



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 01:52 AM UTC

PDB ID : 4RRY / pdb_00004rry
Title : Crystal Structure of Apo Murine H90W Cyclooxygenase-2
Authors : Xu, S.; Blobaum, A.L.; Banerjee, S.; Marnett, L.J.
Deposited on : 2014-11-06
Resolution : 2.43 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

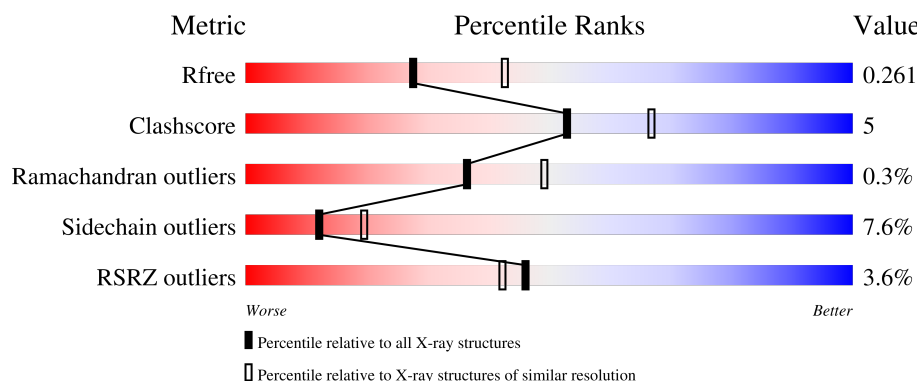
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	587	2% 78% 14% 6%
1	B	587	4% 79% 12% 6%
1	C	587	4% 77% 15% 6%
1	D	587	3% 79% 12% 6%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 100%
2	H	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18993 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 Prostaglandin G/H synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	552	Total	C	N	O	S	0	0	0
			4478	2890	749	814	25			
1	B	552	Total	C	N	O	S	0	0	0
			4478	2890	749	814	25			
1	C	552	Total	C	N	O	S	0	0	0
			4478	2890	749	814	25			
1	D	552	Total	C	N	O	S	0	0	0
			4478	2890	749	814	25			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	TRP	HIS	engineered mutation	UNP Q05769
B	90	TRP	HIS	engineered mutation	UNP Q05769
C	90	TRP	HIS	engineered mutation	UNP Q05769
D	90	TRP	HIS	engineered mutation	UNP Q05769

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



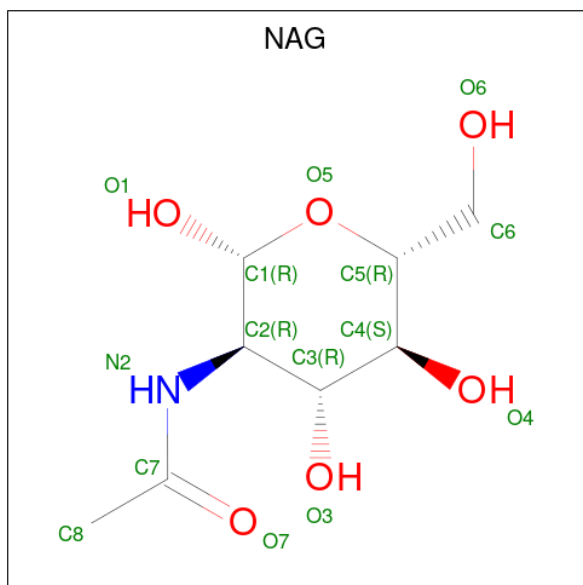
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

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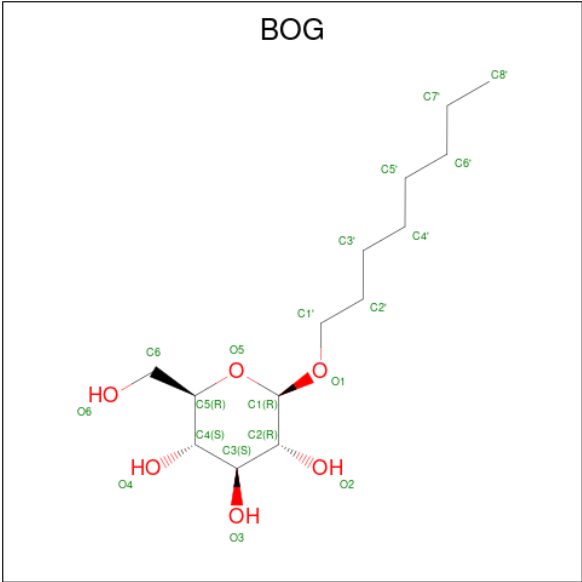
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: $C_{14}H_{28}O_6$).



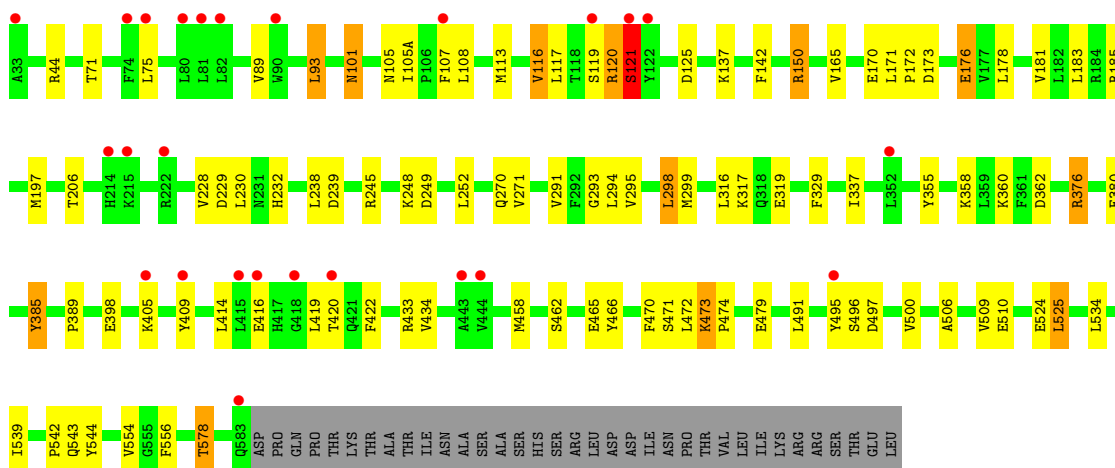
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			20	14	6		
4	A	1	Total	C	O	0	0
			20	14	6		
4	B	1	Total	C	O	0	0
			20	14	6		
4	C	1	Total	C	O	0	0
			20	14	6		
4	C	1	Total	C	O	0	0
			20	14	6		
4	D	1	Total	C	O	0	0
			20	14	6		

- Molecule 5 is water.

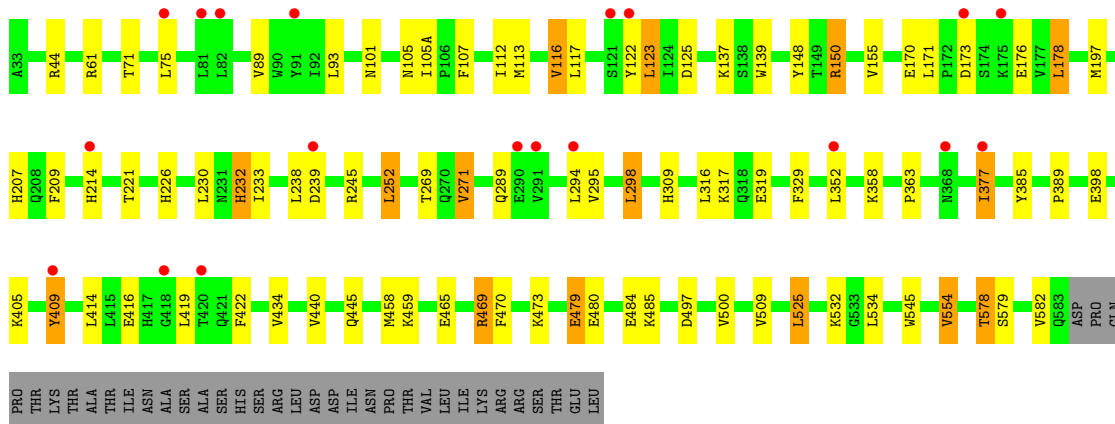
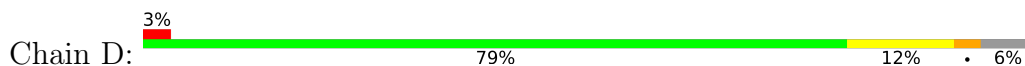
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	214	Total	O	0	0
			214	214		
5	B	212	Total	O	0	0
			212	212		
5	C	145	Total	O	0	0
			145	145		
5	D	166	Total	O	0	0
			166	166		

- Molecule 1: Prostaglandin G/H synthase 2





• Molecule 1: Prostaglandin G/H synthase 2



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%

3AG1
3AG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%

3AG1
3AG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	181.19Å 134.47Å 121.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.36 – 2.43 49.36 – 2.43	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.36-2.43) 87.2 (49.36-2.43)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.42Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.209 , 0.259 0.214 , 0.261	Depositor DCC
R_{free} test set	3370 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.646	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.4	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	18993	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.9529e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NAG, BOG

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	0.40	0/4606	0.74	3/6247 (0.0%)
1	B	0.38	0/4606	0.76	5/6247 (0.1%)
1	C	0.43	0/4606	0.77	6/6247 (0.1%)
1	D	0.40	0/4606	0.76	2/6247 (0.0%)
All	All	0.40	0/18424	0.76	16/24988 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	419	LEU	N-CA-C	-6.79	103.68	112.23
1	B	105(A)	ILE	CA-C-N	6.57	126.07	119.24
1	B	105(A)	ILE	C-N-CA	6.57	126.07	119.24
1	C	105(A)	ILE	CA-C-N	6.37	125.87	119.24
1	C	105(A)	ILE	C-N-CA	6.37	125.87	119.24
1	C	121	SER	N-CA-C	6.00	118.78	111.82
1	C	120	ARG	N-CA-C	-5.90	104.03	111.11
1	B	419	LEU	N-CA-C	-5.84	104.51	111.69
1	C	228	VAL	N-CA-C	5.47	112.06	106.21
1	A	105(A)	ILE	CA-C-N	5.40	124.85	119.24
1	A	105(A)	ILE	C-N-CA	5.40	124.85	119.24
1	B	388	HIS	CA-C-N	-5.37	114.16	120.12
1	B	388	HIS	C-N-CA	-5.37	114.16	120.12
1	D	105(A)	ILE	CA-C-N	5.17	124.62	119.24
1	D	105(A)	ILE	C-N-CA	5.17	124.62	119.24
1	A	228	VAL	N-CA-C	5.08	111.65	106.21

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	4478	0	4376	49	0
1	B	4478	0	4376	45	0
1	C	4478	0	4376	53	0
1	D	4478	0	4376	43	0
2	E	28	0	25	1	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
3	A	28	0	26	0	0
3	B	28	0	26	0	0
3	C	28	0	26	0	0
3	D	28	0	26	0	0
4	A	40	0	56	3	0
4	B	20	0	28	2	0
4	C	40	0	56	5	0
4	D	20	0	28	1	0
5	A	214	0	0	5	0
5	B	212	0	0	6	0
5	C	145	0	0	0	0
5	D	166	0	0	6	0
All	All	18993	0	17876	182	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (182) 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:C:120:ARG:HD3	4:C:706:BOG:O2	1.73	0.88
1:A:44:ARG:HH11	1:A:44:ARG:HG2	1.46	0.80
1:B:150:ARG:HD3	5:B:939:HOH:O	1.82	0.79
1:B:294:LEU:HD22	1:B:409:TYR:HD1	1.49	0.76
1:A:123:LEU:O	1:A:469:ARG:NH2	2.20	0.74
1:C:319:GLU:HG3	1:C:554:VAL:HG11	1.70	0.72
1:C:543:GLN:NE2	1:D:125:ASP:OD1	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:PRO:HG2	1:C:495:TYR:CZ	2.26	0.71
1:D:197:MET:HE2	1:D:578:THR:HG21	1.73	0.71
1:B:197:MET:HE2	1:B:578:THR:HG21	1.71	0.71
1:D:150:ARG:NH2	1:D:458:MET:O	2.25	0.69
1:B:319:GLU:HG3	1:B:554:VAL:HG11	1.75	0.69
1:D:479:GLU:CD	5:D:879:HOH:O	2.36	0.69
1:B:479:GLU:OE2	1:B:485:LYS:HG2	1.94	0.68
1:C:116:VAL:O	1:C:120:ARG:HG2	1.94	0.66
1:C:197:MET:HE2	1:C:578:THR:HG21	1.78	0.66
1:A:319:GLU:HG3	1:A:554:VAL:HG11	1.77	0.65
1:A:142:PHE:O	1:A:376:ARG:NH2	2.21	0.63
1:C:173:ASP:HB3	1:C:176:GLU:HB2	1.80	0.62
1:D:319:GLU:HG3	1:D:554:VAL:HG11	1.81	0.62
1:B:557:LYS:NZ	5:B:965:HOH:O	2.29	0.61
1:D:389:PRO:HG2	1:D:434:VAL:HA	1.81	0.61
1:C:150:ARG:NH2	1:C:458:MET:O	2.33	0.61
1:A:125:ASP:OD1	1:B:543:GLN:NE2	2.30	0.60
1:D:123:LEU:O	1:D:469:ARG:NH2	2.28	0.60
1:B:226:HIS:HA	1:B:377:ILE:HD13	1.83	0.60
1:D:245:ARG:HD3	1:D:329:PHE:CD1	2.36	0.60
1:C:116:VAL:HB	4:C:706:BOG:H2'2	1.83	0.60
1:B:294:LEU:HD22	1:B:409:TYR:CD1	2.34	0.59
1:C:44:ARG:HG2	1:C:44:ARG:HH11	1.68	0.59
1:B:175:LYS:NZ	5:B:822:HOH:O	2.34	0.59
1:A:294:LEU:HD22	1:A:409:TYR:HD1	1.67	0.58
1:A:197:MET:HE2	1:A:578:THR:HG21	1.84	0.58
1:C:294:LEU:HD22	1:C:409:TYR:HD1	1.67	0.58
1:D:294:LEU:HD22	1:D:409:TYR:HD1	1.67	0.58
1:D:209:PHE:HB2	1:D:377:ILE:HD12	1.85	0.58
1:C:172:PRO:CG	1:C:495:TYR:CE1	2.86	0.58
1:C:542:PRO:O	1:D:61:ARG:NH1	2.37	0.57
1:C:470:PHE:O	1:C:471:SER:HB2	2.04	0.56
1:A:495:TYR:O	1:A:496:SER:HB3	2.04	0.56
1:B:389:PRO:HG2	1:B:434:VAL:HA	1.89	0.55
1:B:85:THR:O	1:B:89:VAL:HG23	2.06	0.55
1:C:113:MET:HE3	1:C:117:LEU:HD13	1.89	0.55
1:D:214:HIS:ND1	5:D:946:HOH:O	2.33	0.55
1:C:500:VAL:HG12	1:C:500:VAL:O	2.07	0.55
1:C:543:GLN:HE22	1:D:44:ARG:HH22	1.54	0.55
1:D:479:GLU:HG2	1:D:480:GLU:N	2.22	0.55
1:C:472:LEU:HD21	1:C:524:GLU:HG3	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:178:LEU:HD11	1:D:445:GLN:HB2	1.89	0.54
1:A:150:ARG:NH1	1:A:152:LEU:O	2.40	0.54
1:C:495:TYR:O	1:C:497:ASP:N	2.41	0.54
1:A:472:LEU:HD21	1:A:524:GLU:HG3	1.90	0.54
1:A:93:LEU:HD21	4:A:706:BOG:H4'1	1.89	0.54
1:A:216:ARG:NH1	2:E:2:NAG:O7	2.42	0.53
1:C:142:PHE:O	1:C:376:ARG:NH2	2.25	0.53
1:B:116:VAL:HG12	4:B:705:BOG:H4'2	1.91	0.52
1:B:230:LEU:HD13	1:B:233:ILE:HD12	1.90	0.52
1:C:294:LEU:HD22	1:C:409:TYR:CD1	2.44	0.52
1:A:456:ARG:NH2	1:A:502:GLU:OE1	2.39	0.52
1:A:213:ASP:HB2	1:A:222:ARG:HG3	1.91	0.52
1:C:389:PRO:HG2	1:C:434:VAL:HA	1.92	0.51
1:D:44:ARG:N	5:D:887:HOH:O	2.35	0.51
1:D:485:LYS:NZ	5:D:879:HOH:O	2.32	0.51
1:A:389:PRO:HD3	1:A:440:VAL:HG22	1.92	0.51
1:B:150:ARG:NH2	5:B:811:HOH:O	2.29	0.51
1:D:101:ASN:O	1:D:105:ASN:ND2	2.39	0.51
1:B:209:PHE:O	1:B:377:ILE:HD12	2.11	0.51
1:C:380:GLU:HG2	1:C:466:TYR:CE1	2.46	0.50
1:C:206:THR:HG21	1:C:385:TYR:CE1	2.47	0.50
1:C:44:ARG:NH2	1:C:125:ASP:OD1	2.44	0.50
1:A:497:ASP:HB3	1:A:500:VAL:HG23	1.93	0.50
1:A:44:ARG:HH11	1:A:44:ARG:CG	2.21	0.49
1:B:230:LEU:HA	1:B:232:HIS:CE1	2.47	0.49
1:A:549:THR:OG1	1:B:137:LYS:NZ	2.44	0.49
1:A:553:GLU:HG3	5:A:930:HOH:O	2.13	0.49
1:A:294:LEU:HD22	1:A:409:TYR:CD1	2.47	0.49
1:C:172:PRO:HG2	1:C:495:TYR:CE1	2.48	0.49
1:C:172:PRO:CG	1:C:495:TYR:CZ	2.95	0.49
1:A:116:VAL:HB	4:A:706:BOG:H2'2	1.95	0.48
1:C:495:TYR:O	1:C:496:SER:C	2.54	0.48
1:D:230:LEU:HD13	1:D:233:ILE:HD12	1.94	0.48
1:D:497:ASP:HB3	1:D:500:VAL:HG23	1.96	0.48
1:B:226:HIS:ND1	1:B:377:ILE:HG12	2.29	0.48
1:D:294:LEU:HD22	1:D:409:TYR:CD1	2.47	0.48
1:C:119:SER:O	1:C:120:ARG:C	2.55	0.48
1:C:360:LYS:HE2	1:C:362:ASP:HB2	1.96	0.48
1:B:380:GLU:HG2	1:B:466:TYR:CE1	2.49	0.48
1:D:207:HIS:NE2	5:D:962:HOH:O	2.35	0.47
1:B:342:LYS:HG2	1:B:562:ALA:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:269:THR:OG1	1:D:271:VAL:HG13	2.14	0.47
1:B:417:HIS:O	1:B:421:GLN:HB2	2.15	0.47
1:B:89:VAL:HG11	4:B:705:BOG:H3'2	1.97	0.47
1:A:249:ASP:OD1	1:A:317:LYS:HE3	2.15	0.47
1:B:180:LYS:HB3	1:B:490:GLU:HG2	1.96	0.47
1:B:243:LYS:HB3	1:B:271:VAL:HG12	1.96	0.47
1:D:173:ASP:HB3	1:D:176:GLU:HB2	1.97	0.46
1:B:253:LYS:NZ	5:B:921:HOH:O	2.45	0.46
1:B:112:ILE:O	1:B:116:VAL:HG13	2.15	0.46
1:B:295:VAL:HB	1:B:298:LEU:HD22	1.96	0.46
1:A:467:ARG:NH1	1:A:521:THR:OG1	2.49	0.46
1:A:179:GLU:OE1	5:A:921:HOH:O	2.21	0.46
1:A:492:LYS:NZ	5:A:973:HOH:O	2.49	0.46
1:B:178:LEU:HD11	1:B:445:GLN:HB2	1.97	0.46
1:C:101:ASN:O	1:C:105:ASN:ND2	2.40	0.46
1:C:249:ASP:OD1	1:C:317:LYS:HE3	2.15	0.46
1:A:542:PRO:O	1:B:61:ARG:NH1	2.49	0.45
1:D:112:ILE:O	1:D:116:VAL:HG13	2.17	0.45
1:A:113:MET:HE3	1:A:117:LEU:HD13	1.98	0.45
1:B:418:GLY:O	1:B:422:PHE:HB2	2.17	0.45
1:C:543:GLN:HE22	1:D:44:ARG:NH2	2.15	0.45
1:D:113:MET:HE3	1:D:117:LEU:HD13	1.99	0.44
1:B:271:VAL:HG22	1:B:286:ALA:HB1	1.98	0.44
1:B:276:PRO:HG2	1:B:279:ILE:HG12	1.98	0.44
1:D:470:PHE:CG	1:D:525:LEU:HD22	2.53	0.44
1:B:101:ASN:O	1:B:105:ASN:ND2	2.37	0.44
1:D:89:VAL:HG11	4:D:705:BOG:H3'2	1.99	0.44
1:B:148:TYR:CD1	1:B:377:ILE:HG13	2.53	0.44
1:A:163:MET:HE2	1:A:171:LEU:HD21	1.99	0.44
1:C:117:LEU:O	1:C:121:SER:OG	2.35	0.44
1:C:462:SER:OG	1:C:465:GLU:HG2	2.17	0.44
1:A:491:LEU:HD11	1:A:509:VAL:HG11	1.99	0.44
1:A:34:ASN:HB3	1:A:37:CYS:SG	2.58	0.43
1:A:174:SER:OG	1:A:449:LYS:NZ	2.28	0.43
1:C:473:LYS:HA	1:C:474:PRO:HD3	1.88	0.43
1:A:344:VAL:O	1:A:348:TYR:HB3	2.18	0.43
1:B:539:ILE:HA	1:B:544:TYR:HB3	2.00	0.43
1:C:185:ARG:NH2	4:C:705:BOG:H4'1	2.33	0.43
1:C:89:VAL:HG11	4:C:706:BOG:H3'2	2.00	0.43
1:D:155:VAL:HB	1:D:459:LYS:HE2	2.00	0.43
1:A:382:ASN:OD1	1:A:386:HIS:HE1	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:226:HIS:HA	1:D:377:ILE:HD13	2.00	0.43
1:D:389:PRO:HD3	1:D:440:VAL:HG22	2.01	0.43
1:C:470:PHE:CG	1:C:525:LEU:HD22	2.54	0.42
1:D:363:PRO:HG2	1:D:545:TRP:CD2	2.53	0.42
1:A:511:LYS:O	5:A:828:HOH:O	2.21	0.42
1:B:173:ASP:HB3	1:B:176:GLU:HB2	2.01	0.42
1:D:479:GLU:HG2	1:D:480:GLU:H	1.83	0.42
1:D:578:THR:HG22	1:D:579:SER:H	1.84	0.42
1:B:65:TYR:O	1:B:71:THR:HG23	2.20	0.42
1:D:465:GLU:OE1	5:D:931:HOH:O	2.22	0.42
1:A:44:ARG:NH2	1:A:125:ASP:OD1	2.48	0.42
1:A:334:LEU:HD23	1:A:334:LEU:HA	1.85	0.42
1:C:414:LEU:HA	1:C:422:PHE:CE1	2.54	0.42
1:D:44:ARG:HD2	1:D:469:ARG:HE	1.84	0.42
1:A:93:LEU:HB3	1:A:355:TYR:CD1	2.54	0.42
1:C:229:ASP:HB3	1:D:139:TRP:CZ2	2.54	0.42
1:C:295:VAL:HB	1:C:298:LEU:HD22	2.01	0.42
4:C:705:BOG:H7'1	4:C:705:BOG:H4'2	1.78	0.42
1:A:473:LYS:HA	1:A:474:PRO:HD3	1.91	0.42
1:C:539:ILE:HA	1:C:544:TYR:HB3	2.01	0.42
1:A:388:HIS:N	1:A:389:PRO:HD2	2.34	0.42
1:C:230:LEU:HG	1:C:337:ILE:HG12	2.02	0.42
1:A:180:LYS:HD3	1:A:490:GLU:HG3	2.02	0.42
1:A:89:VAL:HG11	4:A:706:BOG:H3'2	2.02	0.41
1:A:363:PRO:HG2	1:A:545:TRP:CD2	2.55	0.41
1:A:456:ARG:HA	5:A:949:HOH:O	2.21	0.41
1:B:114:LYS:HE2	1:B:365:LEU:O	2.19	0.41
1:D:414:LEU:HA	1:D:422:PHE:CE1	2.55	0.41
1:C:172:PRO:HG3	1:C:495:TYR:CD1	2.54	0.41
1:D:295:VAL:HB	1:D:298:LEU:HD22	2.01	0.41
1:B:386:HIS:HB3	1:B:388:HIS:CE1	2.55	0.41
1:C:245:ARG:HD3	1:C:329:PHE:CD1	2.56	0.41
1:B:148:TYR:HD1	1:B:377:ILE:HG13	1.85	0.41
1:C:506:ALA:O	1:C:510:GLU:HB2	2.21	0.41
1:A:206:THR:HG21	1:A:385:TYR:CE1	2.54	0.41
1:B:292:PHE:O	1:B:299:MET:HE2	2.21	0.41
1:B:530:SER:O	1:B:534:LEU:HD22	2.20	0.41
1:C:181:VAL:HG21	1:C:491:LEU:HD21	2.01	0.41
1:A:173:ASP:HB3	1:A:176:GLU:HB2	2.03	0.41
1:A:386:HIS:HB3	1:A:388:HIS:CE1	2.56	0.41
1:D:252:LEU:HD22	1:D:309:HIS:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:453:ASP:OD2	5:B:867:HOH:O	2.22	0.41
1:C:183:LEU:HD23	1:C:183:LEU:HA	1.93	0.41
1:C:389:PRO:HB2	1:C:433:ARG:O	2.21	0.41
1:D:230:LEU:HA	1:D:232:HIS:CE1	2.56	0.41
1:C:293:GLY:HA2	1:C:299:MET:HE3	2.03	0.41
1:A:497:ASP:OD1	1:A:498:ILE:N	2.53	0.40
1:C:230:LEU:HD22	1:C:232:HIS:HE1	1.86	0.40
1:D:148:TYR:CZ	1:D:221:THR:HB	2.56	0.40
1:A:139:TRP:CZ2	1:B:229:ASP:HB3	2.57	0.40
1:C:93:LEU:HB3	1:C:355:TYR:CD1	2.57	0.40
1:A:119:SER:O	1:A:122:TYR:HD1	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	550/587 (94%)	528 (96%)	21 (4%)	1 (0%)	43 57
1	B	550/587 (94%)	534 (97%)	14 (2%)	2 (0%)	30 42
1	C	550/587 (94%)	523 (95%)	24 (4%)	3 (0%)	24 35
1	D	550/587 (94%)	533 (97%)	16 (3%)	1 (0%)	43 57
All	All	2200/2348 (94%)	2118 (96%)	75 (3%)	7 (0%)	36 49

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	416	GLU
1	A	398	GLU
1	D	398	GLU
1	C	398	GLU

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Mol	Chain	Res	Type
1	B	398	GLU
1	B	416	GLU
1	C	420	THR

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	493/525 (94%)	455 (92%)	38 (8%)	12	19
1	B	493/525 (94%)	456 (92%)	37 (8%)	12	20
1	C	493/525 (94%)	458 (93%)	35 (7%)	13	22
1	D	493/525 (94%)	453 (92%)	40 (8%)	11	17
All	All	1972/2100 (94%)	1822 (92%)	150 (8%)	12	19

All (150) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	71	THR
1	A	75	LEU
1	A	93	LEU
1	A	107	PHE
1	A	116	VAL
1	A	117	LEU
1	A	122	TYR
1	A	123	LEU
1	A	137	LYS
1	A	150	ARG
1	A	165	VAL
1	A	171	LEU
1	A	176	GLU
1	A	178	LEU
1	A	207	HIS
1	A	238	LEU
1	A	245	ARG

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Mol	Chain	Res	Type
1	A	248	LYS
1	A	252	LEU
1	A	271	VAL
1	A	289	GLN
1	A	298	LEU
1	A	316	LEU
1	A	376	ARG
1	A	385	TYR
1	A	405	LYS
1	A	416	GLU
1	A	469	ARG
1	A	473	LYS
1	A	479	GLU
1	A	484	GLU
1	A	525	LEU
1	A	532	LYS
1	A	534	LEU
1	A	554	VAL
1	A	578	THR
1	A	581	ASN
1	B	71	THR
1	B	75	LEU
1	B	93	LEU
1	B	101	ASN
1	B	107	PHE
1	B	116	VAL
1	B	117	LEU
1	B	123	LEU
1	B	137	LYS
1	B	170	GLU
1	B	171	LEU
1	B	176	GLU
1	B	178	LEU
1	B	232	HIS
1	B	238	LEU
1	B	239	ASP
1	B	245	ARG
1	B	248	LYS
1	B	252	LEU
1	B	271	VAL
1	B	289	GLN
1	B	298	LEU

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Mol	Chain	Res	Type
1	B	316	LEU
1	B	377	ILE
1	B	385	TYR
1	B	405	LYS
1	B	409	TYR
1	B	416	GLU
1	B	419	LEU
1	B	473	LYS
1	B	484	GLU
1	B	525	LEU
1	B	534	LEU
1	B	554	VAL
1	B	556	PHE
1	B	578	THR
1	B	581	ASN
1	C	71	THR
1	C	75	LEU
1	C	93	LEU
1	C	101	ASN
1	C	107	PHE
1	C	108	LEU
1	C	116	VAL
1	C	121	SER
1	C	137	LYS
1	C	150	ARG
1	C	165	VAL
1	C	170	GLU
1	C	171	LEU
1	C	176	GLU
1	C	178	LEU
1	C	238	LEU
1	C	239	ASP
1	C	248	LYS
1	C	252	LEU
1	C	270	GLN
1	C	271	VAL
1	C	291	VAL
1	C	298	LEU
1	C	316	LEU
1	C	358	LYS
1	C	376	ARG
1	C	385	TYR

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Mol	Chain	Res	Type
1	C	405	LYS
1	C	473	LYS
1	C	479	GLU
1	C	509	VAL
1	C	525	LEU
1	C	534	LEU
1	C	556	PHE
1	C	578	THR
1	D	71	THR
1	D	75	LEU
1	D	93	LEU
1	D	107	PHE
1	D	116	VAL
1	D	122	TYR
1	D	123	LEU
1	D	137	LYS
1	D	150	ARG
1	D	170	GLU
1	D	171	LEU
1	D	178	LEU
1	D	232	HIS
1	D	238	LEU
1	D	239	ASP
1	D	252	LEU
1	D	271	VAL
1	D	289	GLN
1	D	298	LEU
1	D	316	LEU
1	D	317	LYS
1	D	352	LEU
1	D	358	LYS
1	D	377	ILE
1	D	385	TYR
1	D	405	LYS
1	D	409	TYR
1	D	416	GLU
1	D	419	LEU
1	D	469	ARG
1	D	473	LYS
1	D	479	GLU
1	D	484	GLU
1	D	509	VAL

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Mol	Chain	Res	Type
1	D	525	LEU
1	D	532	LYS
1	D	534	LEU
1	D	554	VAL
1	D	578	THR
1	D	582	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	43	ASN
1	A	203	GLN
1	A	242	HIS
1	A	461	GLN
1	A	571	ASN
1	B	270	GLN
1	B	282	ASN
1	B	571	ASN
1	C	42	GLN
1	C	101	ASN
1	C	270	GLN
1	C	571	ASN
1	D	43	ASN
1	D	374	GLN
1	D	382	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

8 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	E	1	1,2	14,14,15	0.19	0	17,19,21	0.61	0
2	NAG	E	2	2	14,14,15	0.26	0	17,19,21	0.49	0
2	NAG	F	1	1,2	14,14,15	0.35	0	17,19,21	0.49	0
2	NAG	F	2	2	14,14,15	0.25	0	17,19,21	0.45	0
2	NAG	G	1	1,2	14,14,15	0.25	0	17,19,21	0.53	0
2	NAG	G	2	2	14,14,15	0.30	0	17,19,21	0.50	0
2	NAG	H	1	1,2	14,14,15	0.33	0	17,19,21	0.57	0
2	NAG	H	2	2	14,14,15	0.30	0	17,19,21	0.44	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
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	2	NAG	C4-C5-C6-O6
2	H	2	NAG	O5-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6

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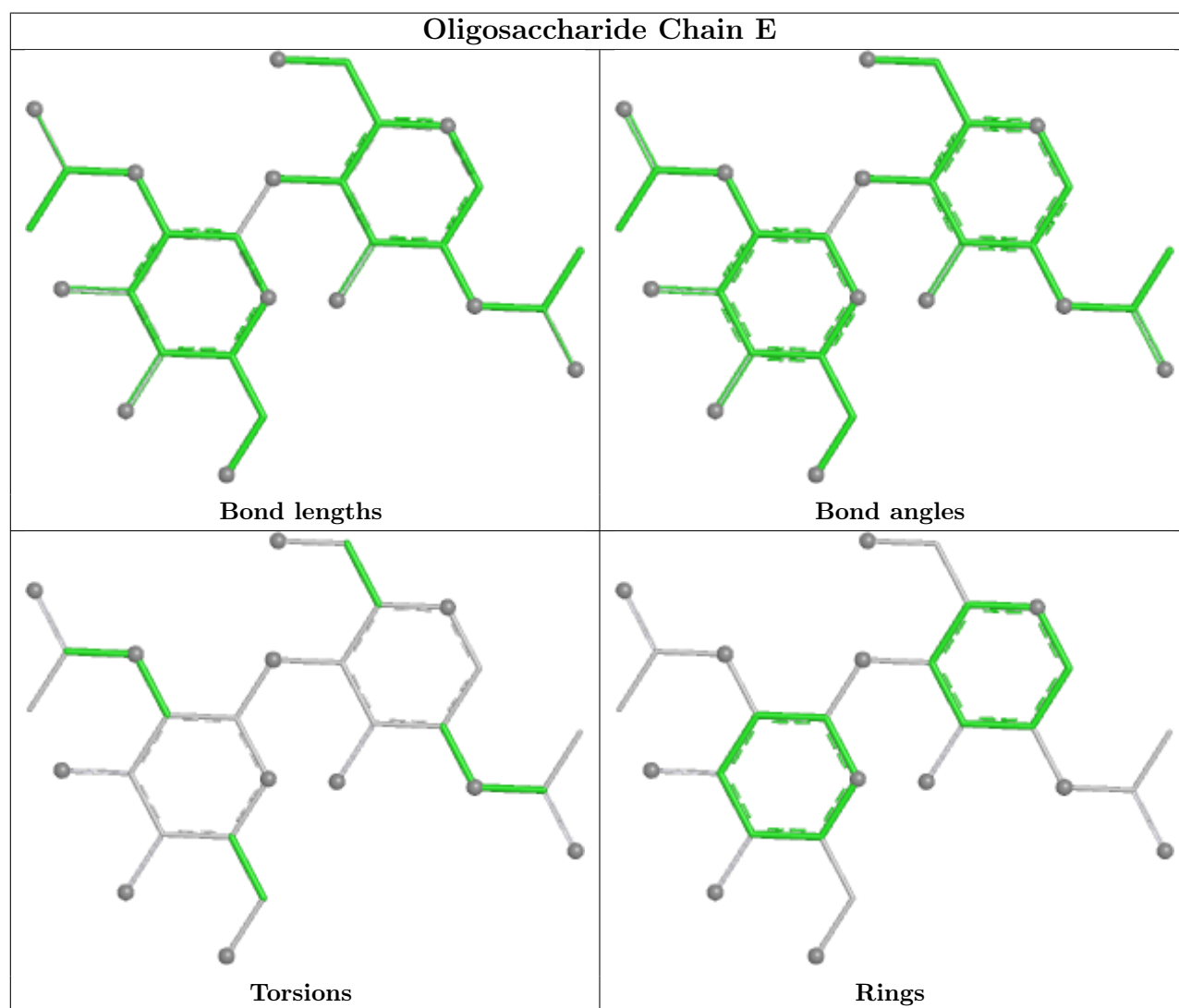
Mol	Chain	Res	Type	Atoms
2	F	2	NAG	O5-C5-C6-O6

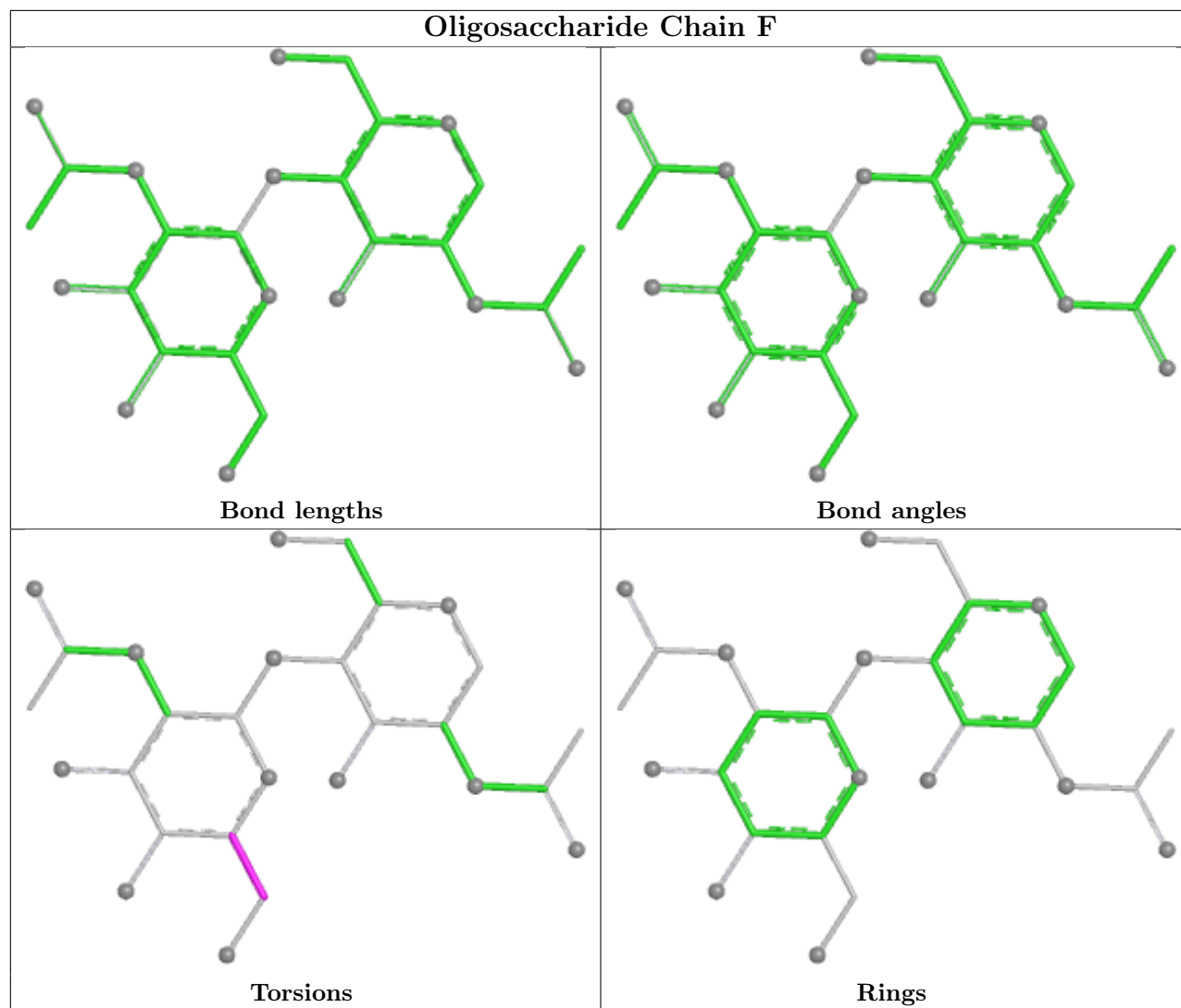
There are no ring outliers.

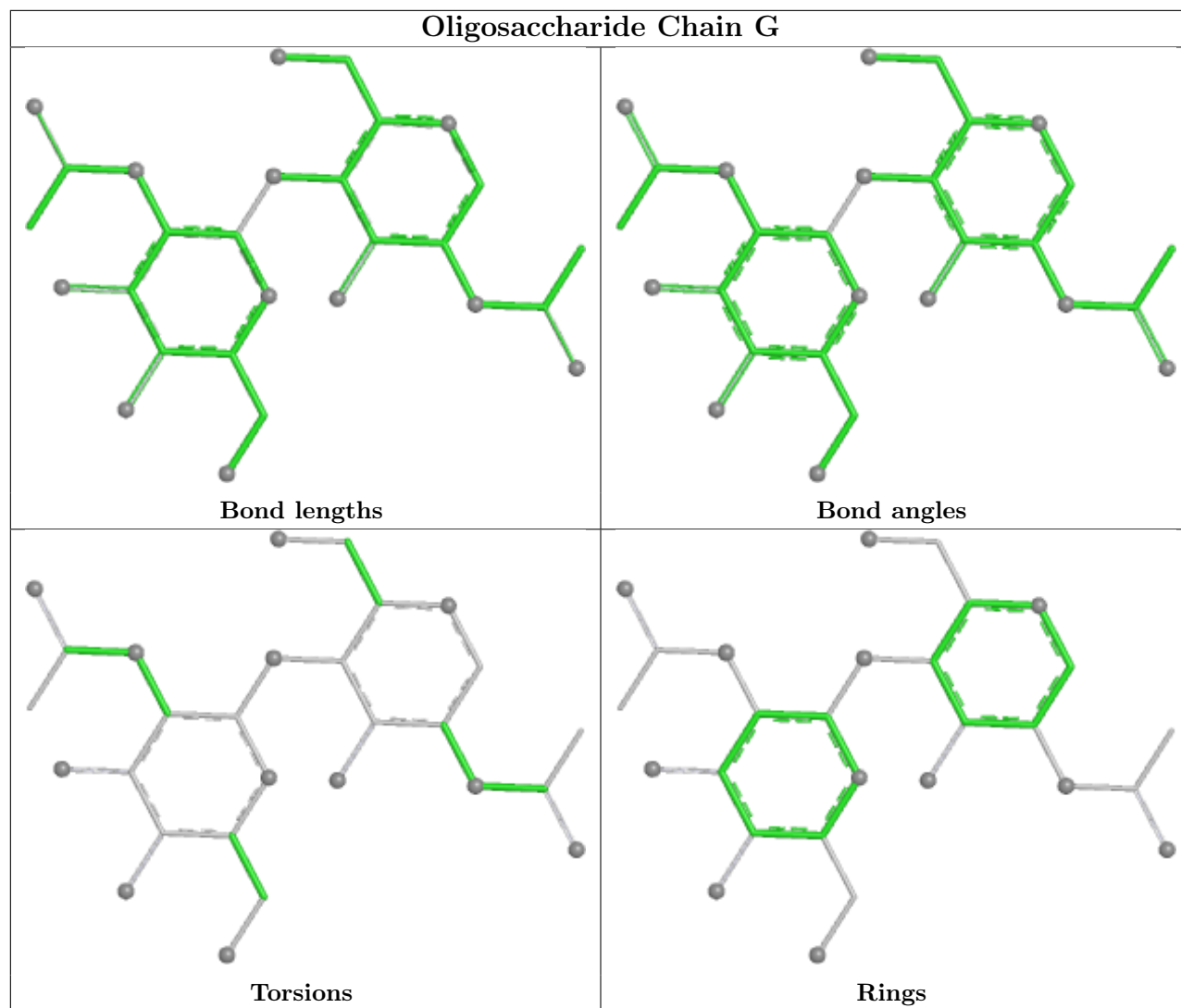
1 monomer is involved in 1 short contact:

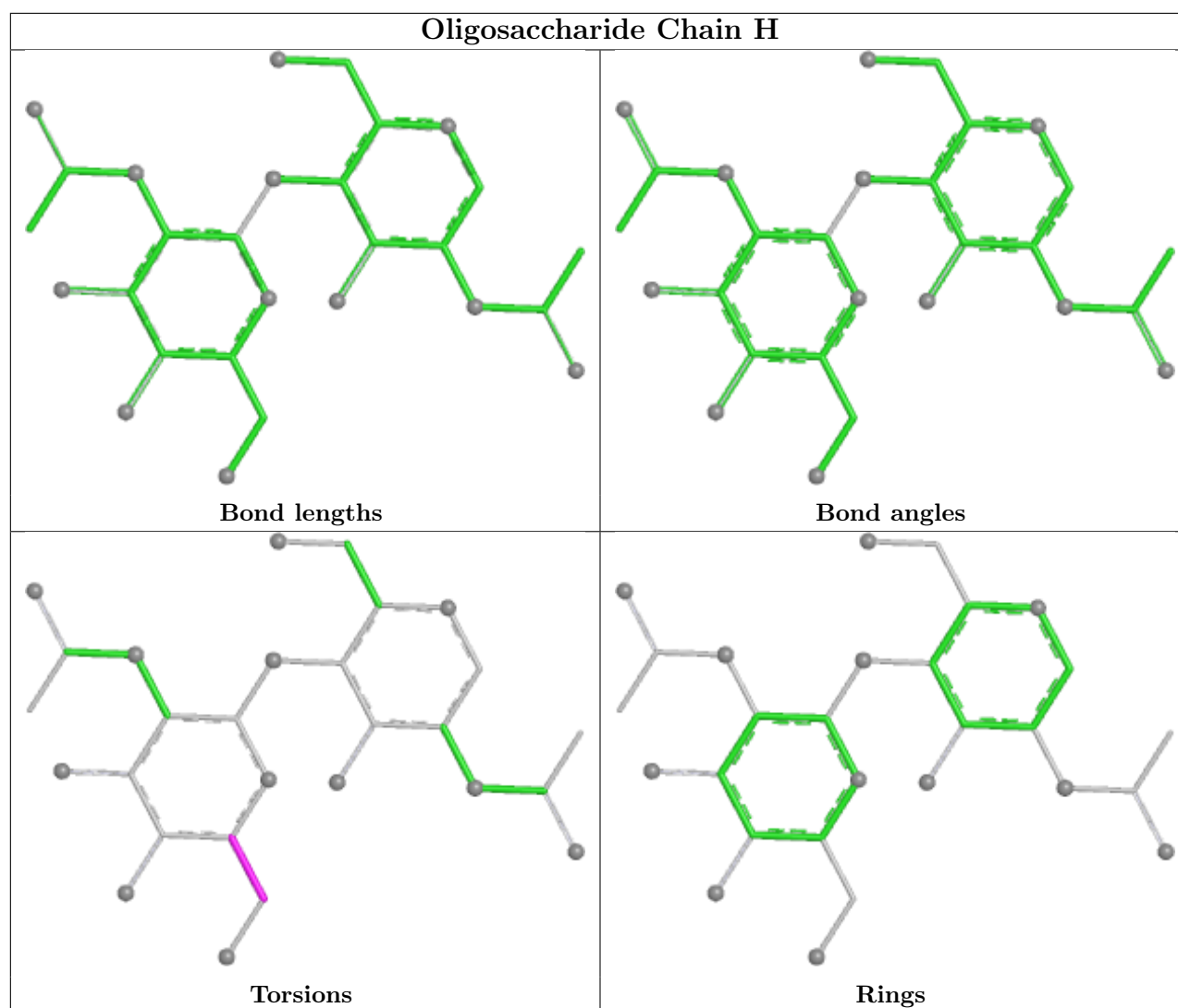
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









5.6 Ligand geometry [i](#)

14 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	$\# Z > 2$
4	BOG	C	706	-	20,20,20	1.05	1 (5%)	25,25,25	1.14	2 (8%)
3	NAG	C	704	1	14,14,15	0.35	0	17,19,21	0.32	0
4	BOG	A	705	-	20,20,20	1.06	1 (5%)	25,25,25	1.13	3 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	704	1	14,14,15	0.25	0	17,19,21	0.35	0
4	BOG	D	705	-	20,20,20	1.05	1 (5%)	25,25,25	1.11	2 (8%)
4	BOG	A	706	-	20,20,20	1.07	1 (5%)	25,25,25	1.16	2 (8%)
3	NAG	D	704	1	14,14,15	0.31	0	17,19,21	0.47	0
3	NAG	B	701	1	14,14,15	0.24	0	17,19,21	0.54	0
4	BOG	B	705	-	20,20,20	1.05	1 (5%)	25,25,25	1.15	2 (8%)
3	NAG	C	701	1	14,14,15	0.24	0	17,19,21	0.48	0
3	NAG	D	701	1	14,14,15	0.45	0	17,19,21	0.44	0
4	BOG	C	705	-	20,20,20	1.02	1 (5%)	25,25,25	1.17	2 (8%)
3	NAG	A	701	1	14,14,15	0.36	0	17,19,21	0.55	0
3	NAG	B	704	1	14,14,15	0.48	0	17,19,21	0.48	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
4	BOG	C	706	-	-	4/11/31/31	0/1/1/1
3	NAG	C	704	1	-	2/6/23/26	0/1/1/1
4	BOG	A	705	-	-	3/11/31/31	0/1/1/1
3	NAG	A	704	1	-	2/6/23/26	0/1/1/1
4	BOG	D	705	-	-	2/11/31/31	0/1/1/1
4	BOG	A	706	-	-	3/11/31/31	0/1/1/1
3	NAG	D	704	1	-	1/6/23/26	0/1/1/1
3	NAG	B	701	1	-	2/6/23/26	0/1/1/1
4	BOG	B	705	-	-	3/11/31/31	0/1/1/1
3	NAG	C	701	1	-	2/6/23/26	0/1/1/1
3	NAG	D	701	1	-	2/6/23/26	0/1/1/1
4	BOG	C	705	-	-	7/11/31/31	0/1/1/1
3	NAG	A	701	1	-	2/6/23/26	0/1/1/1
3	NAG	B	704	1	-	1/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	705	BOG	O2-C2	-2.45	1.36	1.43
4	A	705	BOG	O2-C2	-2.44	1.36	1.43
4	A	706	BOG	O2-C2	-2.43	1.36	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	706	BOG	O2-C2	-2.42	1.37	1.43
4	D	705	BOG	O2-C2	-2.38	1.37	1.43
4	B	705	BOG	O2-C2	-2.37	1.37	1.43

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	705	BOG	C1'-O1-C1	3.70	119.99	113.68
4	B	705	BOG	C1'-O1-C1	3.53	119.71	113.68
4	D	705	BOG	C1'-O1-C1	3.52	119.69	113.68
4	C	706	BOG	C1'-O1-C1	3.45	119.58	113.68
4	A	706	BOG	C1'-O1-C1	3.41	119.51	113.68
4	A	705	BOG	O1-C1-C2	3.13	113.03	108.27
4	A	705	BOG	C1'-O1-C1	2.78	118.43	113.68
4	C	706	BOG	C1-O5-C5	-2.74	108.36	113.72
4	B	705	BOG	C1-O5-C5	-2.61	108.62	113.72
4	A	706	BOG	C1-O5-C5	-2.58	108.67	113.72
4	D	705	BOG	C1-O5-C5	-2.57	108.70	113.72
4	C	705	BOG	C1-O5-C5	-2.23	109.37	113.72
4	A	705	BOG	C1-O5-C5	-2.13	109.57	113.72

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	701	NAG	O5-C5-C6-O6
3	C	701	NAG	C4-C5-C6-O6
3	D	701	NAG	O5-C5-C6-O6
3	D	701	NAG	C4-C5-C6-O6
3	B	701	NAG	O5-C5-C6-O6
3	A	704	NAG	C4-C5-C6-O6
4	C	705	BOG	O1-C1'-C2'-C3'
3	B	701	NAG	C4-C5-C6-O6
3	A	701	NAG	O5-C5-C6-O6
3	C	704	NAG	C4-C5-C6-O6
3	A	701	NAG	C4-C5-C6-O6
4	A	705	BOG	O1-C1'-C2'-C3'
4	A	706	BOG	C4'-C5'-C6'-C7'
3	A	704	NAG	O5-C5-C6-O6
4	A	705	BOG	C3'-C4'-C5'-C6'
4	C	705	BOG	C1'-C2'-C3'-C4'
4	A	705	BOG	C2'-C3'-C4'-C5'

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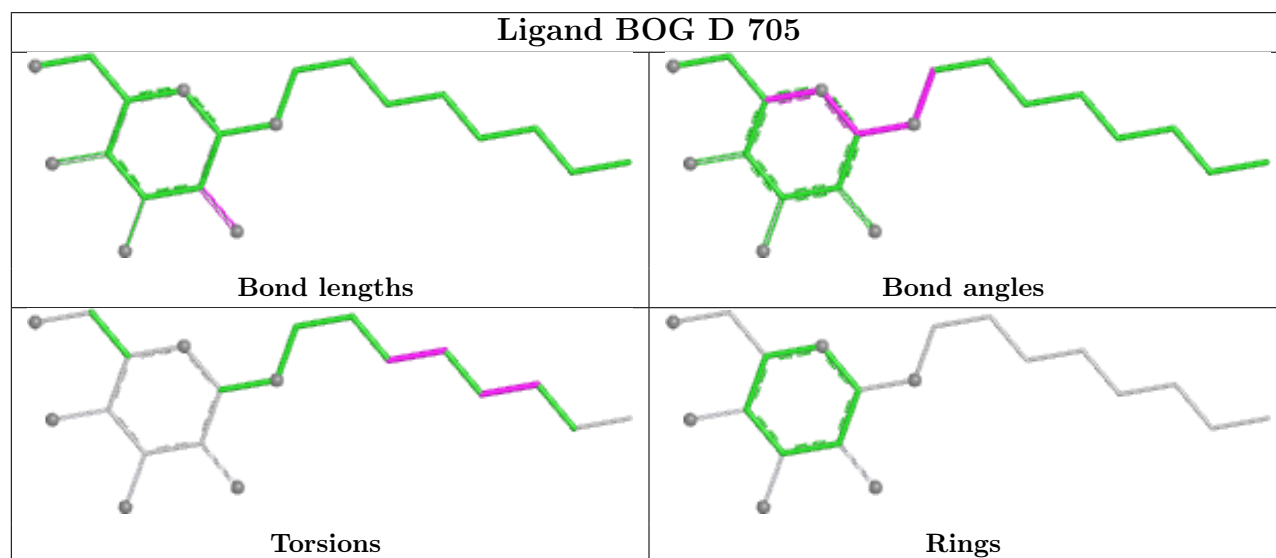
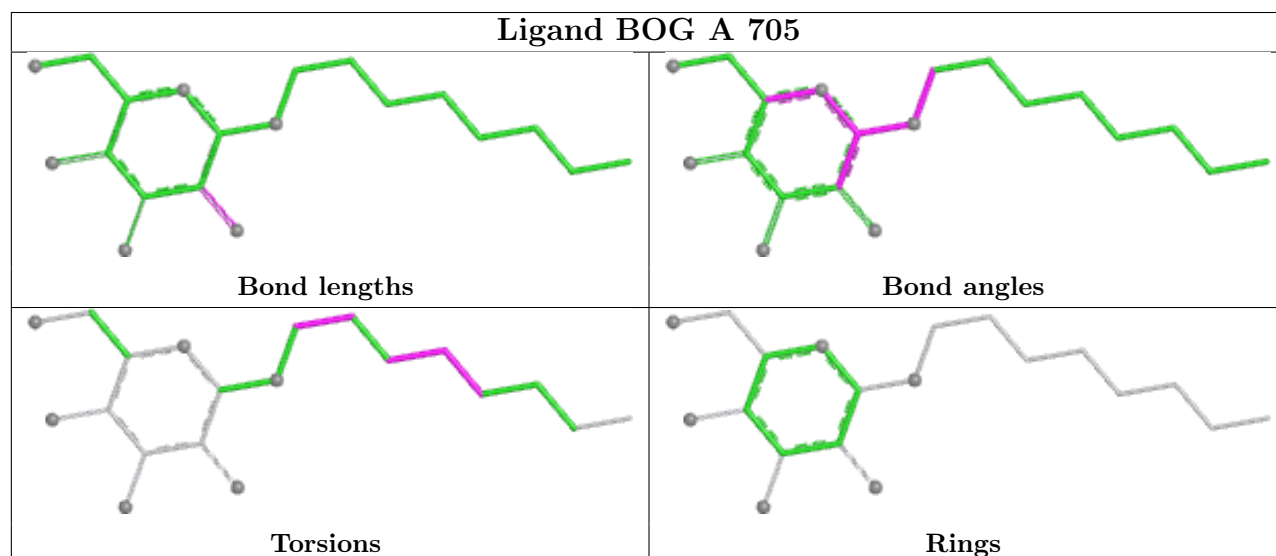
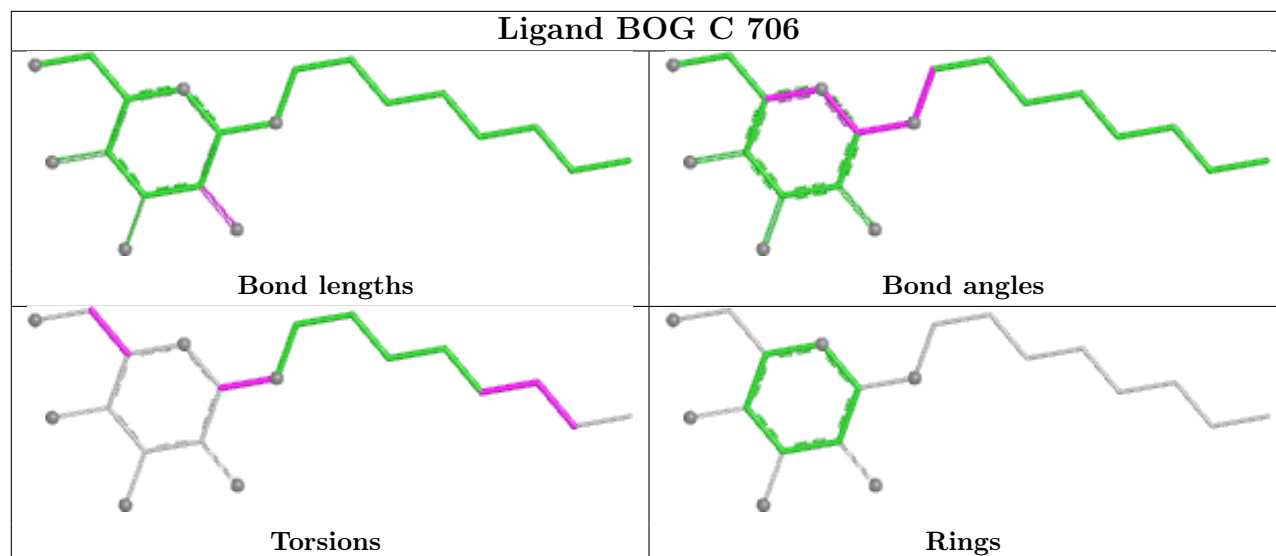
Mol	Chain	Res	Type	Atoms
4	C	706	BOG	C4'-C5'-C6'-C7'
4	B	705	BOG	C4'-C5'-C6'-C7'
4	D	705	BOG	C4'-C5'-C6'-C7'
3	C	704	NAG	O5-C5-C6-O6
4	C	705	BOG	C3'-C4'-C5'-C6'
4	C	705	BOG	C2'-C1'-O1-C1
4	C	705	BOG	C2'-C3'-C4'-C5'
4	B	705	BOG	O5-C1-O1-C1'
4	A	706	BOG	O1-C1'-C2'-C3'
4	B	705	BOG	C2-C1-O1-C1'
4	C	705	BOG	C4-C5-C6-O6
4	C	705	BOG	O5-C5-C6-O6
3	D	704	NAG	C4-C5-C6-O6
4	C	706	BOG	C4-C5-C6-O6
4	D	705	BOG	C2'-C3'-C4'-C5'
3	B	704	NAG	C4-C5-C6-O6
4	A	706	BOG	O5-C1-O1-C1'
4	C	706	BOG	O5-C1-O1-C1'
4	C	706	BOG	C5'-C6'-C7'-C8'

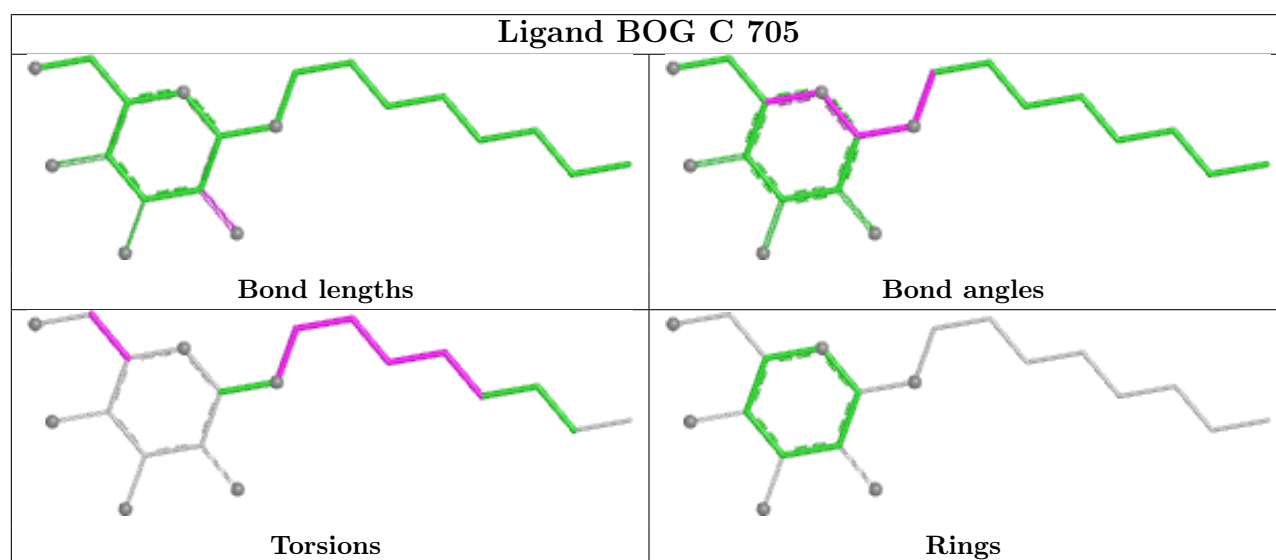
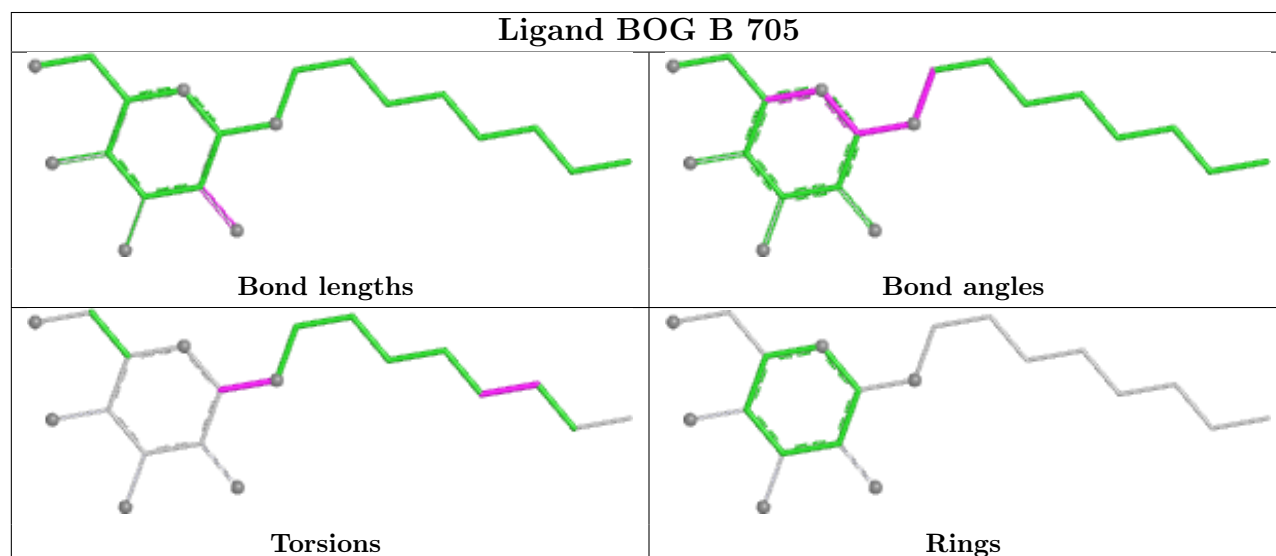
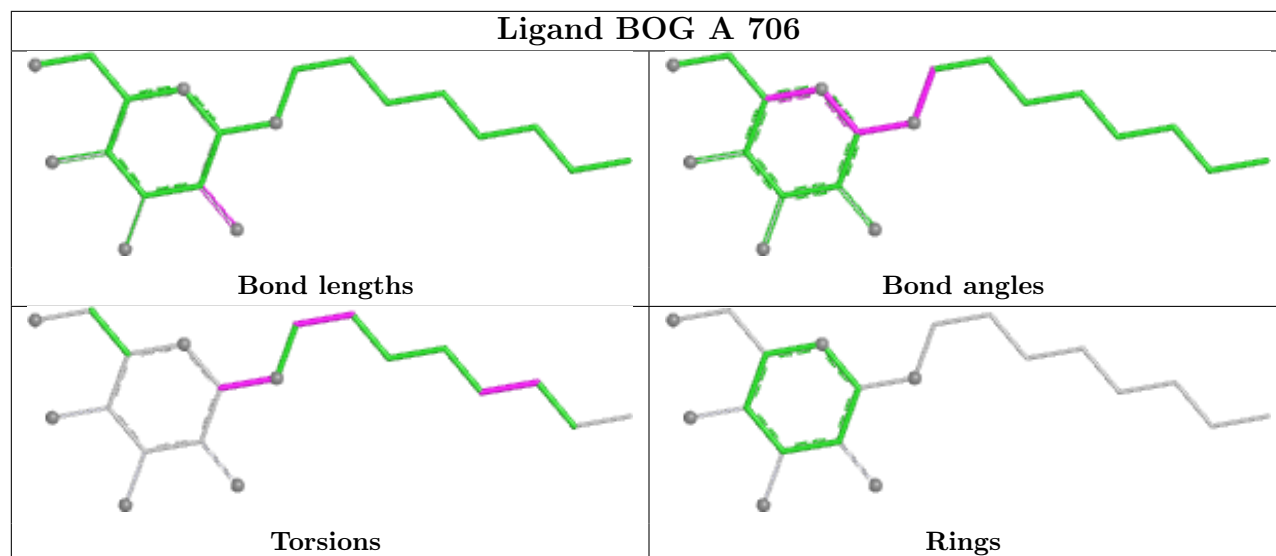
There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	706	BOG	3	0
4	D	705	BOG	1	0
4	A	706	BOG	3	0
4	B	705	BOG	2	0
4	C	705	BOG	2	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 [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	552/587 (94%)	0.06	14 (2%) 58 55	26, 41, 69, 98	0
1	B	552/587 (94%)	0.03	21 (3%) 44 40	25, 40, 69, 90	0
1	C	552/587 (94%)	0.34	25 (4%) 38 34	28, 53, 83, 106	0
1	D	552/587 (94%)	0.25	19 (3%) 48 44	27, 48, 77, 95	0
All	All	2208/2348 (94%)	0.17	79 (3%) 46 42	25, 45, 77, 106	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	418	GLY	5.6
1	B	418	GLY	5.1
1	B	583	GLN	4.2
1	B	420	THR	4.1
1	C	74	PHE	4.1
1	C	420	THR	4.1
1	C	583	GLN	3.9
1	D	121	SER	3.7
1	A	386	HIS	3.6
1	C	495	TYR	3.6
1	C	416	GLU	3.5
1	A	81	LEU	3.5
1	C	81	LEU	3.4
1	D	173	ASP	3.3
1	A	258	GLY	3.3
1	B	416	GLU	3.3
1	A	74	PHE	3.2
1	B	107	PHE	3.2
1	B	409	TYR	3.2
1	B	81	LEU	3.2
1	B	121	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	409	TYR	3.1
1	B	122	TYR	3.0
1	D	352	LEU	3.0
1	C	214	HIS	3.0
1	A	214	HIS	3.0
1	C	75	LEU	3.0
1	C	107	PHE	3.0
1	B	119	SER	3.0
1	C	33	ALA	2.9
1	A	121	SER	2.9
1	C	405	LYS	2.9
1	D	294	LEU	2.9
1	A	443	ALA	2.9
1	D	409	TYR	2.8
1	C	121	SER	2.8
1	C	415	LEU	2.8
1	A	583	GLN	2.7
1	D	81	LEU	2.7
1	D	377	ILE	2.6
1	C	119	SER	2.6
1	D	75	LEU	2.6
1	A	75	LEU	2.6
1	D	175	LYS	2.5
1	B	377	ILE	2.5
1	A	119	SER	2.5
1	B	294	LEU	2.4
1	B	173	ASP	2.4
1	C	90	TRP	2.4
1	C	443	ALA	2.4
1	A	405	LYS	2.4
1	D	239	ASP	2.4
1	B	75	LEU	2.4
1	A	122	TYR	2.4
1	D	291	VAL	2.3
1	B	33	ALA	2.3
1	B	186	GLU	2.3
1	A	79	LYS	2.3
1	C	444	VAL	2.3
1	B	222	ARG	2.3
1	D	290	GLU	2.3
1	D	214	HIS	2.2
1	D	91	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	122	TYR	2.2
1	C	222	ARG	2.2
1	C	122	TYR	2.2
1	D	420	THR	2.2
1	B	290	GLU	2.2
1	C	80	LEU	2.1
1	C	82	LEU	2.1
1	D	418	GLY	2.1
1	B	415	LEU	2.1
1	D	82	LEU	2.1
1	B	214	HIS	2.1
1	D	368	ASN	2.1
1	C	352	LEU	2.1
1	A	82	LEU	2.0
1	B	419	LEU	2.0
1	C	215	LYS	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](#)

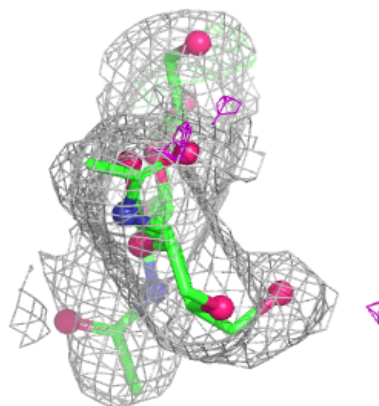
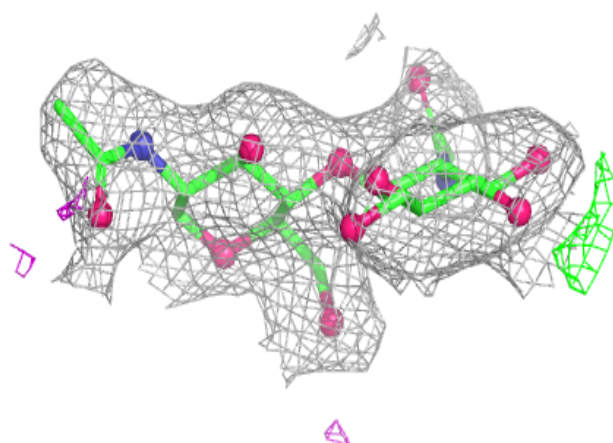
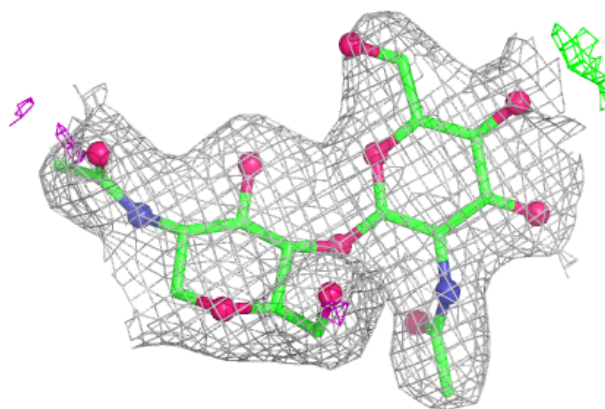
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NAG	E	2	14/15	0.84	0.14	56,66,73,76	0
2	NAG	G	2	14/15	0.87	0.13	54,59,69,72	0
2	NAG	F	2	14/15	0.88	0.11	48,66,73,78	0
2	NAG	H	2	14/15	0.91	0.09	52,60,69,71	0
2	NAG	E	1	14/15	0.93	0.08	28,36,42,53	0
2	NAG	H	1	14/15	0.94	0.07	27,38,45,55	0
2	NAG	G	1	14/15	0.95	0.07	31,44,49,51	0
2	NAG	F	1	14/15	0.95	0.08	30,39,47,59	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

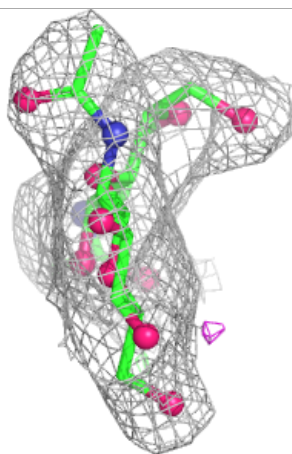
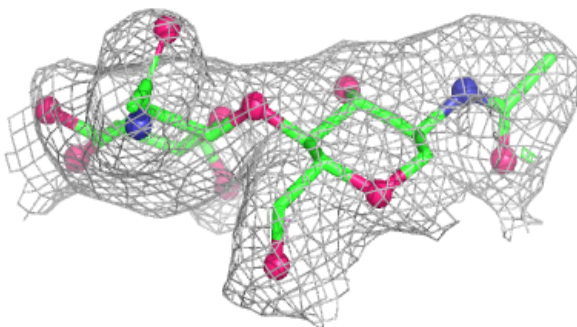
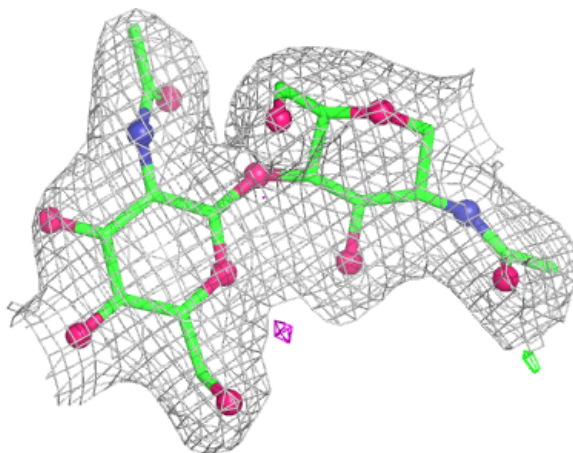
Electron density around Chain E:

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



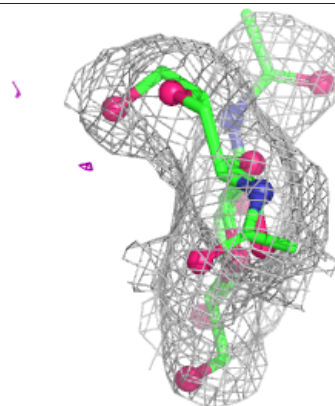
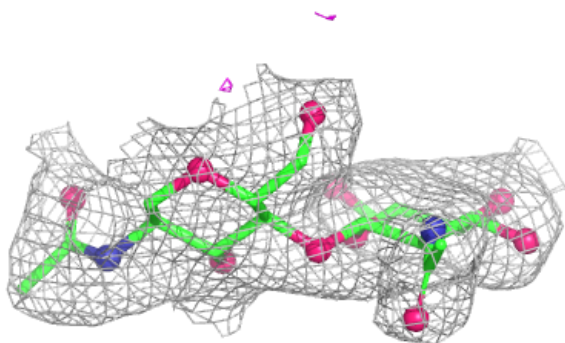
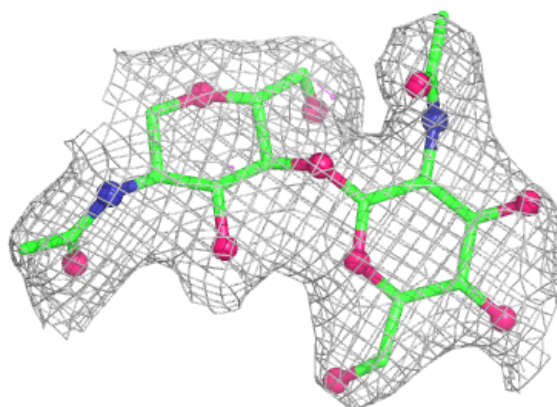
Electron density around Chain F:

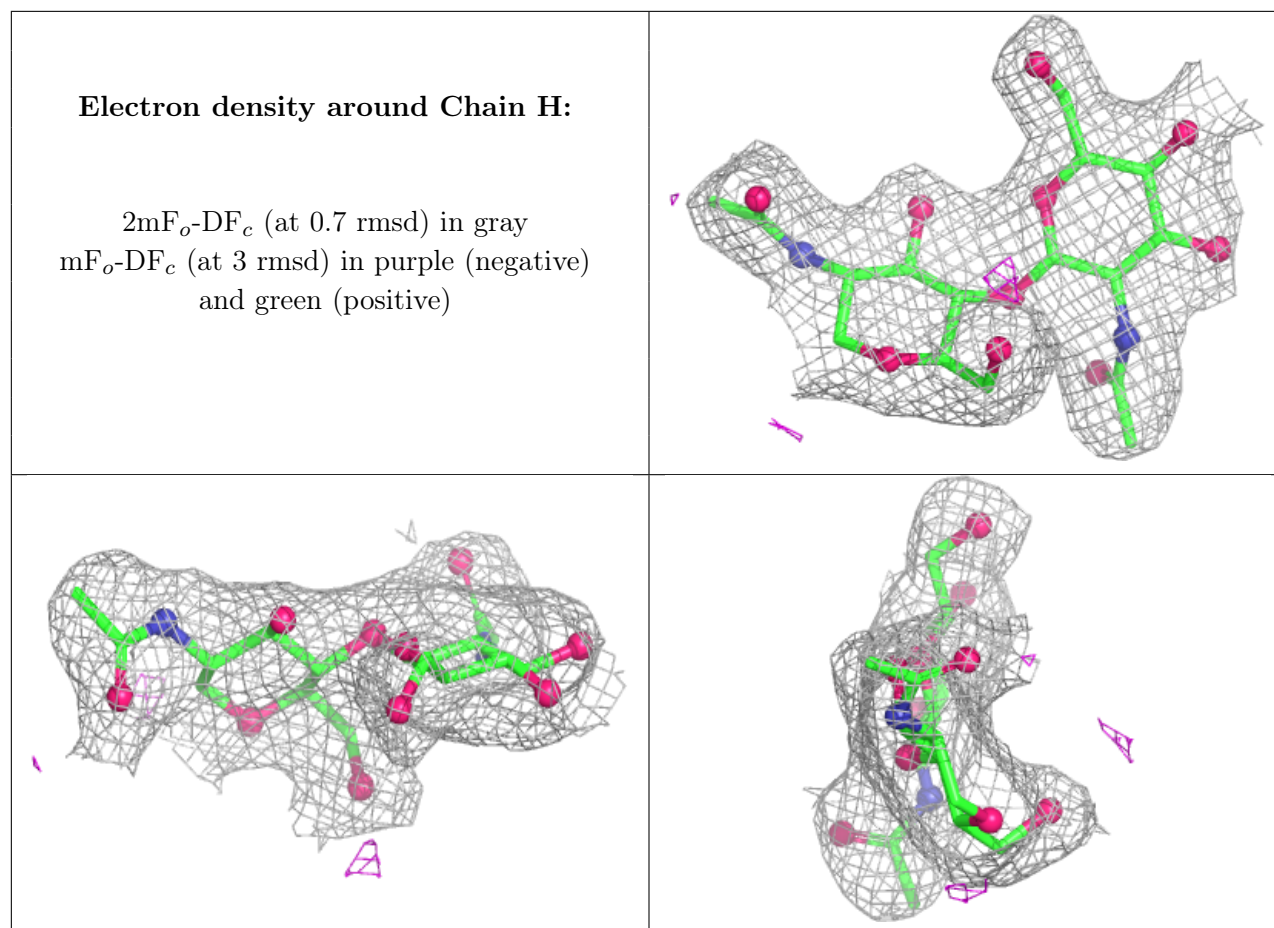
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

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





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.

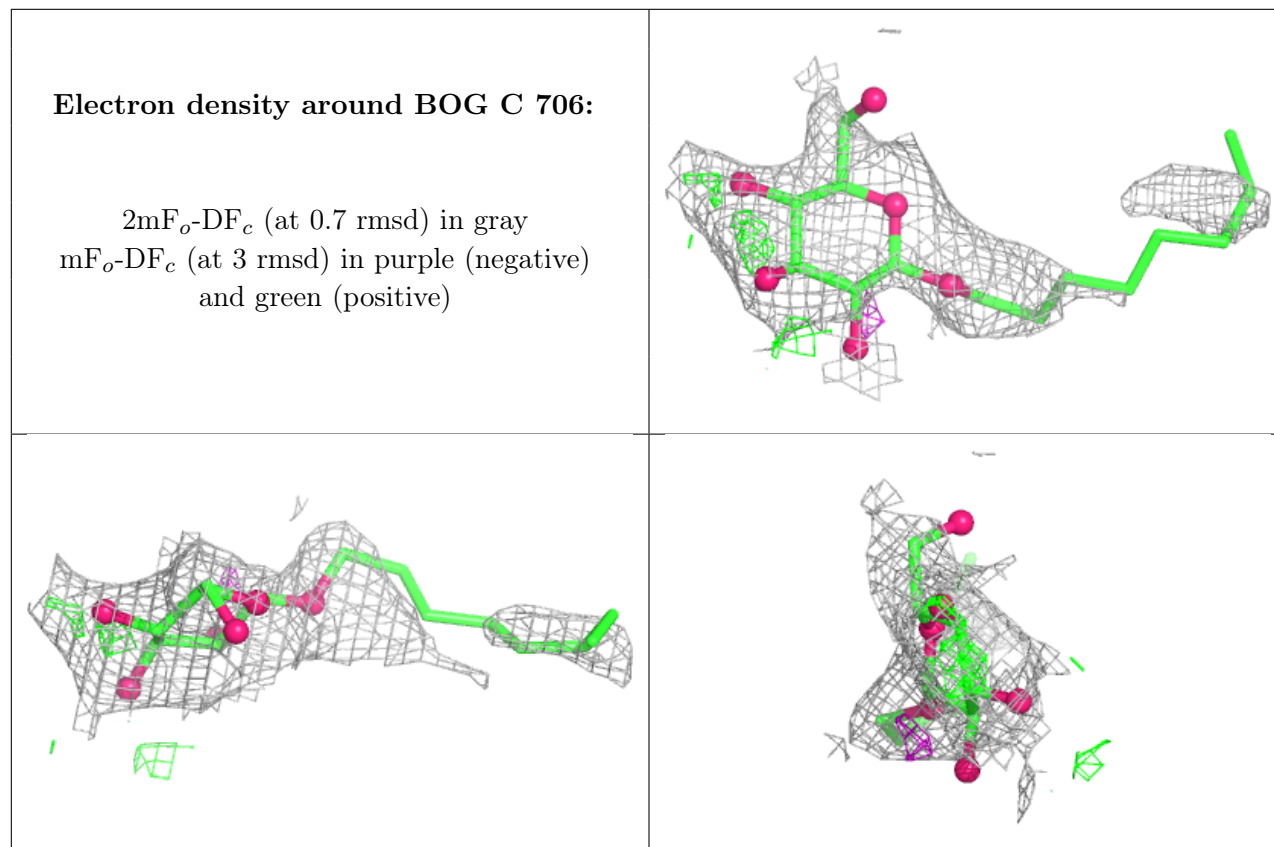
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	B	701	14/15	0.69	0.18	68,79,86,91	0
3	NAG	D	701	14/15	0.70	0.17	63,74,82,85	0
3	NAG	A	701	14/15	0.71	0.15	61,72,88,90	0
3	NAG	C	701	14/15	0.74	0.15	63,80,87,88	0
3	NAG	C	704	14/15	0.75	0.16	63,72,85,92	0
3	NAG	D	704	14/15	0.76	0.16	56,62,73,75	0
4	BOG	C	706	20/20	0.78	0.32	133,145,148,150	0
4	BOG	A	706	20/20	0.80	0.32	134,147,150,153	0
3	NAG	A	704	14/15	0.80	0.14	58,68,76,77	0
4	BOG	C	705	20/20	0.82	0.18	59,72,86,87	0
4	BOG	A	705	20/20	0.82	0.20	44,58,97,99	0
4	BOG	D	705	20/20	0.82	0.29	139,147,151,151	0

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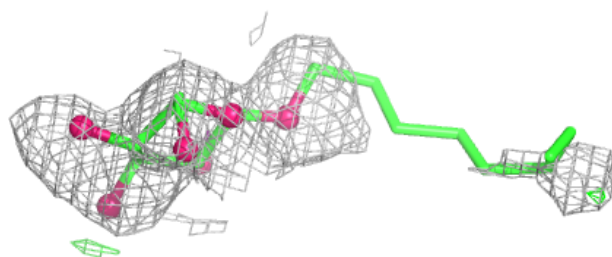
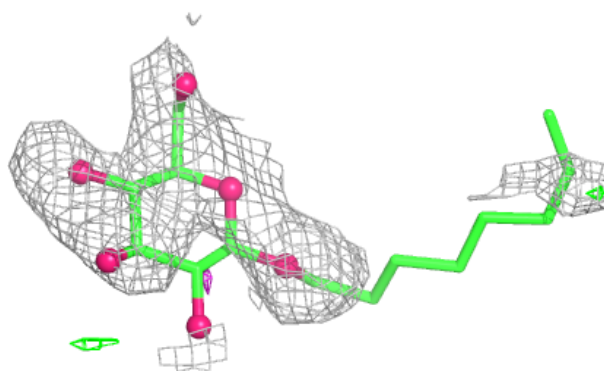
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	B	704	14/15	0.83	0.12	46,55,62,68	0
4	BOG	B	705	20/20	0.85	0.28	137,142,147,147	0

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.

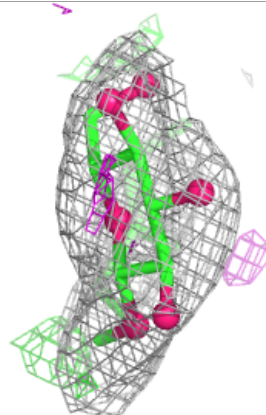
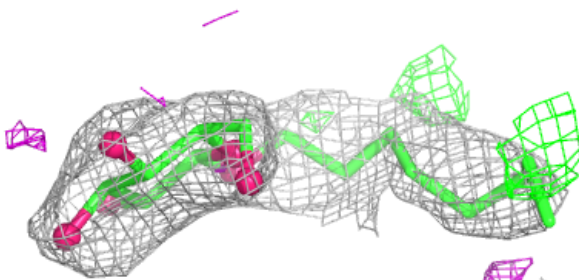
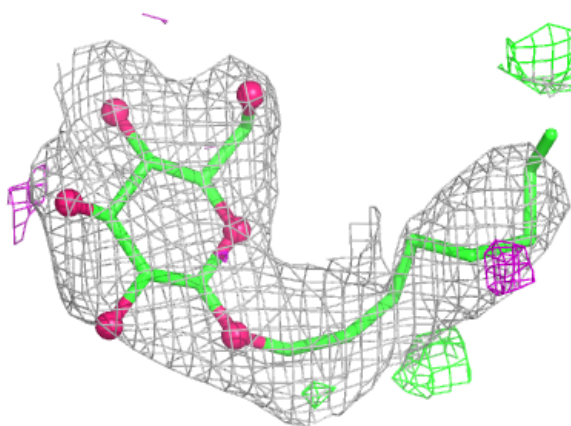


Electron density around BOG A 706:

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

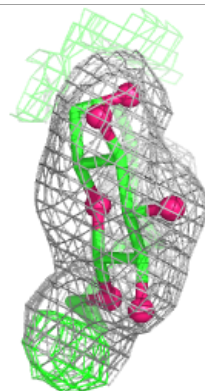
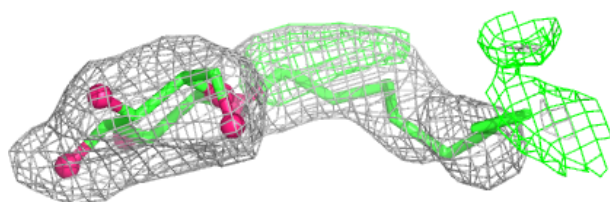
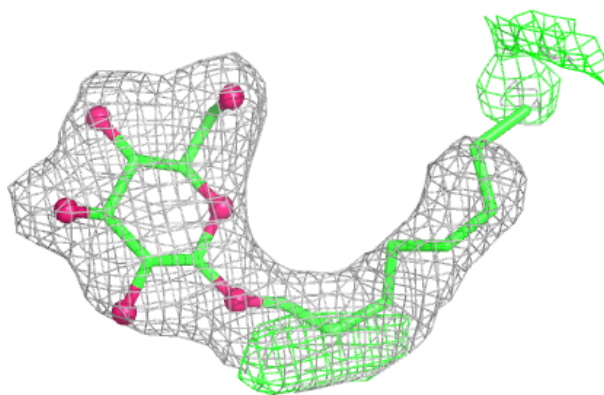
**Electron density around BOG C 705:**

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

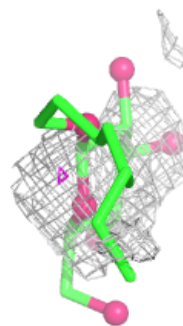
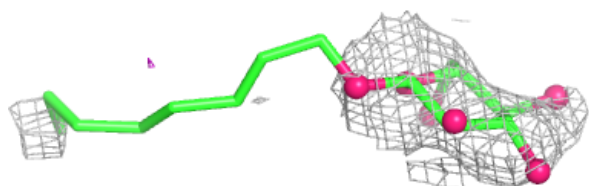
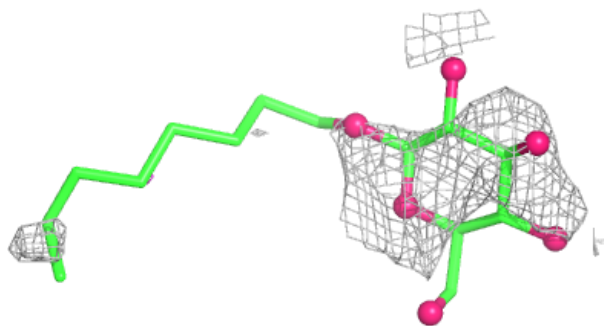


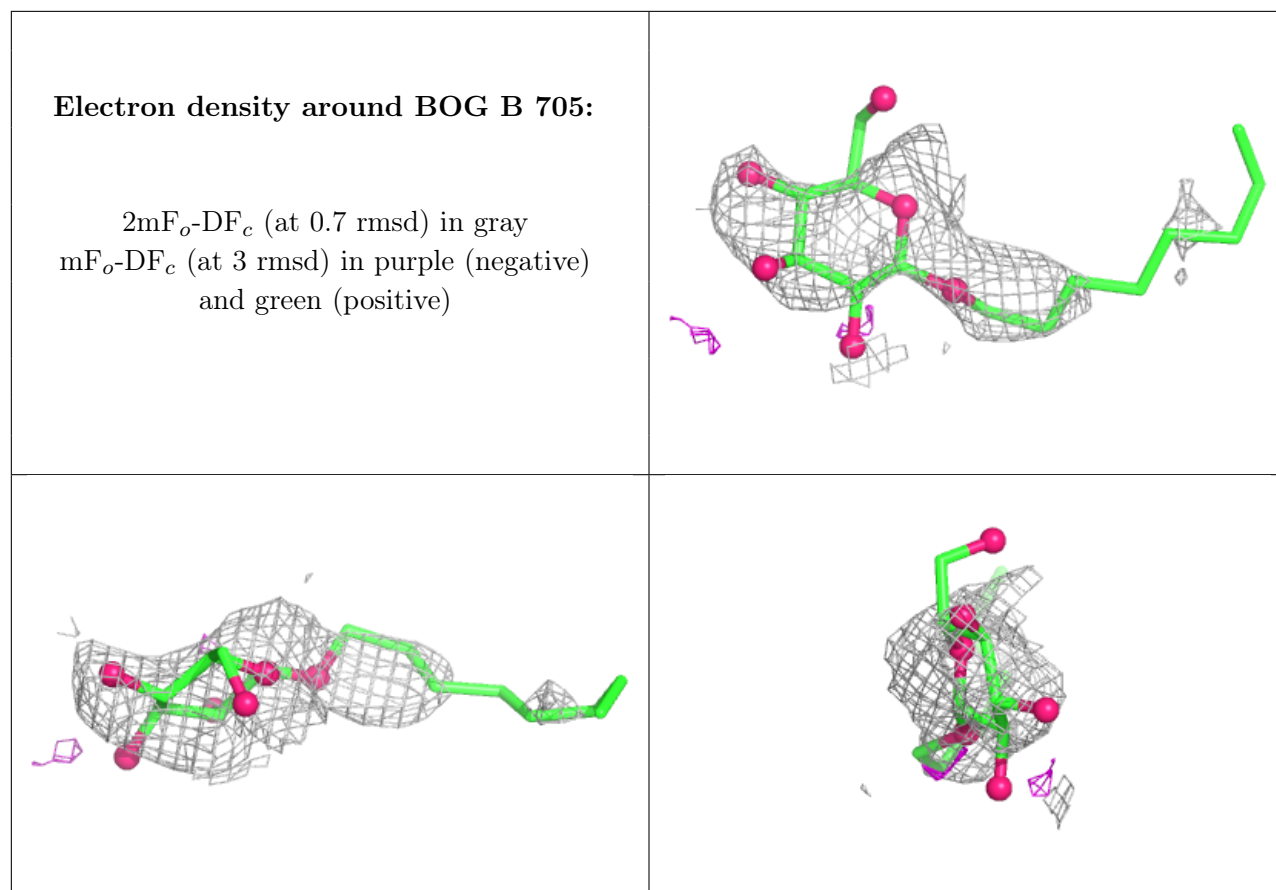
Electron density around BOG A 705:

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

**Electron density around BOG D 705:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.