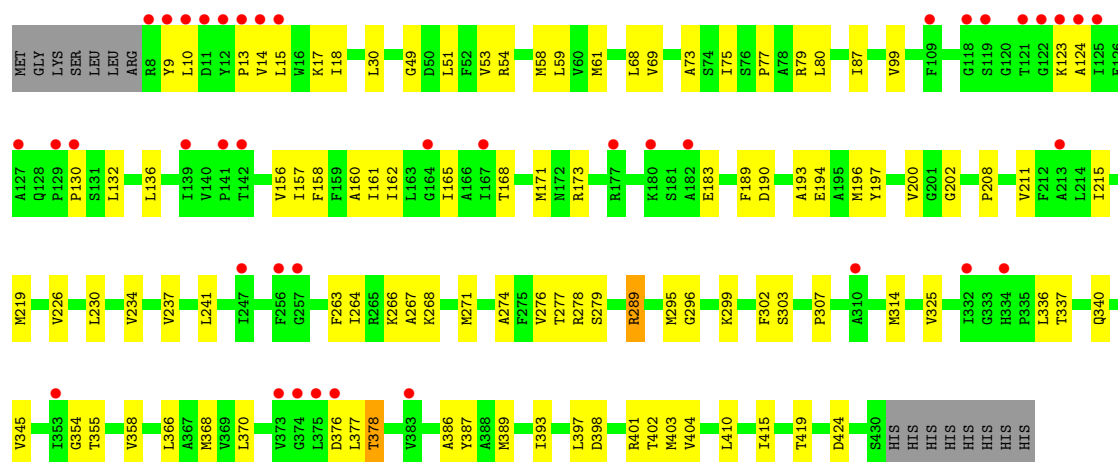
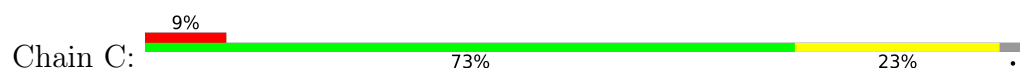
- Molecule 1: Proton/glutamate symporter, SDF family



- Molecule 1: Proton/glutamate symporter, SDF family



- Molecule 1: Proton/glutamate symporter, SDF family



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.79Å 116.79Å 310.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.91 – 2.80 49.91 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.91-2.80) 99.9 (49.91-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.218 , 0.251 0.227 , 0.265	Depositor DCC
R_{free} test set	3067 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	98.6	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9881	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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: QM5, PEG, PGE, DMU, 1PE, PG4, NA

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	0.37	0/3221	0.60	0/4385
1	B	0.38	0/3221	0.62	0/4384
1	C	0.39	0/3221	0.62	0/4384
All	All	0.38	0/9663	0.61	0/13153

There are no bond length outliers.

There are no bond angle outliers.

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	3161	0	3360	59	0
1	B	3159	0	3365	56	0
1	C	3159	0	3366	75	0
2	A	27	0	0	1	0
2	B	27	0	0	0	0
2	C	27	0	0	0	0
3	A	33	0	42	3	0
3	B	33	0	42	1	0
3	C	33	0	42	3	0
4	A	39	0	54	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	20	0	28	1	0
5	B	30	0	42	0	0
5	C	10	0	14	0	0
6	A	3	0	0	0	0
6	B	3	0	0	0	0
6	C	3	0	0	0	0
7	A	14	0	20	0	0
7	B	35	0	50	3	0
7	C	49	0	70	2	0
8	C	16	0	22	1	0
All	All	9881	0	10517	186	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 9.

All (186) 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:278:ARG:HD2	1:B:398:ASP:HB3	1.56	0.87
1:C:157:ILE:HD11	1:C:307:PRO:HB2	1.62	0.80
1:A:364:ILE:HG22	1:A:368:MET:HE2	1.69	0.75
1:B:364:ILE:HG22	1:B:368:MET:HE2	1.71	0.72
1:A:15:LEU:HD13	1:A:268:LYS:HZ1	1.57	0.70
1:C:289:ARG:HH12	3:C:502:DMU:H36	1.56	0.69
1:C:190:ASP:O	1:C:194:GLU:HG2	1.94	0.68
1:B:321:GLN:HG2	1:B:366:LEU:HD13	1.76	0.67
1:A:10:LEU:HD21	3:A:502:DMU:H9	1.77	0.66
1:C:171:MET:HE3	1:C:183:GLU:HA	1.76	0.66
1:C:130:PRO:HG2	1:C:358:VAL:HG21	1.77	0.66
1:C:264:ILE:HG13	1:C:271:MET:HE1	1.78	0.65
1:A:249:TYR:OH	1:A:315:ASP:OD2	2.15	0.61
1:B:157:ILE:HD11	1:B:307:PRO:HB2	1.82	0.60
1:B:211:VAL:HG13	1:B:276:VAL:HG11	1.82	0.60
1:C:15:LEU:HB2	1:C:268:LYS:HE2	1.83	0.60
1:C:325:VAL:HG12	1:C:336:LEU:HD11	1.83	0.60
1:A:141:PRO:HB3	1:A:155:PRO:HB2	1.84	0.59
1:A:215:ILE:HD12	1:A:399:MET:HE1	1.83	0.59
1:A:365:MET:HA	1:A:368:MET:HE3	1.83	0.59
1:C:123:LYS:HG3	1:C:376:ASP:CG	2.28	0.59
1:C:263:PHE:HD2	1:C:264:ILE:HD12	1.67	0.59
1:A:241:LEU:HB3	1:A:404:VAL:HG21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:196:MET:O	1:B:200:VAL:HG23	2.03	0.58
1:C:123:LYS:HG3	1:C:376:ASP:OD2	2.04	0.58
1:B:241:LEU:HB3	1:B:404:VAL:HG21	1.85	0.58
8:C:504:1PE:H242	7:C:511:PEG:H41	1.85	0.58
1:C:61:MET:HE1	1:C:156:VAL:HG21	1.85	0.57
1:B:266:LYS:HB2	1:B:295:MET:HE2	1.85	0.57
1:A:211:VAL:HG22	1:A:276:VAL:HG21	1.86	0.57
1:B:328:VAL:HG12	1:B:375:LEU:HD13	1.87	0.57
1:A:290:VAL:O	1:A:294:GLU:HB2	2.05	0.57
3:A:502:DMU:H35	1:C:173:ARG:HH12	1.69	0.56
1:B:289:ARG:HH22	3:B:505:DMU:H40	1.70	0.56
1:C:132:LEU:O	1:C:136:LEU:HG	2.05	0.56
1:B:321:GLN:O	1:B:325:VAL:HG12	2.06	0.56
1:A:15:LEU:HD22	1:A:268:LYS:HE3	1.88	0.56
1:A:90:TYR:CE2	1:A:412:GLY:HA3	2.41	0.56
1:B:142:THR:HG23	1:C:54:ARG:HH21	1.72	0.55
1:A:177:ARG:NH1	1:B:190:ASP:OD2	2.40	0.55
1:A:325:VAL:HG22	1:A:370:LEU:HD23	1.87	0.55
1:A:79:ARG:NH2	1:A:422:GLU:OE2	2.40	0.55
1:B:68:LEU:HD23	1:B:160:ALA:HB3	1.89	0.55
1:C:366:LEU:HD23	1:C:387:TYR:HE1	1.72	0.55
1:C:278:ARG:HD2	1:C:398:ASP:HB3	1.88	0.54
1:A:366:LEU:HD23	1:A:387:TYR:HE1	1.71	0.54
1:B:132:LEU:O	1:B:136:LEU:HG	2.08	0.54
1:C:99:VAL:HG11	1:C:345:VAL:HA	1.90	0.54
1:B:249:TYR:OH	1:B:315:ASP:OD2	2.18	0.54
1:A:119:SER:HB2	1:A:332:ILE:HB	1.89	0.54
1:C:266:LYS:HB2	1:C:295:MET:HE2	1.88	0.53
1:C:267:ALA:HB3	1:C:271:MET:HE3	1.90	0.53
1:C:196:MET:O	1:C:200:VAL:HG23	2.09	0.53
1:B:193:ALA:O	1:B:197:TYR:HD1	1.89	0.53
1:A:326:LEU:HD23	1:A:336:LEU:HD12	1.92	0.52
1:B:152:GLU:O	1:B:155:PRO:HD2	2.10	0.52
1:C:61:MET:CE	1:C:156:VAL:HG21	2.40	0.52
1:B:149:ALA:HB1	7:B:511:PEG:H32	1.92	0.52
1:C:10:LEU:HD12	1:C:10:LEU:H	1.76	0.51
1:C:234:VAL:HG12	7:C:514:PEG:H22	1.92	0.51
1:C:241:LEU:HB3	1:C:404:VAL:HG21	1.91	0.51
1:A:139:ILE:O	1:A:155:PRO:HA	2.11	0.51
1:A:246:VAL:HG12	1:A:247:ILE:HD12	1.93	0.51
1:C:69:VAL:HG11	1:C:189:PHE:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LEU:HG	1:A:311:THR:HG21	1.93	0.50
1:B:131:SER:O	1:B:135:THR:HG23	2.11	0.50
1:B:73:ALA:O	1:B:168:THR:HG21	2.12	0.50
1:B:79:ARG:NH1	1:B:422:GLU:OE2	2.44	0.50
1:C:211:VAL:HG22	1:C:276:VAL:HG21	1.92	0.50
1:B:75:ILE:HD11	1:B:79:ARG:HG2	1.93	0.50
1:B:365:MET:HA	1:B:368:MET:HE3	1.94	0.50
1:A:337:THR:O	1:A:341:GLN:HG3	2.12	0.49
1:C:68:LEU:HD21	1:C:161:ILE:HG13	1.94	0.49
1:C:49:GLY:O	1:C:53:VAL:HG23	2.13	0.49
1:C:289:ARG:NH1	3:C:502:DMU:H36	2.27	0.49
1:A:158:PHE:O	1:A:162:ILE:HG12	2.12	0.49
1:C:274:ALA:HB1	1:C:402:THR:HG22	1.92	0.49
1:B:82:ARG:HG2	1:B:86:LYS:NZ	2.28	0.49
1:C:30:LEU:HD21	1:C:219:MET:HE3	1.95	0.49
1:C:124:ALA:O	1:C:376:ASP:HB3	2.12	0.49
1:C:193:ALA:O	1:C:197:TYR:HD1	1.96	0.49
1:A:61:MET:HE1	1:A:156:VAL:HG21	1.94	0.49
1:A:9:TYR:HE2	1:A:17:LYS:HD2	1.78	0.49
1:A:397:LEU:O	1:A:401:ARG:HG2	2.13	0.48
1:B:271:MET:HE3	1:B:407:THR:OG1	2.14	0.48
1:A:332:ILE:HD13	1:A:383:VAL:HG22	1.95	0.48
1:A:317:THR:OG1	2:A:501:QM5:O2	2.18	0.48
1:B:314:MET:HG2	1:B:405:ASN:ND2	2.28	0.48
1:B:211:VAL:HG22	1:B:276:VAL:HG21	1.96	0.48
1:C:68:LEU:HD23	1:C:160:ALA:HB3	1.96	0.48
1:C:158:PHE:O	1:C:162:ILE:HG12	2.14	0.48
1:A:340:GLN:HG2	1:A:373:VAL:HG12	1.95	0.47
1:C:68:LEU:HD13	1:C:303:SER:O	2.14	0.47
1:A:193:ALA:O	1:A:197:TYR:HD1	1.98	0.47
1:A:63:ILE:HG23	1:A:288:MET:HE1	1.96	0.47
1:B:141:PRO:O	1:C:58:MET:HB2	2.14	0.47
1:A:278:ARG:HD2	1:A:398:ASP:HB3	1.95	0.47
1:C:14:VAL:HA	1:C:17:LYS:HE2	1.96	0.47
1:B:167:ILE:HG22	1:B:171:MET:HE2	1.96	0.47
1:C:202:GLY:HA2	3:C:502:DMU:H8	1.97	0.46
1:A:415:ILE:O	1:A:419:THR:HG23	2.15	0.46
1:A:264:ILE:HD13	1:A:264:ILE:HA	1.80	0.46
1:C:73:ALA:O	1:C:168:THR:OG1	2.33	0.46
1:C:230:LEU:HD13	1:C:393:ILE:HG23	1.97	0.46
5:A:507:PGE:H32	5:A:507:PGE:H52	1.66	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:ARG:NH1	1:C:190:ASP:OD2	2.49	0.46
1:B:394:ASP:O	1:B:398:ASP:HB2	2.16	0.46
1:C:80:LEU:HD12	1:C:80:LEU:HA	1.77	0.46
1:A:325:VAL:HG12	1:A:336:LEU:HD11	1.97	0.46
1:C:386:ALA:O	1:C:389:MET:HB2	2.14	0.46
1:C:59:LEU:HD13	1:C:200:VAL:HG22	1.98	0.46
1:A:299:LYS:HA	1:A:302:PHE:CE2	2.50	0.46
1:C:15:LEU:HD13	1:C:268:LYS:HE3	1.97	0.46
1:A:176:GLU:HG3	1:A:179:ARG:NH2	2.31	0.45
1:A:366:LEU:HD23	1:A:387:TYR:CE1	2.52	0.45
1:C:296:GLY:HA3	1:C:424:ASP:HB3	1.97	0.45
1:B:82:ARG:HG2	1:B:86:LYS:HZ2	1.81	0.45
1:C:277:THR:C	1:C:279:SER:H	2.25	0.45
1:A:63:ILE:HD11	1:A:197:TYR:CZ	2.52	0.45
1:B:138:ASN:HA	1:C:54:ARG:NH1	2.32	0.44
1:C:415:ILE:O	1:C:419:THR:HG23	2.17	0.44
1:B:139:ILE:O	1:B:155:PRO:HA	2.17	0.44
1:C:75:ILE:HD11	1:C:79:ARG:HG2	1.99	0.44
1:B:280:SER:HB2	1:B:406:VAL:HG23	2.00	0.44
1:A:123:LYS:HB2	1:A:376:ASP:OD2	2.18	0.44
1:B:25:GLY:HA3	1:B:215:ILE:HG23	2.00	0.44
1:A:123:LYS:HB2	1:A:376:ASP:CG	2.43	0.43
1:B:105:VAL:HG21	1:B:240:GLY:HA2	1.99	0.43
1:C:9:TYR:HE2	1:C:17:LYS:HD2	1.83	0.43
1:B:284:LEU:HD23	1:B:284:LEU:HA	1.73	0.43
1:C:226:VAL:HG13	1:C:234:VAL:HG21	1.98	0.43
1:A:321:GLN:HG2	1:A:366:LEU:HD13	2.00	0.43
1:B:101:PHE:O	1:B:105:VAL:HG23	2.18	0.43
1:A:83:VAL:HG13	1:A:416:VAL:HG11	1.99	0.43
1:A:266:LYS:HB2	1:A:295:MET:HE2	2.00	0.43
1:C:124:ALA:HB3	1:C:378:THR:HG23	2.00	0.43
1:B:366:LEU:HD23	1:B:387:TYR:CE1	2.53	0.43
1:C:230:LEU:HB3	1:C:393:ILE:HD13	2.01	0.43
1:C:397:LEU:O	1:C:401:ARG:HB2	2.19	0.43
1:A:75:ILE:HD11	1:A:79:ARG:HG2	2.01	0.43
1:B:245:ILE:O	1:B:249:TYR:HB2	2.18	0.42
1:B:397:LEU:O	1:B:401:ARG:HG2	2.19	0.42
1:C:299:LYS:HA	1:C:302:PHE:CE2	2.54	0.42
1:A:225:ARG:NH1	1:A:392:GLY:O	2.47	0.42
1:A:180:LYS:HE3	1:B:187[A]:ARG:CZ	2.49	0.42
1:B:183:GLU:O	1:B:187[A]:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:297:VAL:HG11	1:B:413:THR:HG22	2.02	0.42
1:C:403:MET:HE2	1:C:403:MET:HB3	1.83	0.42
1:C:370:LEU:HD12	1:C:377:LEU:HD11	2.02	0.42
1:C:124:ALA:HB3	1:C:378:THR:CG2	2.49	0.42
1:A:68:LEU:HD21	1:A:161:ILE:HG13	2.02	0.42
1:B:338:LEU:HD12	1:B:338:LEU:HA	1.84	0.42
1:C:376:ASP:OD2	1:C:376:ASP:N	2.52	0.42
1:B:15:LEU:H	1:B:15:LEU:HG	1.69	0.42
1:B:410:LEU:HA	1:B:410:LEU:HD23	1.78	0.42
1:A:314:MET:HB3	1:A:317:THR:HB	2.02	0.41
1:B:15:LEU:HD22	1:B:268:LYS:HE2	2.02	0.41
1:B:59:LEU:HD13	1:B:200:VAL:HG22	2.02	0.41
1:C:355:THR:HG22	1:C:368:MET:HE1	2.02	0.41
1:A:59:LEU:O	1:A:63:ILE:HG22	2.20	0.41
7:B:511:PEG:H41	7:B:511:PEG:H21	1.97	0.41
1:C:87:ILE:HD12	1:C:87:ILE:HA	1.88	0.41
7:B:503:PEG:H22	7:B:503:PEG:H41	1.72	0.41
1:C:13:PRO:O	1:C:17:LYS:HG3	2.21	0.41
1:C:211:VAL:O	1:C:215:ILE:HG22	2.19	0.41
1:A:141:PRO:O	1:B:58:MET:HB2	2.20	0.41
1:B:68:LEU:HD13	1:B:303:SER:O	2.20	0.41
1:A:198:LEU:CD1	3:A:502:DMU:H30	2.51	0.41
1:B:326:LEU:HD23	1:B:336:LEU:HD12	2.01	0.41
1:C:132:LEU:HD23	1:C:354:GLY:HA2	2.03	0.41
1:A:230:LEU:HD23	1:A:230:LEU:HA	1.91	0.41
1:A:281:SER:O	1:A:284:LEU:HB2	2.21	0.41
1:A:338:LEU:HD12	1:A:338:LEU:HA	1.91	0.41
1:C:18:ILE:HG13	1:C:208:PRO:HG3	2.01	0.41
1:C:337:THR:HG23	1:C:340:GLN:H	1.86	0.41
1:C:355:THR:CG2	1:C:368:MET:HE1	2.51	0.41
1:A:390:ILE:HD13	1:A:390:ILE:HA	1.96	0.41
1:B:247:ILE:HG23	1:B:251:ILE:HD12	2.03	0.41
1:C:410:LEU:HD23	1:C:410:LEU:HA	1.87	0.40
1:A:292:GLU:HB2	1:A:302:PHE:CZ	2.56	0.40
1:B:140:VAL:HG21	1:C:51:LEU:HD11	2.03	0.40
1:C:299:LYS:HG3	1:C:302:PHE:CZ	2.57	0.40
1:C:77:PRO:HG3	1:C:165:ILE:HD13	2.03	0.40
1:C:237:VAL:O	1:C:241:LEU:HG	2.20	0.40
1:A:337:THR:HG22	1:A:338:LEU:N	2.37	0.40
1:A:58:MET:HE2	1:A:58:MET:HB3	1.89	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	422/438 (96%)	411 (97%)	11 (3%)	0	100	100
1	B	422/438 (96%)	409 (97%)	13 (3%)	0	100	100
1	C	422/438 (96%)	410 (97%)	12 (3%)	0	100	100
All	All	1266/1314 (96%)	1230 (97%)	36 (3%)	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	332/345 (96%)	328 (99%)	4 (1%)	63	87
1	B	332/345 (96%)	329 (99%)	3 (1%)	70	89
1	C	332/345 (96%)	329 (99%)	3 (1%)	70	89
All	All	996/1035 (96%)	986 (99%)	10 (1%)	68	88

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ILE
1	A	209	ILE
1	A	314	MET
1	A	378	THR
1	B	121	THR

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Mol	Chain	Res	Type
1	B	314	MET
1	B	326	LEU
1	C	289	ARG
1	C	314	MET
1	C	378	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	134	GLN
1	A	334	HIS
1	B	172	ASN
1	C	134	GLN
1	C	172	ASN

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 39 ligands modelled in this entry, 9 are monoatomic - leaving 30 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
7	PEG	C	509	-	6,6,6	0.51	0	5,5,5	0.51	0
4	PG4	A	504	-	12,12,12	0.57	0	11,11,11	0.29	0
5	PGE	B	502	-	9,9,9	0.41	0	8,8,8	0.34	0
4	PG4	A	503	-	12,12,12	0.55	0	11,11,11	0.36	0
4	PG4	A	506	-	12,12,12	0.56	0	11,11,11	0.42	0
7	PEG	C	511	-	6,6,6	0.50	0	5,5,5	0.48	0
3	DMU	A	502	-	34,34,34	1.58	8 (23%)	45,45,45	1.25	5 (11%)
5	PGE	A	507	-	9,9,9	0.39	0	8,8,8	0.22	0
7	PEG	B	504	-	6,6,6	0.54	0	5,5,5	0.32	0
2	QM5	C	501	6	27,28,28	2.01	9 (33%)	34,37,37	2.95	14 (41%)
7	PEG	C	512	-	6,6,6	0.52	0	5,5,5	0.33	0
5	PGE	C	503	-	9,9,9	0.36	0	8,8,8	0.36	0
8	1PE	C	504	-	15,15,15	0.56	0	14,14,14	0.25	0
7	PEG	C	508	-	6,6,6	0.49	0	5,5,5	0.34	0
2	QM5	A	501	-	27,28,28	2.20	13 (48%)	34,37,37	1.45	4 (11%)
7	PEG	B	512	-	6,6,6	0.55	0	5,5,5	0.26	0
7	PEG	C	510	-	6,6,6	0.57	0	5,5,5	0.62	0
7	PEG	C	513	-	6,6,6	0.50	0	5,5,5	0.36	0
7	PEG	B	511	-	6,6,6	0.51	0	5,5,5	0.42	0
3	DMU	B	505	-	34,34,34	1.55	7 (20%)	45,45,45	1.52	7 (15%)
5	PGE	B	506	-	9,9,9	0.39	0	8,8,8	0.23	0
7	PEG	C	514	-	6,6,6	0.54	0	5,5,5	0.30	0
7	PEG	B	513	-	6,6,6	0.50	0	5,5,5	0.37	0
3	DMU	C	502	-	34,34,34	1.56	7 (20%)	45,45,45	1.38	6 (13%)
7	PEG	A	511	-	6,6,6	0.51	0	5,5,5	0.55	0
7	PEG	B	503	-	6,6,6	0.51	0	5,5,5	0.34	0
7	PEG	A	512	-	6,6,6	0.51	0	5,5,5	0.32	0
5	PGE	B	507	-	9,9,9	0.35	0	8,8,8	0.32	0
2	QM5	B	501	-	27,28,28	2.06	12 (44%)	34,37,37	1.32	2 (5%)
5	PGE	A	505	-	9,9,9	0.40	0	8,8,8	0.33	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
7	PEG	C	509	-	-	2/4/4/4	-
4	PG4	A	504	-	-	4/10/10/10	-
5	PGE	B	502	-	-	4/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PG4	A	503	-	-	5/10/10/10	-
4	PG4	A	506	-	-	5/10/10/10	-
7	PEG	C	511	-	-	1/4/4/4	-
3	DMU	A	502	-	-	10/19/59/59	0/2/2/2
5	PGE	A	507	-	-	3/7/7/7	-
7	PEG	B	504	-	-	2/4/4/4	-
2	QM5	C	501	6	-	10/24/24/24	0/2/2/2
7	PEG	C	512	-	-	2/4/4/4	-
5	PGE	C	503	-	-	4/7/7/7	-
8	1PE	C	504	-	-	9/13/13/13	-
7	PEG	C	508	-	-	1/4/4/4	-
2	QM5	A	501	-	-	12/24/24/24	0/2/2/2
7	PEG	B	512	-	-	3/4/4/4	-
7	PEG	C	510	-	-	2/4/4/4	-
7	PEG	C	513	-	-	3/4/4/4	-
7	PEG	B	511	-	-	4/4/4/4	-
3	DMU	B	505	-	-	9/19/59/59	0/2/2/2
5	PGE	B	506	-	-	5/7/7/7	-
7	PEG	C	514	-	-	0/4/4/4	-
7	PEG	B	513	-	-	2/4/4/4	-
3	DMU	C	502	-	-	8/19/59/59	0/2/2/2
7	PEG	A	511	-	-	0/4/4/4	-
7	PEG	B	503	-	-	2/4/4/4	-
7	PEG	A	512	-	-	2/4/4/4	-
5	PGE	B	507	-	-	2/7/7/7	-
2	QM5	B	501	-	-	10/24/24/24	0/2/2/2
5	PGE	A	505	-	-	3/7/7/7	-

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	QM5	N3-N2	-4.78	1.24	1.39
3	A	502	DMU	O1-C9	4.30	1.54	1.44
2	A	501	QM5	C1-C6	4.29	1.47	1.38
3	B	505	DMU	O1-C9	4.24	1.54	1.44
3	C	502	DMU	O1-C9	4.11	1.54	1.44
2	A	501	QM5	C3-N2	3.96	1.52	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	QM5	C1-C6	3.86	1.46	1.38
2	A	501	QM5	O6-C15	3.82	1.45	1.37
2	C	501	QM5	C4-C3	3.76	1.45	1.39
2	B	501	QM5	O6-C15	3.66	1.44	1.37
2	B	501	QM5	C3-N2	3.62	1.51	1.39
2	A	501	QM5	C2-C3	3.50	1.45	1.39
2	C	501	QM5	C5-C4	3.21	1.44	1.38
3	A	502	DMU	O1-C10	3.04	1.49	1.41
2	B	501	QM5	O1-C8	-3.03	1.38	1.42
3	C	502	DMU	O1-C10	3.03	1.49	1.41
2	C	501	QM5	O1-C8	-2.93	1.38	1.42
2	C	501	QM5	C3-N2	2.90	1.48	1.39
2	A	501	QM5	C7-C6	2.87	1.57	1.50
2	A	501	QM5	C12-N3	2.72	1.48	1.39
3	B	505	DMU	O1-C10	2.71	1.48	1.41
3	A	502	DMU	C11-C9	-2.67	1.42	1.51
2	A	501	QM5	C5-C4	2.67	1.43	1.38
3	C	502	DMU	C11-C9	-2.66	1.42	1.51
3	B	505	DMU	C11-C9	-2.66	1.42	1.51
3	B	505	DMU	O5-C6	2.60	1.48	1.41
2	B	501	QM5	C4-C3	2.59	1.43	1.39
2	A	501	QM5	O3-C9	-2.57	1.22	1.30
2	A	501	QM5	C4-C3	2.56	1.43	1.39
2	C	501	QM5	O4-C11	-2.55	1.22	1.30
2	B	501	QM5	O3-C9	-2.53	1.22	1.30
3	A	502	DMU	O5-C6	2.51	1.48	1.41
3	B	505	DMU	O3-C5	2.48	1.49	1.43
3	B	505	DMU	O4-C7	2.48	1.49	1.43
3	A	502	DMU	O3-C5	2.47	1.49	1.43
3	C	502	DMU	O5-C6	2.47	1.48	1.41
2	B	501	QM5	O1-C7	-2.46	1.36	1.42
2	B	501	QM5	C2-C3	2.45	1.43	1.39
3	A	502	DMU	O4-C7	2.44	1.49	1.43
2	B	501	QM5	C12-N3	2.43	1.47	1.39
3	C	502	DMU	O3-C5	2.42	1.49	1.43
2	B	501	QM5	C7-C6	2.42	1.56	1.50
3	C	502	DMU	C7-C5	-2.34	1.46	1.52
2	B	501	QM5	O6-C18	-2.34	1.36	1.42
2	A	501	QM5	O6-C18	-2.32	1.36	1.42
3	C	502	DMU	O4-C7	2.31	1.48	1.43
3	A	502	DMU	C7-C5	-2.21	1.46	1.52
2	A	501	QM5	C2-C1	2.21	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	QM5	C2-C1	-2.18	1.35	1.38
3	A	502	DMU	O5-C4	2.17	1.49	1.44
3	B	505	DMU	C7-C5	-2.16	1.46	1.52
2	C	501	QM5	O3-C9	-2.16	1.23	1.30
2	B	501	QM5	C5-C4	2.10	1.42	1.38
2	A	501	QM5	O1-C7	-2.10	1.37	1.42
2	C	501	QM5	C2-C3	2.09	1.42	1.39
2	A	501	QM5	C5-C6	2.06	1.43	1.38

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	QM5	C12-N3-N2	8.26	141.26	119.14
2	C	501	QM5	C2-C1-C6	7.00	130.20	121.00
2	C	501	QM5	O1-C8-C9	-6.65	102.33	112.26
2	C	501	QM5	C7-O1-C8	5.48	121.26	113.55
2	C	501	QM5	C1-C2-C3	-5.03	114.51	120.30
2	A	501	QM5	C7-O1-C8	4.37	119.69	113.55
2	B	501	QM5	O1-C8-C9	-4.12	106.10	112.26
3	B	505	DMU	C1-C2-C3	3.95	118.66	109.68
3	C	502	DMU	O1-C10-C5	3.95	118.48	110.37
3	B	505	DMU	C6-C1-C2	3.90	118.22	110.01
3	A	502	DMU	C10-C5-C7	3.50	117.37	110.01
3	C	502	DMU	C10-C5-C7	3.45	117.27	110.01
3	B	505	DMU	C8-C7-C5	3.33	116.67	110.83
3	A	502	DMU	O5-C4-C3	3.32	116.59	109.72
2	A	501	QM5	C11-C10-N1	3.26	116.35	109.49
3	B	505	DMU	C10-C5-C7	3.26	116.87	110.01
2	C	501	QM5	C2-C3-N2	-3.09	112.44	120.50
2	C	501	QM5	C18-O6-C15	-3.08	110.90	117.50
2	C	501	QM5	C13-C12-N3	-2.98	112.71	120.50
3	B	505	DMU	C7-C8-C9	2.90	115.50	110.23
3	C	502	DMU	C1-C2-C3	2.85	116.14	109.68
2	C	501	QM5	C11-C10-N1	2.82	115.41	109.49
2	B	501	QM5	O1-C7-C6	-2.72	103.67	109.91
3	A	502	DMU	O1-C10-C5	2.71	115.94	110.37
3	C	502	DMU	O5-C4-C3	2.59	115.07	109.72
2	A	501	QM5	O4-C11-O5	-2.54	118.31	124.08
2	C	501	QM5	C4-C3-N2	2.54	127.11	120.50
3	A	502	DMU	C1-C2-C3	2.53	115.43	109.68
3	C	502	DMU	C6-C1-C2	2.49	115.25	110.01
3	C	502	DMU	C10-O1-C9	2.47	118.55	113.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	QM5	O1-C7-C6	-2.40	104.39	109.91
3	A	502	DMU	C10-O1-C9	2.38	118.38	113.72
2	C	501	QM5	C16-C17-C12	-2.25	117.71	120.30
3	B	505	DMU	C10-O1-C9	2.09	117.80	113.72
2	C	501	QM5	C17-C12-N3	2.08	125.93	120.50
3	B	505	DMU	C10-O7-C3	-2.07	113.08	117.98
2	C	501	QM5	O1-C7-C6	-2.04	105.23	109.91
2	C	501	QM5	C4-C5-C6	-2.01	118.36	121.00

There are no chirality outliers.

All (129) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	QM5	O1-C8-C9-O2
2	A	501	QM5	O1-C8-C9-O3
2	A	501	QM5	C11-C10-C8-C9
2	A	501	QM5	N1-C10-C8-O1
2	B	501	QM5	C11-C10-C8-C9
2	B	501	QM5	N1-C10-C8-O1
2	B	501	QM5	C13-C12-N3-N2
2	B	501	QM5	C17-C12-N3-N2
2	C	501	QM5	O1-C8-C9-O2
2	C	501	QM5	O1-C8-C9-O3
2	C	501	QM5	C11-C10-C8-C9
7	C	509	PEG	C1-C2-O2-C3
7	C	510	PEG	C1-C2-O2-C3
2	B	501	QM5	C16-C15-O6-C18
2	B	501	QM5	C14-C15-O6-C18
2	C	501	QM5	C16-C15-O6-C18
7	B	511	PEG	C4-C3-O2-C2
2	C	501	QM5	C14-C15-O6-C18
7	C	511	PEG	C1-C2-O2-C3
3	A	502	DMU	O6-C11-C9-O1
2	A	501	QM5	C14-C15-O6-C18
2	A	501	QM5	C16-C15-O6-C18
5	A	507	PGE	O2-C3-C4-O3
3	A	502	DMU	O5-C6-O16-C18
4	A	504	PG4	O2-C3-C4-O3
3	B	505	DMU	O6-C11-C9-O1
3	C	502	DMU	O6-C11-C9-O1
5	C	503	PGE	O2-C3-C4-O3
3	B	505	DMU	O6-C11-C9-C8

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Mol	Chain	Res	Type	Atoms
4	A	503	PG4	O4-C7-C8-O5
3	C	502	DMU	O6-C11-C9-C8
4	A	506	PG4	O2-C3-C4-O3
4	A	506	PG4	O4-C7-C8-O5
5	A	507	PGE	O1-C1-C2-O2
7	C	512	PEG	O2-C3-C4-O4
8	C	504	1PE	OH2-C12-C22-OH3
7	B	503	PEG	C4-C3-O2-C2
2	B	501	QM5	C4-C3-N2-N3
2	B	501	QM5	C2-C3-N2-N3
3	A	502	DMU	O6-C11-C9-C8
7	C	510	PEG	O2-C3-C4-O4
7	C	513	PEG	O2-C3-C4-O4
8	C	504	1PE	OH6-C15-C25-OH5
5	A	507	PGE	C3-C4-O3-C5
5	B	506	PGE	O1-C1-C2-O2
7	B	513	PEG	O1-C1-C2-O2
3	B	505	DMU	O5-C6-O16-C18
5	B	502	PGE	O1-C1-C2-O2
5	B	506	PGE	O2-C3-C4-O3
3	C	502	DMU	C28-C31-C34-C37
3	A	502	DMU	C28-C31-C34-C37
3	C	502	DMU	C18-C19-C22-C25
8	C	504	1PE	OH4-C13-C23-OH3
3	B	505	DMU	C25-C28-C31-C34
3	C	502	DMU	O16-C18-C19-C22
3	C	502	DMU	C25-C28-C31-C34
3	B	505	DMU	O5-C4-C57-O61
5	B	507	PGE	O1-C1-C2-O2
7	B	504	PEG	O2-C3-C4-O4
7	B	513	PEG	O2-C3-C4-O4
3	A	502	DMU	C25-C28-C31-C34
3	B	505	DMU	C18-C19-C22-C25
7	A	512	PEG	O2-C3-C4-O4
7	C	508	PEG	O1-C1-C2-O2
7	C	509	PEG	O2-C3-C4-O4
4	A	503	PG4	C1-C2-O2-C3
3	B	505	DMU	C19-C22-C25-C28
3	A	502	DMU	C18-C19-C22-C25
7	B	512	PEG	O2-C3-C4-O4
3	B	505	DMU	C22-C25-C28-C31
3	C	502	DMU	C19-C18-O16-C6

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Mol	Chain	Res	Type	Atoms
5	B	502	PGE	O3-C5-C6-O4
7	B	511	PEG	O2-C3-C4-O4
2	A	501	QM5	C9-C8-O1-C7
2	C	501	QM5	C9-C8-O1-C7
4	A	503	PG4	O2-C3-C4-O3
8	C	504	1PE	C13-C23-OH3-C22
7	B	511	PEG	O1-C1-C2-O2
4	A	504	PG4	C5-C6-O4-C7
2	C	501	QM5	N1-C10-C11-O4
5	B	506	PGE	C1-C2-O2-C3
5	A	505	PGE	C4-C3-O2-C2
5	B	502	PGE	C1-C2-O2-C3
8	C	504	1PE	C24-C14-OH5-C25
5	C	503	PGE	C3-C4-O3-C5
8	C	504	1PE	C12-C22-OH3-C23
4	A	506	PG4	C8-C7-O4-C6
5	B	507	PGE	C4-C3-O2-C2
7	B	503	PEG	C1-C2-O2-C3
7	B	504	PEG	C1-C2-O2-C3
7	B	511	PEG	C1-C2-O2-C3
8	C	504	1PE	OH5-C14-C24-OH4
7	B	512	PEG	C4-C3-O2-C2
2	C	501	QM5	N1-C10-C8-O1
5	B	502	PGE	C3-C4-O3-C5
4	A	503	PG4	C3-C4-O3-C5
5	B	506	PGE	C6-C5-O3-C4
7	B	512	PEG	C1-C2-O2-C3
7	C	513	PEG	O1-C1-C2-O2
2	A	501	QM5	C8-C10-C11-O4
2	A	501	QM5	C8-C10-C11-O5
3	A	502	DMU	C2-C3-O7-C10
2	A	501	QM5	C11-C10-C8-O1
3	A	502	DMU	C22-C25-C28-C31
5	B	506	PGE	C3-C4-O3-C5
4	A	504	PG4	C6-C5-O3-C4
8	C	504	1PE	C16-C26-OH6-C15
4	A	506	PG4	C5-C6-O4-C7
5	A	505	PGE	O1-C1-C2-O2
5	C	503	PGE	C4-C3-O2-C2
5	A	505	PGE	C1-C2-O2-C3
8	C	504	1PE	C25-C15-OH6-C26
3	A	502	DMU	C4-C3-O7-C10

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Mol	Chain	Res	Type	Atoms
3	C	502	DMU	C22-C25-C28-C31
3	A	502	DMU	C19-C22-C25-C28
4	A	504	PG4	C1-C2-O2-C3
7	C	513	PEG	C1-C2-O2-C3
7	A	512	PEG	C1-C2-O2-C3
2	B	501	QM5	O1-C8-C9-O2
4	A	503	PG4	O1-C1-C2-O2
7	C	512	PEG	O1-C1-C2-O2
5	C	503	PGE	C1-C2-O2-C3
2	A	501	QM5	C10-C8-O1-C7
2	C	501	QM5	C10-C8-O1-C7
4	A	506	PG4	O3-C5-C6-O4
3	B	505	DMU	C31-C34-C37-C40
2	A	501	QM5	N1-C10-C8-C9
2	B	501	QM5	N1-C10-C8-C9
2	C	501	QM5	C8-C10-C11-O5

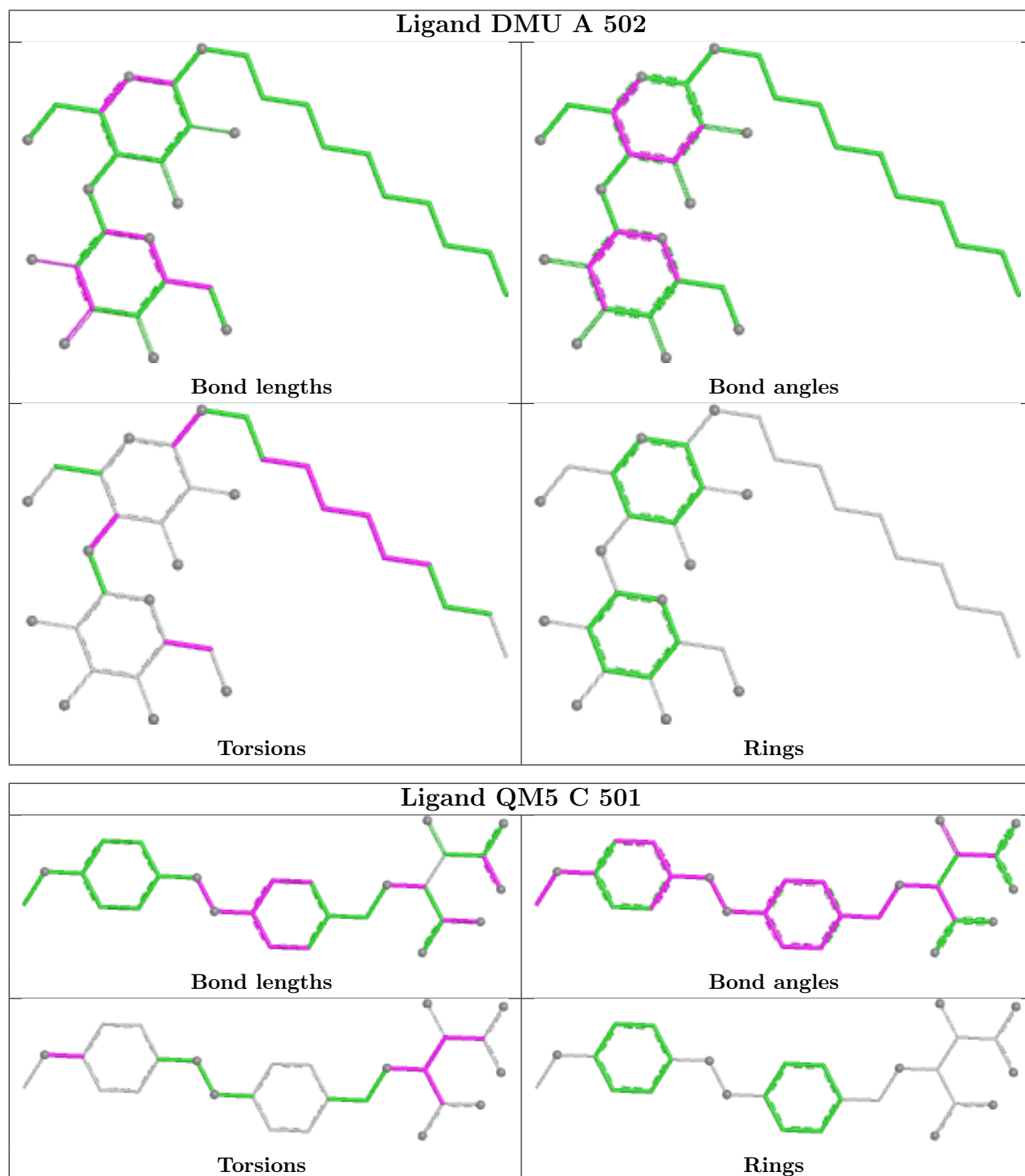
There are no ring outliers.

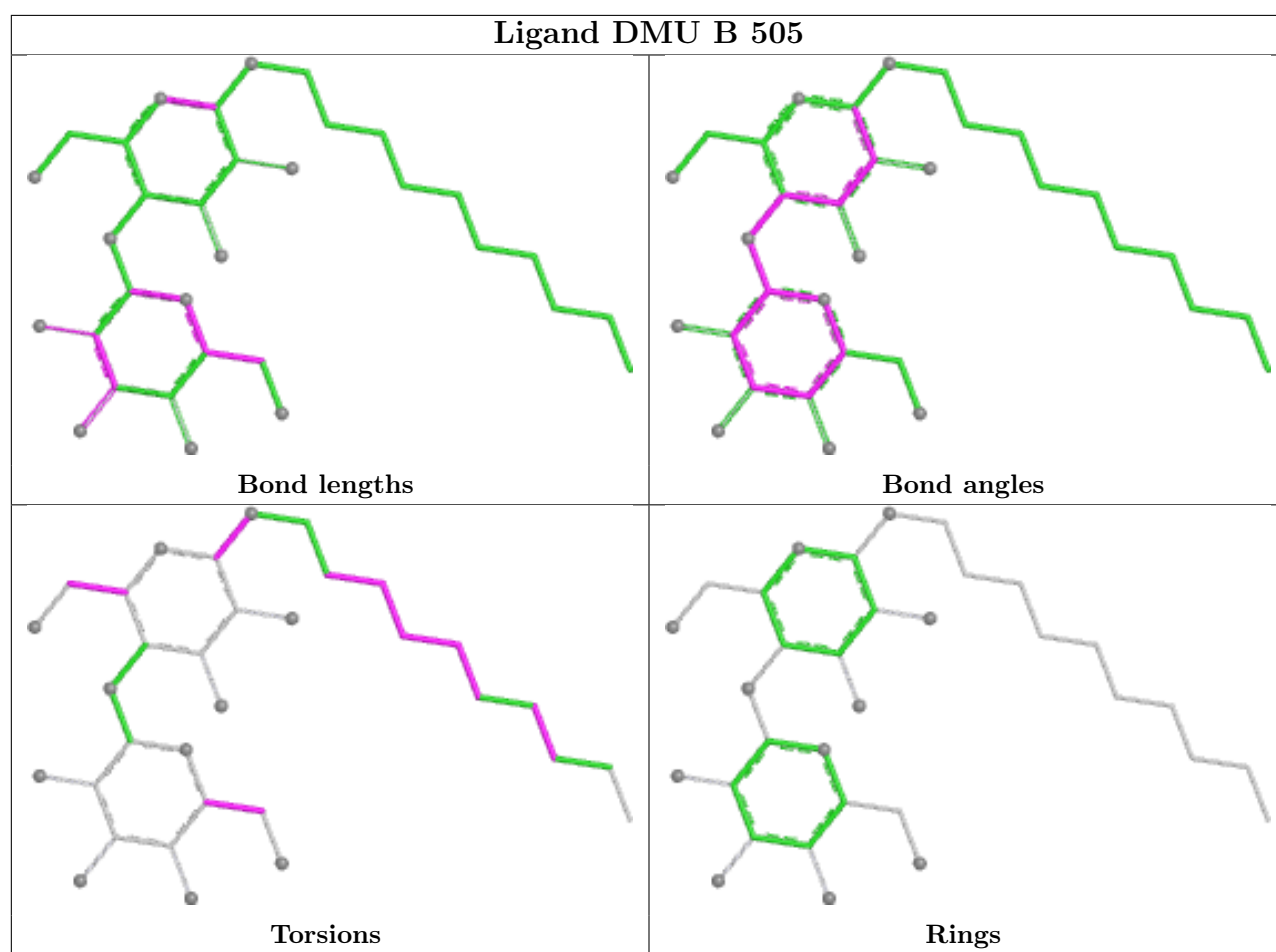
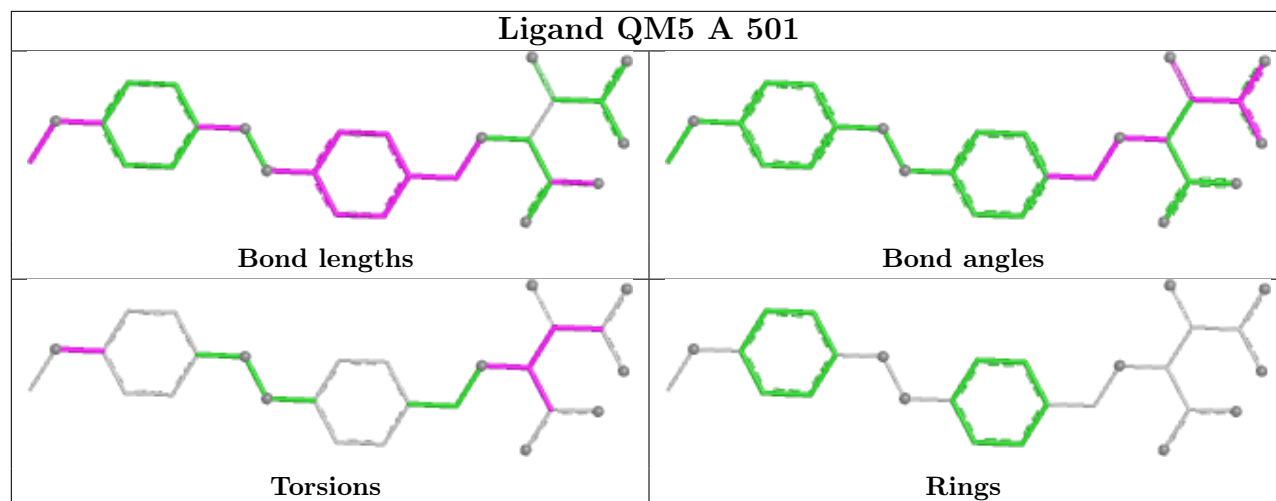
10 monomers are involved in 14 short contacts:

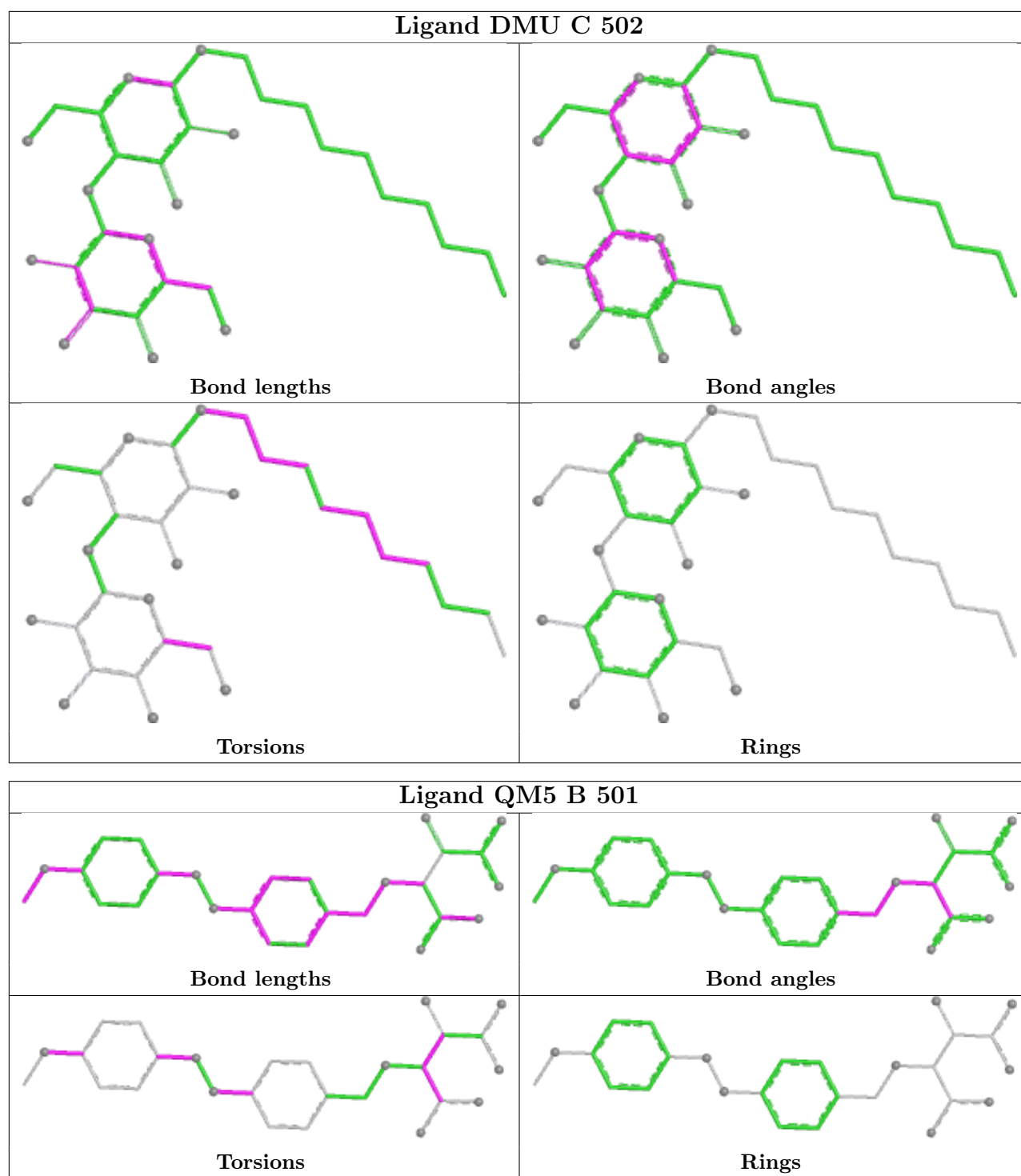
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	511	PEG	1	0
3	A	502	DMU	3	0
5	A	507	PGE	1	0
8	C	504	1PE	1	0
2	A	501	QM5	1	0
7	B	511	PEG	2	0
3	B	505	DMU	1	0
7	C	514	PEG	1	0
3	C	502	DMU	3	0
7	B	503	PEG	1	0

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 ⓘ

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	424/438 (96%)	0.26	38 (8%) 15 11	79, 107, 169, 284	0
1	B	423/438 (96%)	0.54	44 (10%) 11 8	62, 107, 158, 254	1 (0%)
1	C	423/438 (96%)	0.35	40 (9%) 14 10	53, 104, 149, 351	1 (0%)
All	All	1270/1314 (96%)	0.39	122 (9%) 13 10	53, 106, 160, 351	2 (0%)

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	11	ASP	11.0
1	C	121	THR	7.8
1	B	377	LEU	6.9
1	B	126	GLU	6.6
1	B	376	ASP	6.1
1	B	125	ILE	6.0
1	C	375	LEU	5.8
1	C	118	GLY	5.7
1	C	127	ALA	5.7
1	B	387	TYR	5.5
1	B	384	ALA	5.3
1	C	122	GLY	5.3
1	B	383	VAL	5.3
1	B	375	LEU	5.1
1	A	421	LYS	5.0
1	A	428	TRP	5.0
1	B	421	LYS	4.9
1	A	332	ILE	4.9
1	C	256	PHE	4.8
1	C	12	TYR	4.5
1	A	294	GLU	4.5
1	B	386	ALA	4.4
1	B	385	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	121	THR	4.2
1	B	370	LEU	4.2
1	C	10	LEU	4.2
1	B	378	THR	4.1
1	A	334	HIS	4.1
1	A	375	LEU	4.1
1	B	9	TYR	4.1
1	A	266	LYS	4.0
1	C	119	SER	4.0
1	C	142	THR	4.0
1	B	84	GLY	3.8
1	A	187	ARG	3.8
1	C	13	PRO	3.7
1	C	376	ASP	3.7
1	B	124	ALA	3.7
1	A	424	ASP	3.7
1	A	359	PRO	3.6
1	C	125	ILE	3.6
1	B	15	LEU	3.6
1	A	293	GLU	3.6
1	A	16	TRP	3.4
1	A	122	GLY	3.3
1	B	8	ARG	3.3
1	B	28	PHE	3.3
1	B	256	PHE	3.2
1	B	248	THR	3.2
1	A	430	SER	3.2
1	C	9	TYR	3.1
1	A	124	ALA	3.1
1	C	109	PHE	3.1
1	C	8	ARG	3.0
1	C	257	GLY	3.0
1	B	328	VAL	3.0
1	A	431	HIS	3.0
1	B	268	LYS	2.9
1	A	123	LYS	2.9
1	B	247	ILE	2.8
1	C	383	VAL	2.8
1	B	380	GLY	2.8
1	A	353	ILE	2.8
1	C	374	GLY	2.8
1	C	334	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	379	PRO	2.7
1	C	124	ALA	2.7
1	B	31	ILE	2.7
1	C	310	ALA	2.7
1	A	374	GLY	2.7
1	C	180	LYS	2.6
1	B	418	LYS	2.6
1	C	332	ILE	2.6
1	A	333	GLY	2.6
1	A	127	ALA	2.6
1	B	123	LYS	2.6
1	A	337	THR	2.6
1	C	123	LYS	2.5
1	C	129	PRO	2.5
1	C	247	ILE	2.5
1	A	129	PRO	2.5
1	B	388	ALA	2.5
1	B	130	PRO	2.5
1	A	14	VAL	2.5
1	B	374	GLY	2.4
1	A	176	GLU	2.4
1	C	177	ARG	2.4
1	A	340	GLN	2.4
1	C	373	VAL	2.4
1	B	372	SER	2.4
1	A	350	LEU	2.4
1	C	15	LEU	2.4
1	B	47	PRO	2.4
1	A	224	VAL	2.4
1	B	174	ASN	2.4
1	A	57	LYS	2.4
1	C	353	ILE	2.4
1	A	194	GLU	2.3
1	C	182	ALA	2.3
1	A	296	GLY	2.3
1	A	427	LYS	2.3
1	C	139	ILE	2.2
1	A	125	ILE	2.2
1	B	249	TYR	2.2
1	B	201	GLY	2.2
1	B	26	ALA	2.2
1	C	167	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	371	GLN	2.2
1	A	354	GLY	2.2
1	B	101	PHE	2.2
1	C	213	ALA	2.2
1	B	114	ASN	2.1
1	A	335	PRO	2.1
1	C	164	GLY	2.1
1	A	193	ALA	2.1
1	B	430	SER	2.1
1	C	14	VAL	2.1
1	C	141	PRO	2.0
1	B	342	LEU	2.0
1	B	187[A]	ARG	2.0
1	C	130	PRO	2.0
1	A	15	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	DMU	B	505	33/33	0.38	0.24	118,194,218,219	0
4	PG4	A	503	13/13	0.62	0.15	137,143,152,154	0
5	PGE	B	507	10/10	0.63	0.24	114,125,132,135	0
5	PGE	A	507	10/10	0.68	0.14	146,148,153,153	0
7	PEG	C	513	7/7	0.68	0.14	116,129,140,140	0
7	PEG	C	509	7/7	0.69	0.17	119,123,124,126	0
4	PG4	A	504	13/13	0.73	0.18	161,162,169,170	0
4	PG4	A	506	13/13	0.73	0.12	123,128,136,137	0

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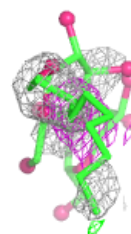
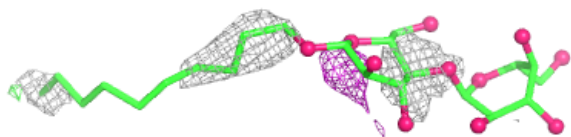
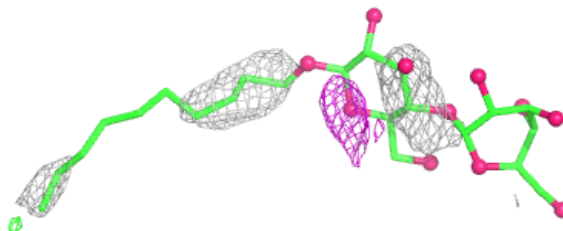
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	PEG	B	504	7/7	0.75	0.14	90,106,117,118	0
7	PEG	C	512	7/7	0.76	0.13	149,150,154,154	0
5	PGE	A	505	10/10	0.76	0.25	135,147,162,163	0
5	PGE	B	506	10/10	0.79	0.12	143,149,159,159	0
7	PEG	C	511	7/7	0.79	0.16	106,112,118,118	0
6	NA	B	510	1/1	0.80	0.32	104,104,104,104	0
3	DMU	C	502	33/33	0.80	0.17	90,150,188,190	0
5	PGE	C	503	10/10	0.81	0.15	158,167,171,172	0
7	PEG	B	513	7/7	0.81	0.15	125,127,137,139	0
7	PEG	A	512	7/7	0.82	0.12	98,113,125,131	0
3	DMU	A	502	33/33	0.83	0.20	129,182,215,216	0
7	PEG	C	514	7/7	0.84	0.19	118,124,137,138	0
2	QM5	C	501	27/27	0.86	0.18	99,125,180,183	0
8	1PE	C	504	16/16	0.86	0.20	99,125,136,139	0
7	PEG	B	503	7/7	0.87	0.12	104,108,113,114	0
5	PGE	B	502	10/10	0.88	0.09	110,116,120,121	0
6	NA	B	508	1/1	0.90	0.18	99,99,99,99	0
6	NA	A	510	1/1	0.90	0.31	110,110,110,110	0
7	PEG	C	510	7/7	0.90	0.23	116,129,140,142	0
6	NA	C	507	1/1	0.90	0.24	97,97,97,97	0
2	QM5	A	501	27/27	0.91	0.16	100,121,165,166	0
2	QM5	B	501	27/27	0.92	0.16	96,131,177,179	0
7	PEG	B	512	7/7	0.92	0.21	117,126,129,131	0
7	PEG	B	511	7/7	0.93	0.14	107,112,118,123	0
7	PEG	A	511	7/7	0.93	0.16	114,118,122,125	0
6	NA	C	505	1/1	0.94	0.12	93,93,93,93	0
7	PEG	C	508	7/7	0.95	0.12	123,126,136,136	0
6	NA	A	508	1/1	0.96	0.14	100,100,100,100	0
6	NA	A	509	1/1	0.96	0.09	100,100,100,100	0
6	NA	B	509	1/1	0.98	0.06	94,94,94,94	0
6	NA	C	506	1/1	0.98	0.04	96,96,96,96	0

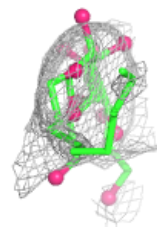
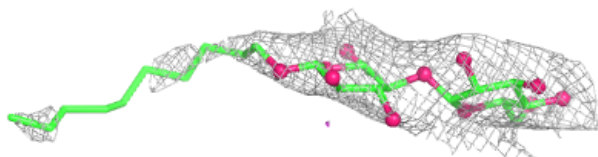
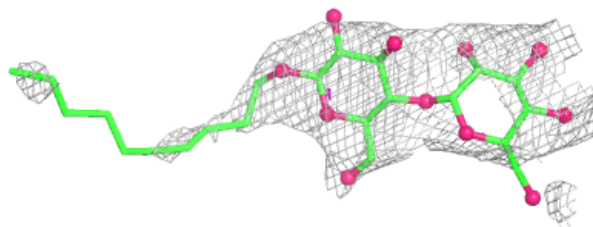
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DMU B 505:

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

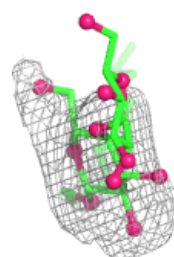
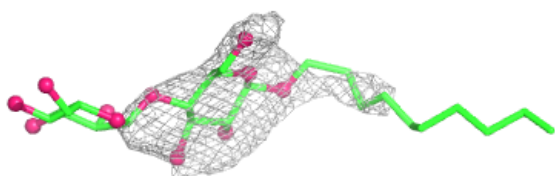
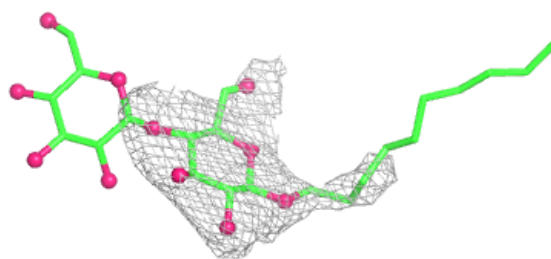
**Electron density around DMU C 502:**

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

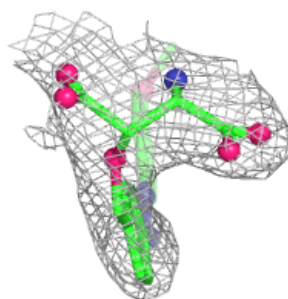
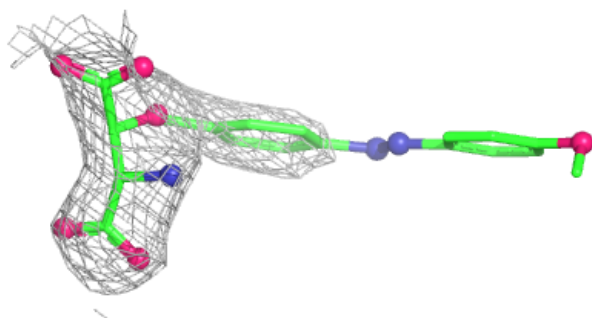
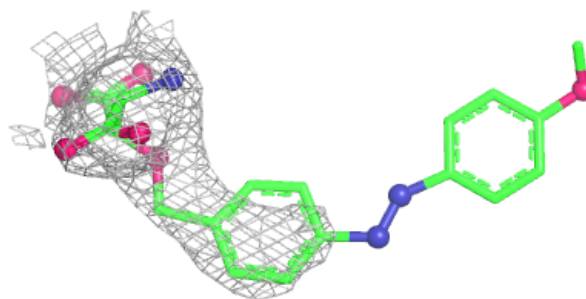


Electron density around DMU A 502:

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

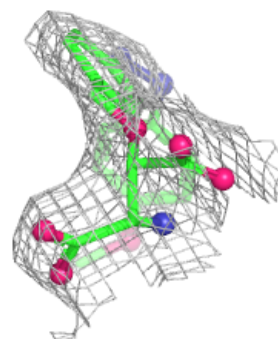
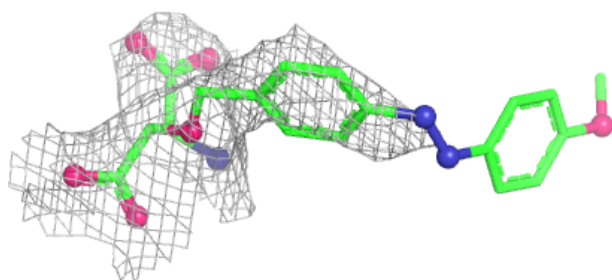
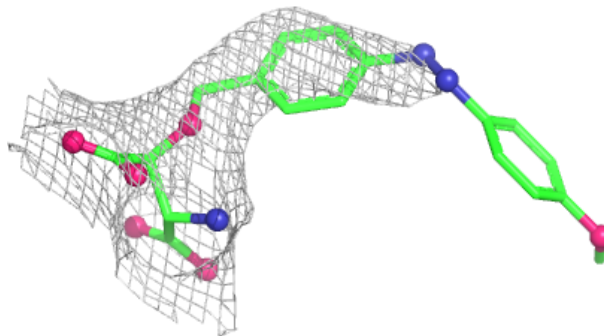
**Electron density around QM5 C 501:**

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

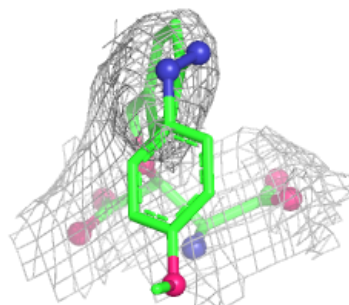
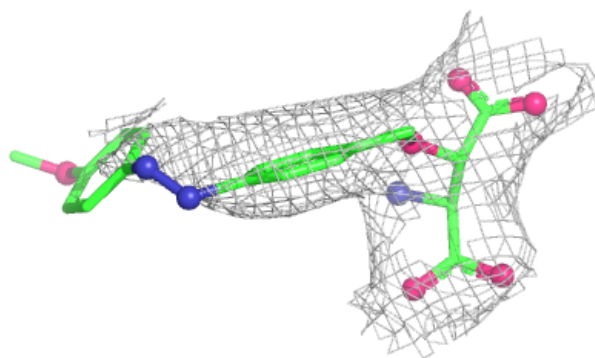
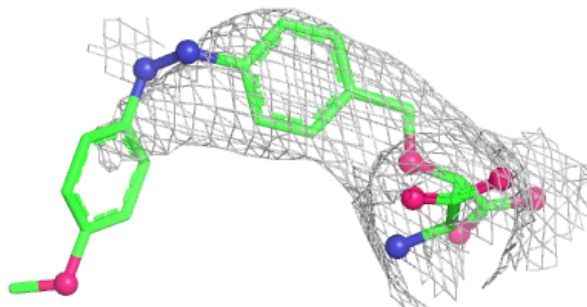


Electron density around QM5 A 501:

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

**Electron density around QM5 B 501:**

$2mF_o-DF_c$ (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.