



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:27 AM UTC

PDB ID : 6V7Y / pdb_00006v7y
Title : Human CD1d presenting alpha-Galactosylceramide in complex with VHH nanobody 1D5
Authors : Shahine, A.; Rossjohn, J.
Deposited on : 2019-12-10
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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

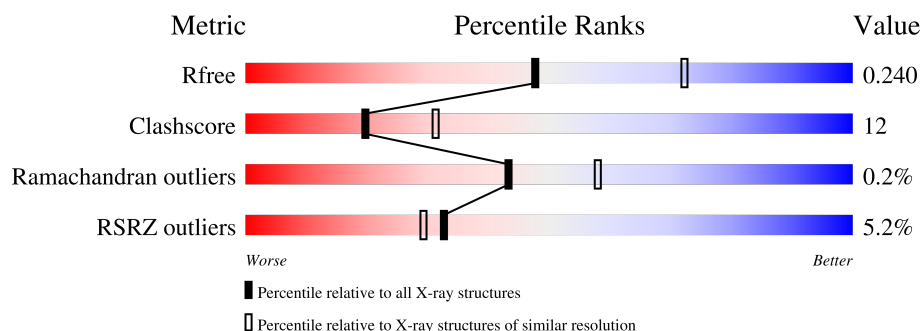
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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)
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	347	5% 58%20%22%
2	B	100	2% 85%14%
3	F	127	4% 78%20%
4	C	2	50%50%
5	D	3	100%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 4324 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 Antigen-presenting glycoprotein CD1d.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	S	2	6	0
			2160	1387	374	391	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P15813

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	1	0
			823	529	134	156	4			

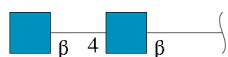
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called Nanobody VHH ID5.

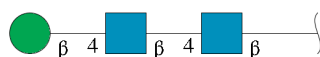
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	126	Total	C	N	O	S	0	2	0
			962	606	167	184	5			

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



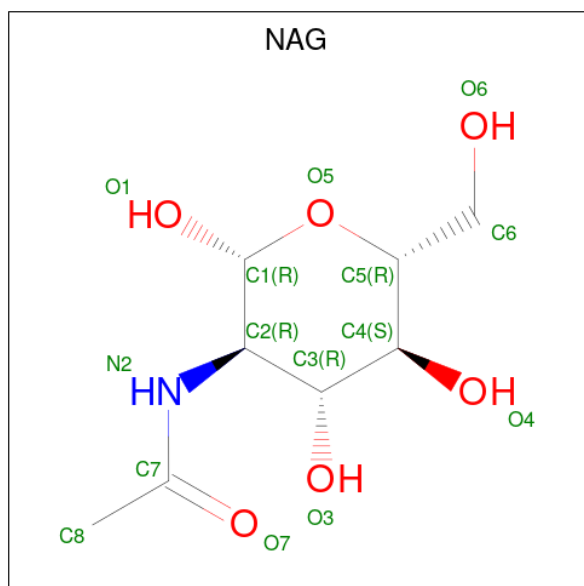
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



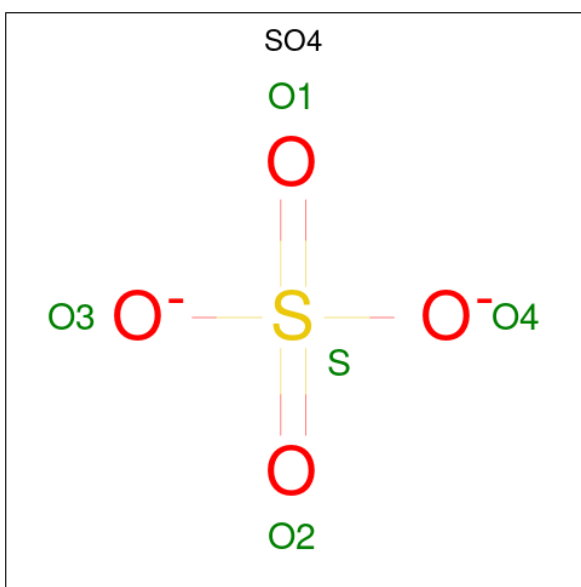
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



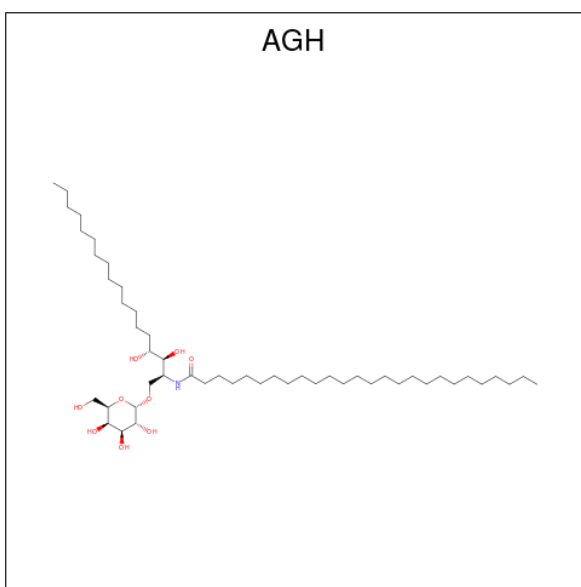
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is N-{(1S,2R,3S)-1-[(ALPHA-D-GALACTOPYRANOSYLOXY)METHYL]-2,3-DIHYDROXYHEPTADECYL}HEXACOSANAMIDE (CCD ID: AGH) (formula: C₅₀H₉₉NO₉) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			60	50	1	9		

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	4	Total	Cl	0	0
			4	4		
9	B	1	Total	Cl	0	0
			1	1		

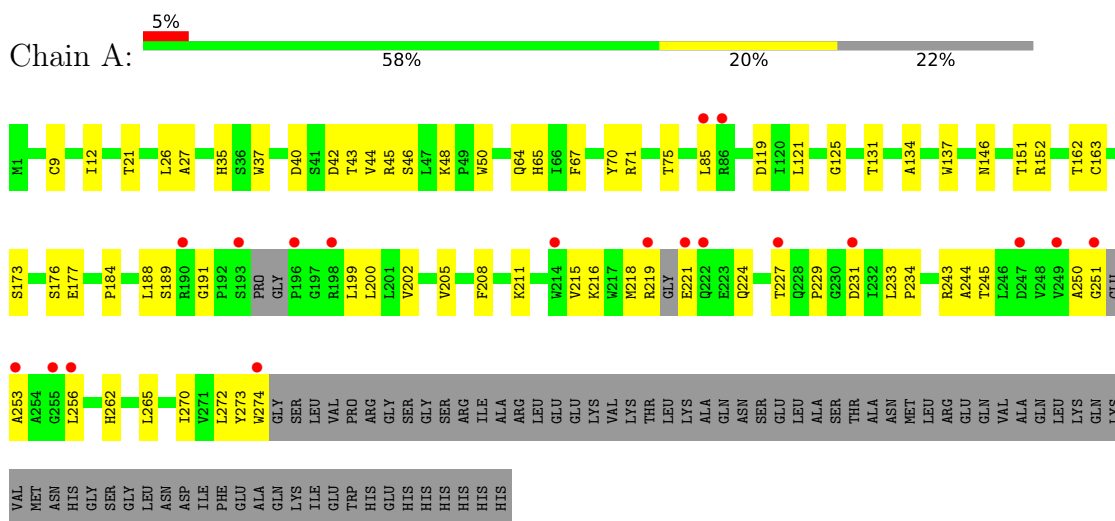
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	111	Total	O	0	0
			111	111		
10	B	45	Total	O	0	0
			45	45		
10	F	38	Total	O	0	0
			38	38		

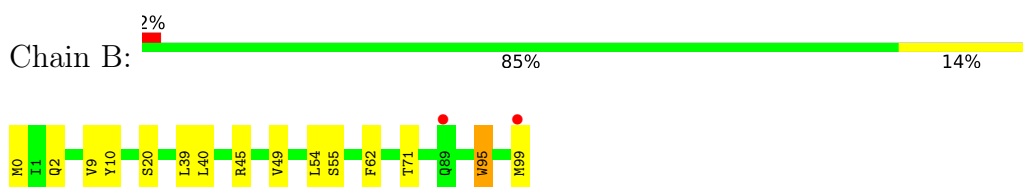
3 Residue-property plots [i](#)

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.

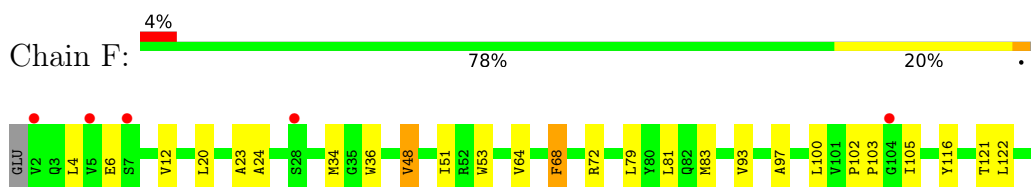
- Molecule 1: Antigen-presenting glycoprotein CD1d



- Molecule 2: Beta-2-microglobulin



- Molecule 3: Nanobody VHH ID5



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



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

HA01
HA02
EM03

4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	73.27 Å 73.27 Å 261.08 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.73 – 2.40 31.73 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (31.73-2.40) 99.9 (31.73-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.40 Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.241 , 0.276 (Not available) , 0.240	Depositor DCC
R_{free} test set	1713 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 60.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.037 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4324	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% 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: NAG, BMA, AGH, SO4, CL

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	0.91	1/2241 (0.0%)	1.29	6/3054 (0.2%)
2	B	0.91	0/851	1.22	4/1158 (0.3%)
3	F	0.81	0/989	1.22	3/1341 (0.2%)
All	All	0.89	1/4081 (0.0%)	1.26	13/5553 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	234	PRO	C-O	-5.34	1.17	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	95[A]	TRP	N-CA-C	5.85	117.74	108.67
2	B	95[B]	TRP	N-CA-C	5.85	117.74	108.67
1	A	71	ARG	CA-C-N	5.58	128.02	120.38
1	A	71	ARG	C-N-CA	5.58	128.02	120.38
1	A	262	HIS	CA-C-N	5.52	127.94	120.38
1	A	262	HIS	C-N-CA	5.52	127.94	120.38
1	A	42	ASP	CA-CB-CG	5.43	118.03	112.60
3	F	105	ILE	N-CA-C	5.34	113.71	107.89
1	A	176	SER	N-CA-C	5.23	116.67	111.07
3	F	48	VAL	N-CA-C	-5.20	107.09	111.56
2	B	95[A]	TRP	CA-C-O	5.11	126.50	120.98
2	B	95[B]	TRP	CA-C-O	5.11	126.50	120.98
3	F	68	PHE	CA-CB-CG	5.00	118.80	113.80

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	2160	0	2047	61	0
2	B	823	0	752	13	0
3	F	962	0	949	22	0
4	C	28	0	25	1	0
5	D	39	0	34	0	0
6	A	28	0	26	1	0
7	A	5	0	0	0	0
7	B	20	0	0	0	0
8	A	60	0	99	11	0
9	A	4	0	0	0	0
9	B	1	0	0	0	0
10	A	111	0	0	4	0
10	B	45	0	0	0	0
10	F	38	0	0	0	0
All	All	4324	0	3932	93	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 12.

All (93) 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:45:ARG:HG2	10:A:592:HOH:O	1.60	1.01
8:A:403:AGH:H72	8:A:403:AGH:H5	1.45	0.95
1:A:218:MET:HE3	1:A:224:GLN:HG2	1.53	0.88
1:A:40:ASP:OD1	10:A:501:HOH:O	2.00	0.80
1:A:218:MET:CE	1:A:224:GLN:CG	2.63	0.77
1:A:218:MET:CE	1:A:224:GLN:HG2	2.15	0.76
1:A:85:LEU:HD22	1:A:137:TRP:HB2	1.68	0.74
1:A:273:TYR:O	1:A:274:TRP:HB3	1.87	0.73
1:A:216:LYS:HA	1:A:227:THR:HG21	1.73	0.70
1:A:119:ASP:HB3	1:A:131:THR:HG21	1.76	0.68
1:A:273:TYR:O	1:A:274:TRP:CB	2.43	0.65
1:A:218:MET:HE1	1:A:224:GLN:HG3	1.78	0.64
1:A:273:TYR:N	10:A:502:HOH:O	2.21	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:THR:OG1	8:A:403:AGH:O3	1.99	0.63
1:A:48:LYS:NZ	1:A:177:GLU:OE2	2.29	0.63
3:F:20:LEU:HG	3:F:83:MET:CE	2.28	0.63
2:B:0:MET:HE3	2:B:2:GLN:HB2	1.80	0.62
1:A:70:TYR:CG	8:A:403:AGH:HAF1	2.35	0.61
3:F:12:VAL:O	3:F:125:VAL:HA	2.01	0.61
1:A:218:MET:HE2	1:A:224:GLN:HA	1.83	0.60
3:F:6:GLU:HB2	3:F:121[A]:THR:HG23	1.83	0.60
3:F:68:PHE:CE2	3:F:83:MET:HG2	2.38	0.59
3:F:20:LEU:HD22	3:F:121[B]:THR:HG21	1.83	0.59
1:A:50:TRP:HB2	1:A:173:SER:HB3	1.85	0.59
1:A:211:LYS:HD3	10:A:591:HOH:O	2.02	0.58
3:F:51:ILE:HD13	3:F:72:ARG:HD2	1.84	0.58
1:A:218:MET:CE	1:A:224:GLN:HG3	2.34	0.58
1:A:243:ARG:HH11	2:B:99:MET:HA	1.69	0.57
1:A:243:ARG:NH1	2:B:99:MET:HA	2.20	0.56
1:A:231:ASP:HB2	1:A:233:LEU:CD2	2.35	0.56
3:F:34:MET:HB3	3:F:79:LEU:HD22	1.87	0.55
1:A:45:ARG:HD3	1:A:46:SER:H	1.72	0.55
1:A:184:PRO:HB3	1:A:208:PHE:HB3	1.89	0.54
3:F:20:LEU:HG	3:F:83:MET:HE2	1.91	0.53
1:A:163:CYS:HB2	8:A:403:AGH:HAW1	1.90	0.53
1:A:70:TYR:CD1	8:A:403:AGH:HAF1	2.43	0.53
3:F:20:LEU:HG	3:F:83:MET:HE1	1.90	0.53
1:A:21:THR:HG21	1:A:75:THR:HG21	1.90	0.52
1:A:218:MET:HE1	1:A:224:GLN:CG	2.36	0.52
1:A:218:MET:HE2	1:A:224:GLN:CA	2.40	0.52
3:F:48:VAL:HG13	3:F:64:VAL:HG21	1.92	0.52
2:B:10:TYR:HB3	2:B:99:MET:HE2	1.91	0.52
1:A:188:LEU:HD11	1:A:272:LEU:HB3	1.91	0.51
1:A:21:THR:HG21	1:A:75:THR:CG2	2.43	0.49
1:A:231:ASP:HB2	1:A:233:LEU:HD23	1.93	0.49
1:A:151:THR:HG23	8:A:403:AGH:HAB1	1.95	0.49
3:F:53:TRP:HH2	3:F:103:PRO:HA	1.78	0.48
1:A:251:GLY:HA3	1:A:253:ALA:N	2.28	0.47
3:F:97:ALA:HA	3:F:116:TYR:O	2.14	0.47
3:F:93:VAL:HG22	3:F:122:LEU:HD22	1.97	0.47
1:A:162:THR:OG1	3:F:102:PRO:HB2	2.15	0.47
1:A:265:LEU:HD13	1:A:270:ILE:HG13	1.96	0.47
1:A:205:VAL:HG21	1:A:215:VAL:HG21	1.97	0.47
1:A:191:GLY:O	1:A:200:LEU:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ARG:HD3	1:A:46:SER:N	2.30	0.46
8:A:403:AGH:CAB	8:A:403:AGH:C3	2.94	0.46
3:F:20:LEU:HD12	3:F:81:LEU:HD23	1.97	0.45
2:B:0:MET:HE1	2:B:2:GLN:CD	2.41	0.45
2:B:39:LEU:HB2	2:B:49:VAL:HG11	1.99	0.45
1:A:125:GLY:HA2	6:A:404:NAG:H5	1.99	0.44
1:A:199:LEU:HD23	1:A:250:ALA:HA	2.00	0.44
1:A:218:MET:CE	1:A:224:GLN:HA	2.46	0.44
1:A:12:ILE:HD13	2:B:54:LEU:HD23	1.99	0.44
1:A:12:ILE:HG12	2:B:62:PHE:HE1	1.83	0.44
1:A:65:HIS:HD2	3:F:100:LEU:HD11	1.83	0.44
1:A:229:PRO:HA	1:A:244:ALA:HA	1.99	0.43
8:A:403:AGH:H5	8:A:403:AGH:CAB	2.48	0.43
2:B:9:VAL:HG11	2:B:95[A]:TRP:HB2	2.01	0.43
1:A:121:LEU:C	1:A:121:LEU:HD12	2.44	0.43
1:A:200:LEU:HG	1:A:245:THR:OG1	2.18	0.43
1:A:27:ALA:HB2	8:A:403:AGH:HAO2	2.01	0.43
1:A:189:SER:HB3	1:A:202:VAL:HG23	2.01	0.43
1:A:256:LEU:O	1:A:273:TYR:O	2.37	0.42
2:B:20:SER:HA	2:B:71:THR:HG22	2.00	0.42
1:A:37:TRP:CG	1:A:44:VAL:HG22	2.54	0.42
1:A:9:CYS:HB3	8:A:403:AGH:HAM1	2.00	0.42
2:B:0:MET:HE1	2:B:2:GLN:OE1	2.18	0.42
1:A:218:MET:HE2	1:A:224:GLN:N	2.35	0.42
3:F:48:VAL:CG1	3:F:64:VAL:HG21	2.49	0.42
1:A:27:ALA:HB3	1:A:35:HIS:HB2	2.02	0.42
1:A:43:THR:OG1	1:A:64:GLN:NE2	2.53	0.42
3:F:68:PHE:CZ	3:F:83:MET:HG2	2.54	0.42
3:F:4:LEU:HA	3:F:23:ALA:O	2.20	0.41
1:A:219:ARG:C	1:A:221:GLU:N	2.78	0.41
3:F:53:TRP:CH2	3:F:103:PRO:HA	2.55	0.41
4:C:2:NAG:O7	4:C:2:NAG:H3	2.21	0.41
1:A:146:ASN:HA	1:A:152:ARG:HD2	2.03	0.41
1:A:26:LEU:HD21	2:B:55:SER:HB2	2.02	0.41
1:A:67:PHE:CE2	8:A:403:AGH:HAS2	2.56	0.41
2:B:40:LEU:HD23	2:B:45:ARG:HA	2.01	0.41
3:F:36:TRP:CD1	3:F:81:LEU:HB2	2.56	0.41
1:A:231:ASP:HB2	1:A:233:LEU:HD21	2.01	0.40
3:F:4:LEU:HD23	3:F:24:ALA:HA	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	268/347 (77%)	255 (95%)	12 (4%)	1 (0%)	30	43
2	B	99/100 (99%)	94 (95%)	5 (5%)	0	100	100
3	F	126/127 (99%)	124 (98%)	2 (2%)	0	100	100
All	All	493/574 (86%)	473 (96%)	19 (4%)	1 (0%)	43	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	ALA

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

5 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	$\# Z > 2$
4	NAG	C	1	4,1	14,14,15	0.29	0	17,19,21	0.65	0
4	NAG	C	2	4	14,14,15	0.43	0	17,19,21	1.23	3 (17%)
5	NAG	D	1	1,5	14,14,15	0.28	0	17,19,21	0.59	0
5	NAG	D	2	5	14,14,15	0.31	0	17,19,21	0.76	0
5	BMA	D	3	5	11,11,12	0.33	0	15,15,17	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	NAG	C	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	C	2	4	-	1/6/23/26	0/1/1/1
5	NAG	D	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	D	2	5	-	0/6/23/26	0/1/1/1
5	BMA	D	3	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	2	NAG	O5-C1-C2	-2.84	106.89	111.29
4	C	2	NAG	C1-C2-N2	2.66	114.62	110.43
4	C	2	NAG	C2-N2-C7	2.60	126.38	122.90

There are no chirality outliers.

All (3) torsion outliers are listed below:

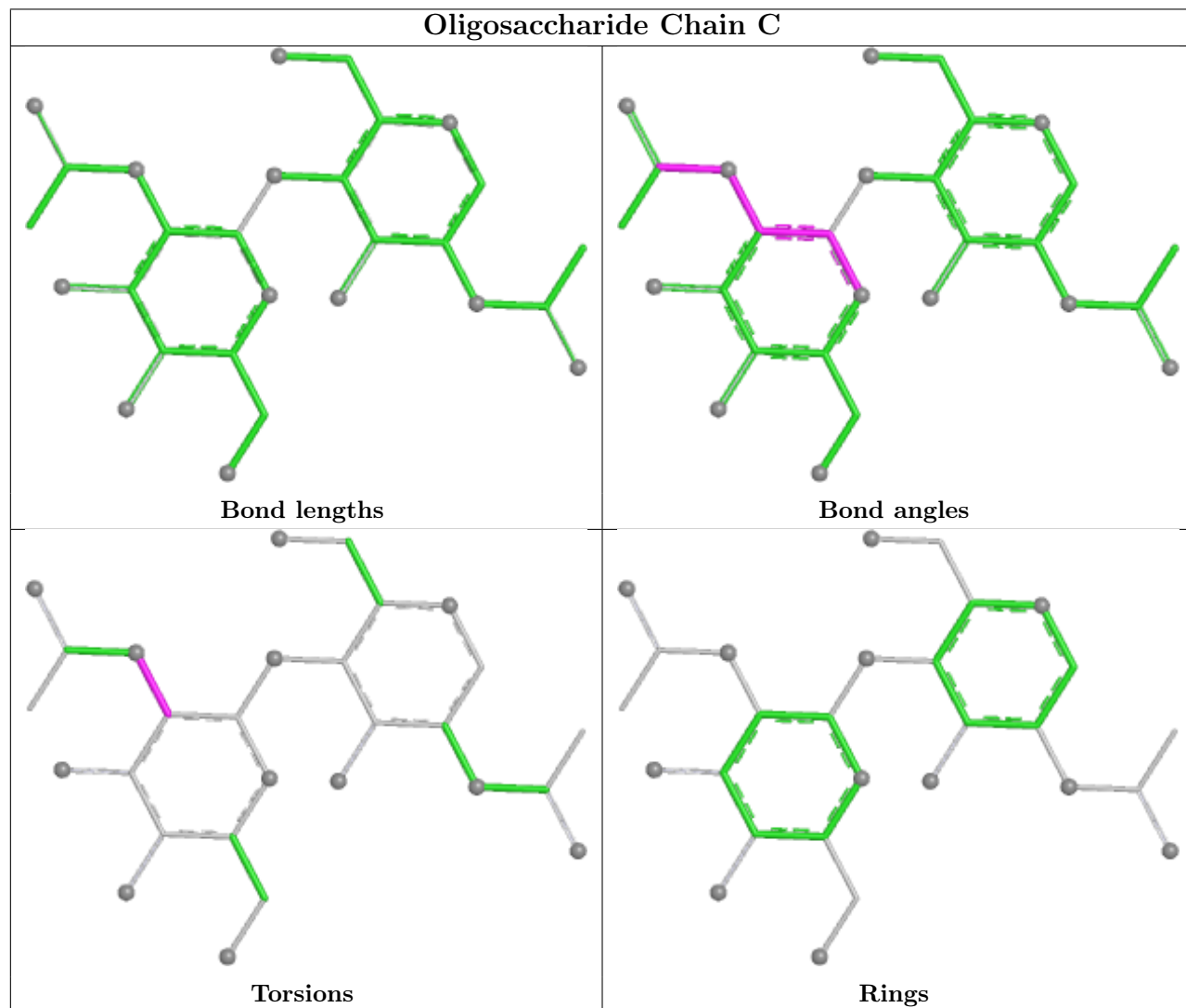
Mol	Chain	Res	Type	Atoms
4	C	2	NAG	C3-C2-N2-C7
5	D	1	NAG	C8-C7-N2-C2
5	D	1	NAG	O7-C7-N2-C2

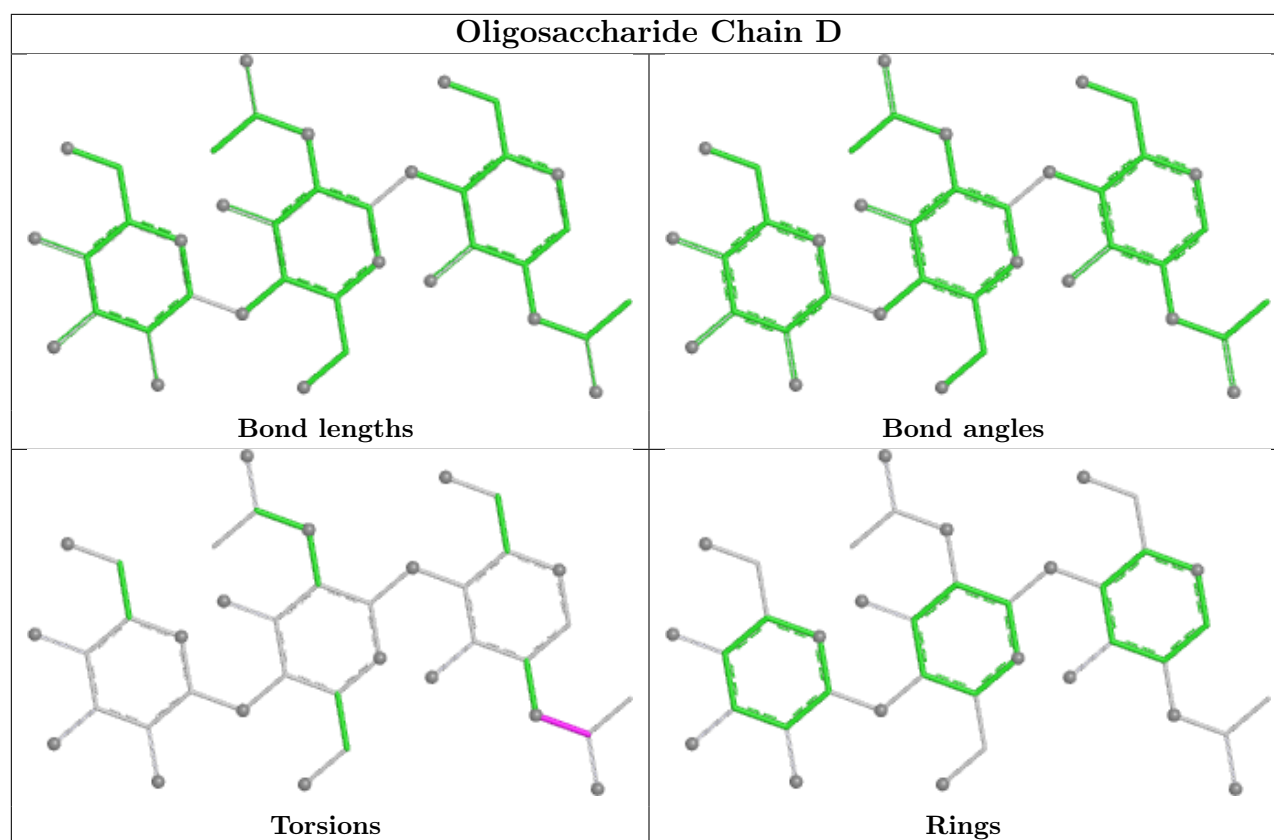
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	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](#)

Of 13 ligands modelled in this entry, 5 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NAG	A	401	1	14,14,15	0.38	0	17,19,21	0.84	1 (5%)
6	NAG	A	404	1	14,14,15	0.36	0	17,19,21	0.46	0
7	SO4	B	103	-	4,4,4	0.34	0	6,6,6	0.17	0
7	SO4	B	101	-	4,4,4	0.35	0	6,6,6	0.15	0
7	SO4	B	102	-	4,4,4	0.58	0	6,6,6	0.24	0
8	AGH	A	403	-	60,60,60	0.77	2 (3%)	66,69,69	1.48	10 (15%)
7	SO4	A	402	-	4,4,4	0.28	0	6,6,6	0.13	0
7	SO4	B	104	-	4,4,4	0.22	0	6,6,6	0.13	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
6	NAG	A	401	1	-	2/6/23/26	0/1/1/1
6	NAG	A	404	1	-	0/6/23/26	0/1/1/1
8	AGH	A	403	-	-	26/58/78/78	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	403	AGH	OAA-CAA	-2.73	1.17	1.23
8	A	403	AGH	C3-C2	-2.35	1.49	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	403	AGH	C2-N2-CAA	5.67	132.86	123.40
8	A	403	AGH	CAB-CAA-N2	5.22	125.06	115.86
8	A	403	AGH	OAA-CAA-CAB	-3.66	115.38	122.02
8	A	403	AGH	C1-C2-N2	3.41	114.51	109.66
8	A	403	AGH	C6A-C5M-C4A	-2.96	105.74	113.02
6	A	401	NAG	C1-O5-C5	2.88	116.04	112.19
8	A	403	AGH	C6-C5-C4	-2.87	109.41	114.11
8	A	403	AGH	O2A-C2A-C3A	-2.29	104.97	110.38
8	A	403	AGH	C5-C4-C3	-2.07	110.69	113.97
8	A	403	AGH	OAA-CAA-N2	-2.03	119.52	122.95
8	A	403	AGH	O4A-C4A-C5M	-2.00	104.39	109.32

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	403	AGH	O1A-C1-C2-C3
8	A	403	AGH	C3-C2-N2-CAA
8	A	403	AGH	C2-C3-C4-C5
8	A	403	AGH	O3-C3-C4-C5
8	A	403	AGH	OAA-CAA-N2-C2
8	A	403	AGH	CAB-CAA-N2-C2
8	A	403	AGH	O3-C3-C4-O4
8	A	403	AGH	C2-C3-C4-O4

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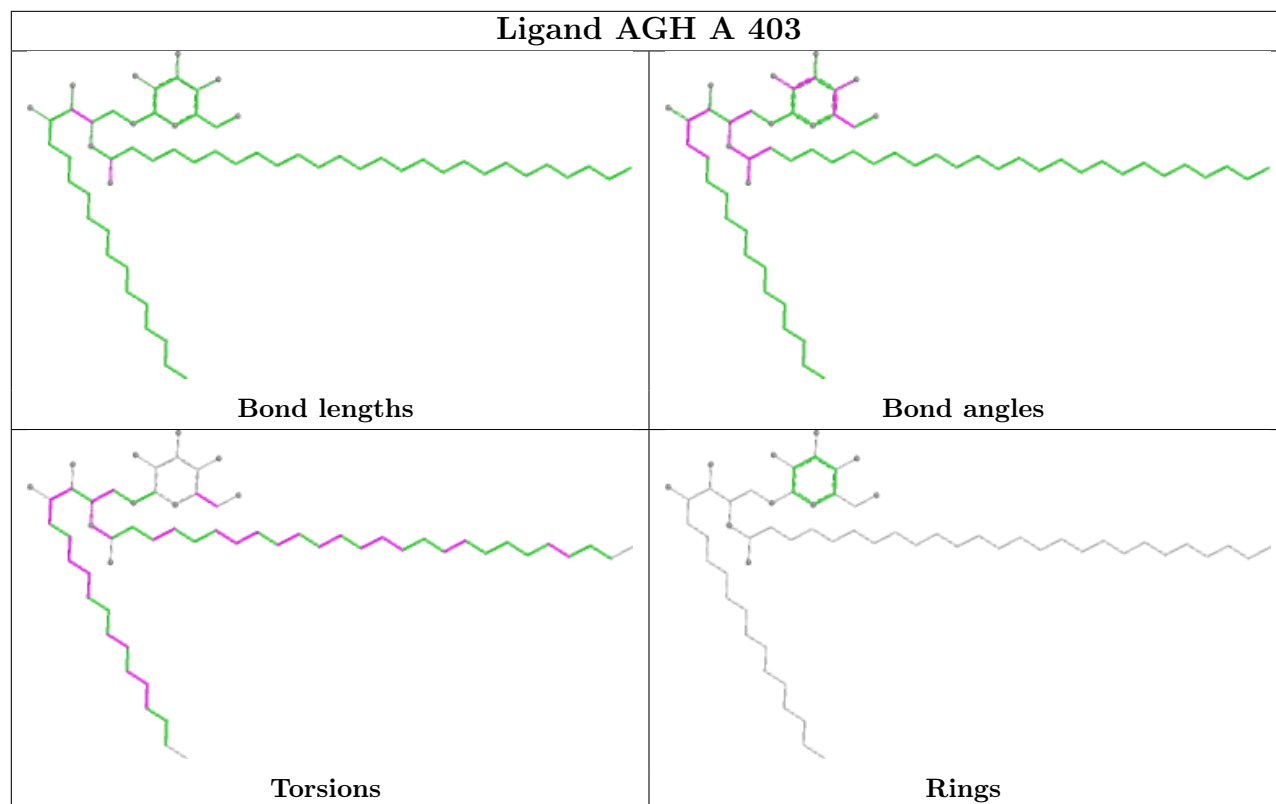
Mol	Chain	Res	Type	Atoms
8	A	403	AGH	CAU-CAV-CAW-CAX
6	A	401	NAG	C4-C5-C6-O6
8	A	403	AGH	CAB-CAC-CAD-CAE
8	A	403	AGH	CAJ-CAK-CAL-CAM
6	A	401	NAG	O5-C5-C6-O6
8	A	403	AGH	CAP-CAQ-CAR-CAS
8	A	403	AGH	C12-C13-C14-C15
8	A	403	AGH	CAF-CAG-CAH-CAI
8	A	403	AGH	CAL-CAM-CAN-CAO
8	A	403	AGH	CAE-CAF-CAG-CAH
8	A	403	AGH	C10-C11-C12-C13
8	A	403	AGH	CAH-CAI-CAJ-CAK
8	A	403	AGH	O1A-C1-C2-N2
8	A	403	AGH	CAM-CAN-CAO-CAP
8	A	403	AGH	C6-C7-C8-C9
8	A	403	AGH	C7-C8-C9-C10
8	A	403	AGH	C5-C6-C7-C8
8	A	403	AGH	O6A-C5M-C6A-O5A
8	A	403	AGH	O4-C4-C5-C6
8	A	403	AGH	C13-C14-C15-C16

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	404	NAG	1	0
8	A	403	AGH	11	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	270/347 (77%)	0.26	19 (7%)	22	19	30, 50, 88, 101	7 (2%)
2	B	100/100 (100%)	0.09	2 (2%)	65	60	33, 50, 84, 106	1 (1%)
3	F	126/127 (99%)	0.42	5 (3%)	42	38	41, 68, 94, 107	2 (1%)
All	All	496/574 (86%)	0.26	26 (5%)	33	29	30, 56, 88, 107	10 (2%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	222	GLN	4.6
1	A	86	ARG	4.5
3	F	2	VAL	4.2
1	A	251	GLY	3.9
1	A	247	ASP	3.6
2	B	99	MET	3.6
1	A	221	GLU	3.6
1	A	274	TRP	3.4
1	A	198	ARG	3.1
1	A	219	ARG	3.0
1	A	193	SER	3.0
1	A	190	ARG	2.9
1	A	231	ASP	2.9
1	A	227	THR	2.7
1	A	255	GLY	2.7
1	A	256	LEU	2.6
3	F	28	SER	2.6
1	A	196	PRO	2.4
2	B	89	GLN	2.3
1	A	85	LEU	2.3
1	A	249	VAL	2.3
1	A	253	ALA	2.2
3	F	7	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	214[A]	TRP	2.1
3	F	5	VAL	2.0
3	F	104	GLY	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](#)

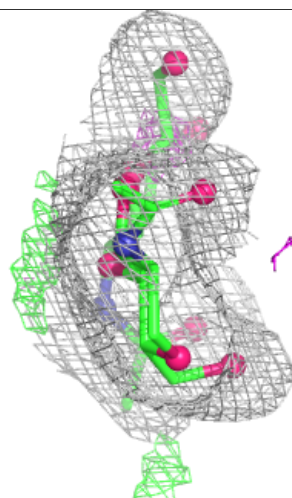
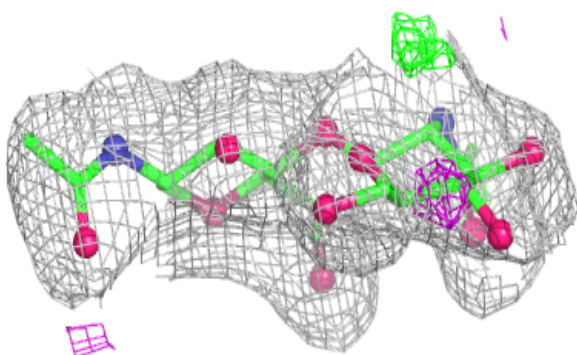
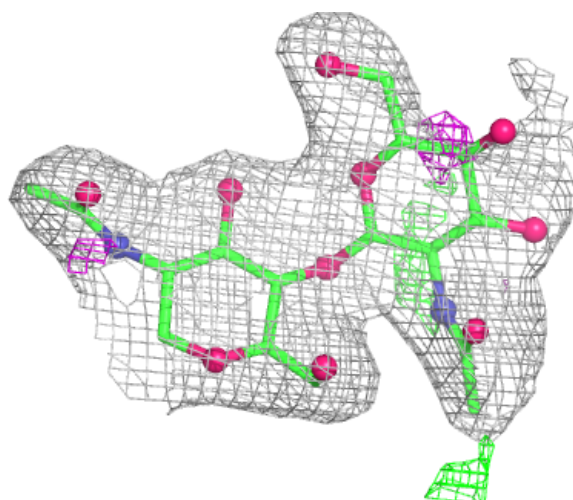
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

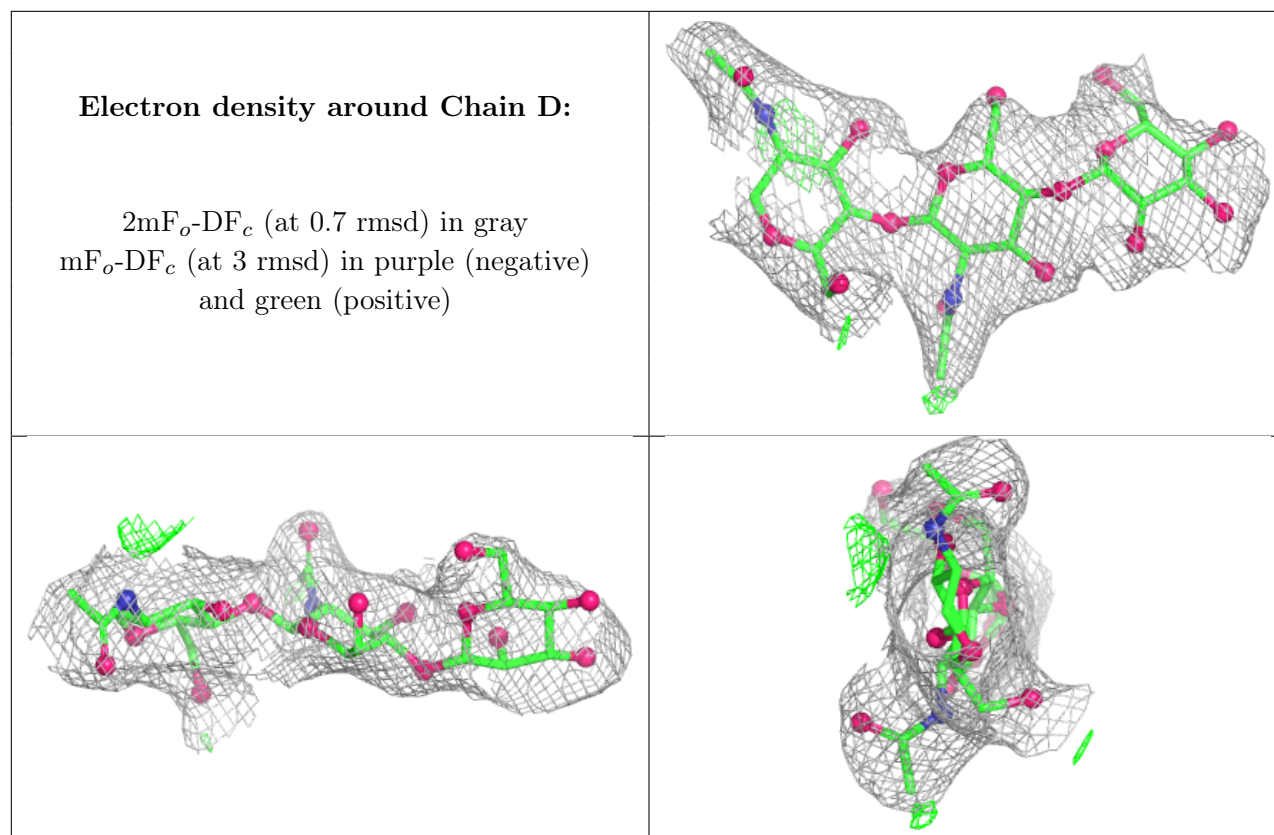
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	C	1	14/15	-	-	49,58,68,76	0
4	NAG	C	2	14/15	-	-	84,87,93,94	0
5	NAG	D	2	14/15	0.65	0.14	107,113,119,123	0
5	NAG	D	1	14/15	0.94	0.06	76,79,87,98	0
5	BMA	D	3	11/12	-	-	127,129,130,131	0

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 C:

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





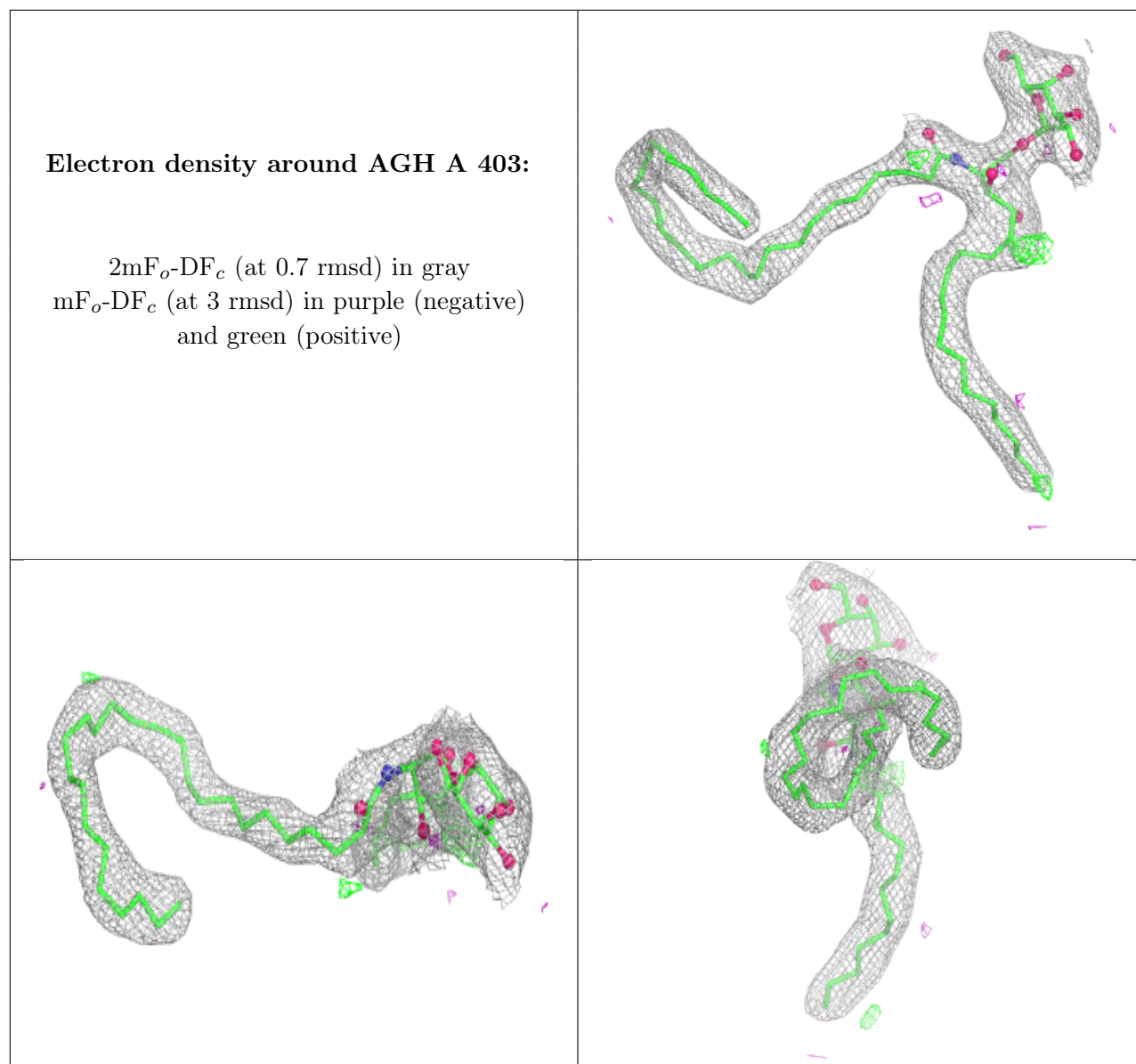
6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	SO4	B	103	5/5	0.67	0.14	125,126,128,129	0
7	SO4	A	402	5/5	0.71	0.10	105,106,106,106	0
7	SO4	B	101	5/5	0.79	0.12	124,125,125,125	0
6	NAG	A	401	14/15	0.79	0.13	91,95,99,99	0
6	NAG	A	404	14/15	0.83	0.11	69,73,75,77	0
7	SO4	B	104	5/5	0.84	0.09	103,104,104,105	0
7	SO4	B	102	5/5	0.91	0.11	59,60,60,63	0
8	AGH	A	403	60/60	0.92	0.11	29,43,58,67	0
9	CL	A	405	1/1	0.93	0.16	72,72,72,72	0
9	CL	B	105	1/1	0.93	0.11	76,76,76,76	0
9	CL	A	407	1/1	0.94	0.15	86,86,86,86	0
9	CL	A	406	1/1	0.94	0.09	69,69,69,69	0
9	CL	A	408	1/1	0.95	0.23	30,30,30,30	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.