



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:30 PM UTC

PDB ID : 3HE7 / pdb_00003he7
Title : Crystal structure of mouse CD1d-alpha-galactosylceramide with mouse Valpha14-Vbeta7 NKT TCR
Authors : Patel, O.; Rossjohn, J.
Deposited on : 2009-05-08
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

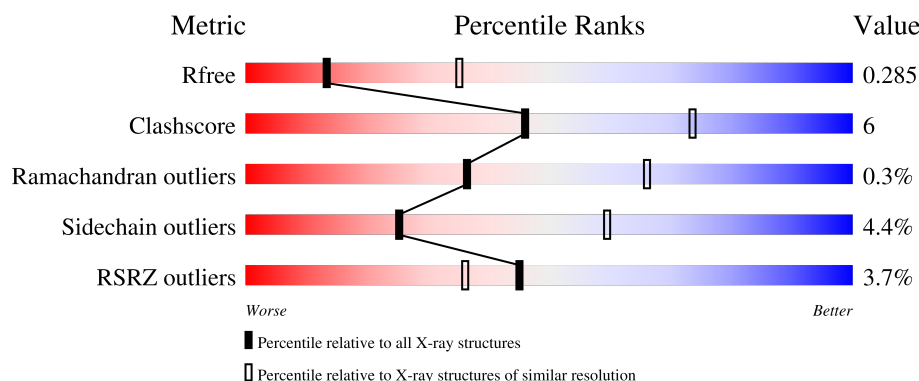
1 Overall quality at a glance

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	302	4% 75% 17% • 7%
2	B	99	79% 16% • •
3	C	207	3% 86% 8% • 5%
4	D	242	5% 81% 17% • •
5	E	2	100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6689 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 CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2273	1449	402	409	13			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	HIS	ASP	conflict	UNP P11609
A	280	GLY	-	expression tag	UNP P11609
A	281	SER	-	expression tag	UNP P11609
A	282	LEU	-	expression tag	UNP P11609
A	283	HIS	-	expression tag	UNP P11609
A	284	HIS	-	expression tag	UNP P11609
A	285	ILE	-	expression tag	UNP P11609
A	286	LEU	-	expression tag	UNP P11609
A	287	ASP	-	expression tag	UNP P11609
A	288	ALA	-	expression tag	UNP P11609
A	289	GLN	-	expression tag	UNP P11609
A	290	LYS	-	expression tag	UNP P11609
A	291	MET	-	expression tag	UNP P11609
A	292	VAL	-	expression tag	UNP P11609
A	293	TRP	-	expression tag	UNP P11609
A	294	ASN	-	expression tag	UNP P11609
A	295	HIS	-	expression tag	UNP P11609
A	296	ARG	-	expression tag	UNP P11609
A	297	HIS	-	expression tag	UNP P11609
A	298	HIS	-	expression tag	UNP P11609
A	299	HIS	-	expression tag	UNP P11609
A	300	HIS	-	expression tag	UNP P11609
A	301	HIS	-	expression tag	UNP P11609
A	302	HIS	-	expression tag	UNP P11609

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	97	Total	C	N	O	S	0	0	0
			802	512	136	147	7			

- Molecule 3 is a protein called Valpha14(mouse variable domain, human constant domain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	197	Total	C	N	O	S	0	0	0
			1522	945	262	308	7			

- Molecule 4 is a protein called Vbeta7(mouse variable domain, human constant domain).

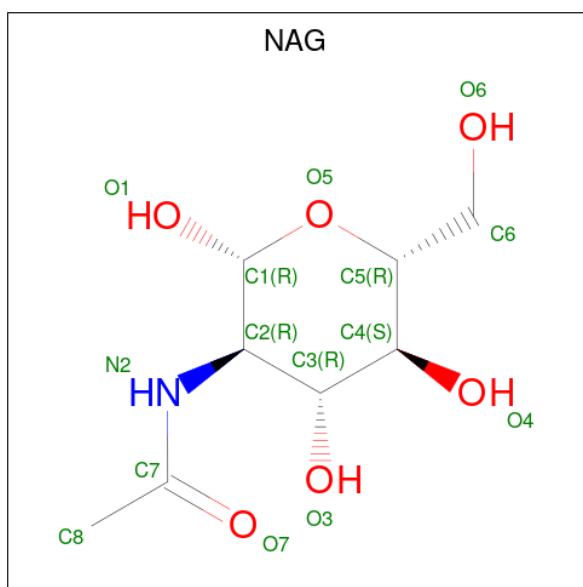
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	240	Total	C	N	O	S	0	0	0
			1931	1219	333	369	10			

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



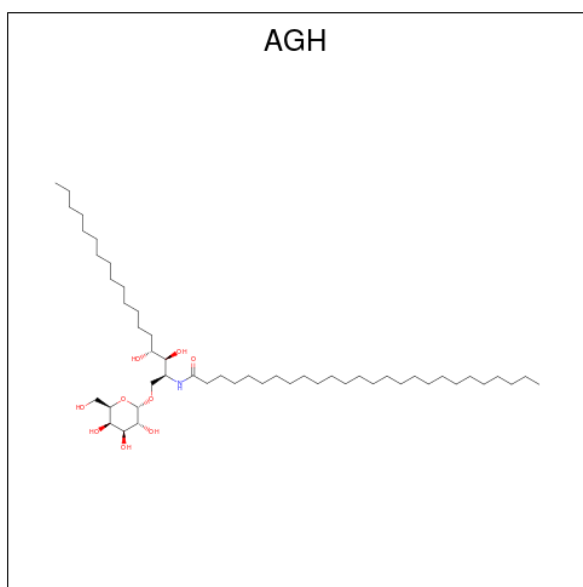
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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 N-{(1S,2R,3S)-1-[(ALPHA-D-GALACTOPYRANOSYLOXY)METHYL]-2,3-DIHYDROXYHEPTADECYL}HEXACOSANAMIDE (CCD ID: AGH) (formula: C₅₀H₉₉NO₉).



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

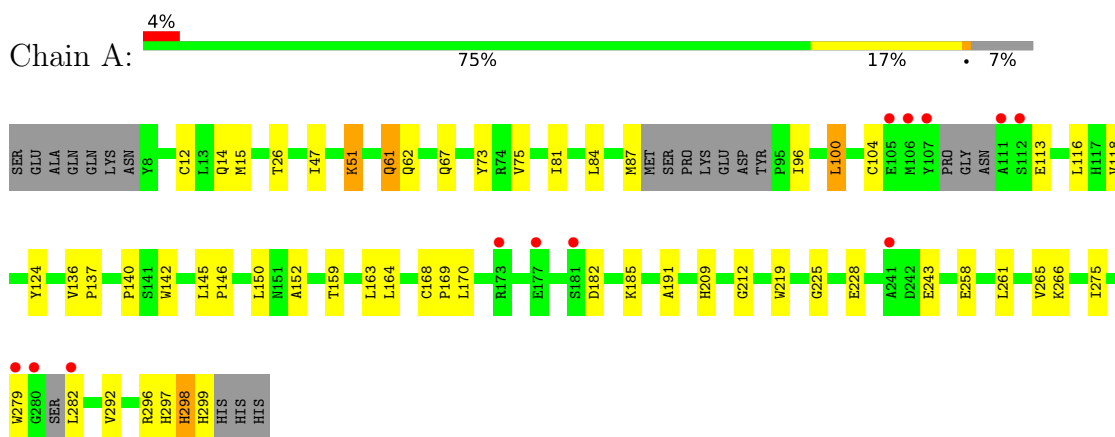
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	9	Total 9	O 9	0	0
8	B	6	Total 6	O 6	0	0
8	C	14	Total 14	O 14	0	0
8	D	16	Total 16	O 16	0	0

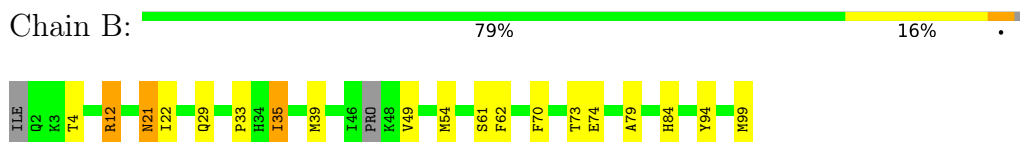
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

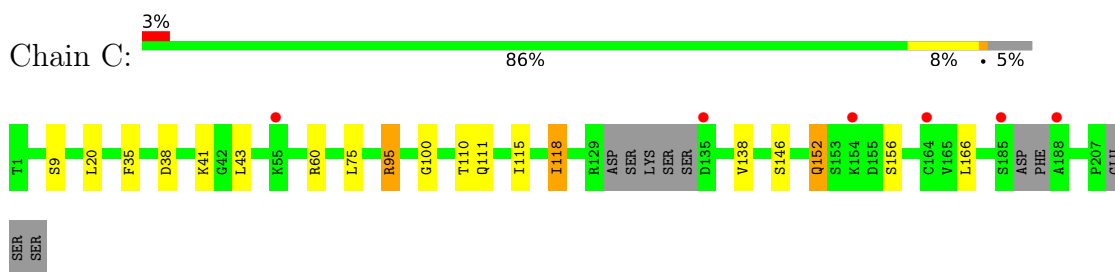
- Molecule 1: Antigen-presenting glycoprotein CD1d1



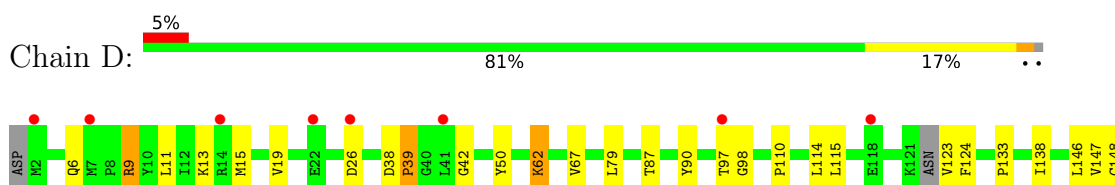
- Molecule 2: Beta-2-microglobulin



- Molecule 3: Valpha14(mouse variable domain, human constant domain)



- Molecule 4: Vbeta7(mouse variable domain, human constant domain)





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

Chain E:

100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.23Å 81.91Å 243.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.80) 99.6 (50.00-2.80)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.224 , 0.271 0.245 , 0.285	Depositor DCC
R_{free} test set	1477 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 28.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6689	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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: NAG, AGH

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	0.44	0/2340	0.74	1/3175 (0.0%)
2	B	0.42	0/826	0.72	0/1118
3	C	0.44	0/1548	0.72	0/2102
4	D	0.42	0/1980	0.71	0/2686
All	All	0.43	0/6694	0.72	1/9081 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	298	HIS	N-CA-C	5.13	117.26	111.11

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	2273	0	2174	32	0
2	B	802	0	775	18	0
3	C	1522	0	1474	10	0
4	D	1931	0	1853	23	0
5	E	28	0	25	0	0
6	A	28	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	60	0	99	3	0
8	A	9	0	0	0	0
8	B	6	0	0	0	0
8	C	14	0	0	0	0
8	D	16	0	0	1	0
All	All	6689	0	6426	75	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (75) 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)
4:D:9:ARG:HH22	4:D:110:PRO:HB2	1.60	0.66
1:A:168:CYS:HB3	1:A:169:PRO:HD3	1.77	0.65
1:A:145:LEU:HB3	1:A:146:PRO:HD3	1.80	0.64
1:A:118:VAL:HG11	7:A:307:AGH:H122	1.79	0.63
2:B:21:ASN:HD22	2:B:22:ILE:N	1.97	0.63
4:D:87:THR:HG23	4:D:115:LEU:HA	1.81	0.63
2:B:21:ASN:ND2	2:B:22:ILE:H	2.00	0.60
4:D:147:VAL:HG22	4:D:196:ARG:HG2	1.83	0.60
1:A:15:MET:HG2	2:B:62:PHE:HE2	1.66	0.60
1:A:219:TRP:HB3	1:A:266:LYS:HB2	1.83	0.59
4:D:124:PHE:CD2	4:D:190:ARG:HD3	2.38	0.57
1:A:191:ALA:HA	1:A:209:HIS:O	2.05	0.57
4:D:62:LYS:HE3	4:D:62:LYS:H	1.69	0.56
3:C:166:LEU:HB3	4:D:174:CYS:HB3	1.89	0.55
3:C:152:GLN:HE21	3:C:152:GLN:HA	1.72	0.54
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.42	0.53
1:A:12:CYS:HB3	7:A:307:AGH:HAM2	1.92	0.52
2:B:33:PRO:HG3	2:B:62:PHE:CE1	2.45	0.52
1:A:136:VAL:CG1	1:A:137:PRO:HD2	2.39	0.52
2:B:21:ASN:ND2	2:B:22:ILE:N	2.57	0.51
3:C:118:ILE:O	3:C:118:ILE:HG13	2.09	0.51
4:D:6:GLN:NE2	4:D:90:TYR:O	2.42	0.51
3:C:20:LEU:HD22	3:C:110:THR:HG21	1.92	0.50
1:A:140:PRO:HB2	1:A:142:TRP:CE2	2.46	0.49
2:B:33:PRO:HG3	2:B:62:PHE:CZ	2.47	0.49
2:B:35:ILE:HD12	2:B:84:HIS:CD2	2.47	0.49
1:A:104:CYS:HG	1:A:168:CYS:HG	1.61	0.49
2:B:29:GLN:HA	2:B:61:SER:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:38:ASP:HB2	3:C:41:LYS:HG3	1.95	0.49
1:A:182:ASP:O	1:A:185:LYS:HE2	2.13	0.48
1:A:152:ALA:HB1	4:D:98:GLY:HA2	1.94	0.48
4:D:19:VAL:HB	4:D:79:LEU:HB2	1.96	0.48
4:D:123:VAL:HG11	4:D:220:LEU:HD13	1.95	0.47
1:A:47:ILE:HD12	1:A:67:GLN:HG3	1.97	0.47
1:A:299:HIS:HD2	2:B:99:MET:HG3	1.78	0.47
2:B:39:MET:HG3	2:B:49:VAL:HG11	1.96	0.47
2:B:21:ASN:HD22	2:B:22:ILE:H	1.60	0.46
1:A:81:ILE:HD13	1:A:84:LEU:HD12	1.98	0.46
1:A:116:LEU:HB2	1:A:164:LEU:HD21	1.96	0.46
1:A:292:VAL:O	2:B:74:GLU:HB3	2.16	0.46
3:C:20:LEU:HD12	3:C:75:LEU:HD23	1.97	0.45
1:A:61:GLN:HG3	1:A:62:GLN:N	2.32	0.45
1:A:124:TYR:CZ	1:A:136:VAL:HG21	2.51	0.45
1:A:212:GLY:HA3	2:B:12:ARG:HH22	1.82	0.45
1:A:15:MET:HE1	2:B:54:MET:HB3	1.99	0.45
3:C:9:SER:HA	3:C:111:GLN:O	2.17	0.45
4:D:9:ARG:HH11	4:D:9:ARG:HA	1.82	0.45
1:A:159:THR:O	1:A:163:LEU:HG	2.17	0.44
4:D:42:GLY:HA2	8:D:250:HOH:O	2.17	0.44
4:D:148:CYS:HB2	4:D:162:TRP:CZ2	2.53	0.44
1:A:136:VAL:HG12	1:A:137:PRO:HD2	1.99	0.44
2:B:79:ALA:HB2	2:B:94:TYR:CD2	2.52	0.44
1:A:87:MET:HE2	4:D:50:TYR:CD2	2.53	0.43
4:D:11:LEU:HD23	4:D:114:LEU:HD13	2.00	0.43
4:D:206:ASN:HA	4:D:207:PRO:HD3	1.84	0.43
4:D:214:GLN:HG3	4:D:237:ILE:HG23	2.01	0.43
4:D:216:GLN:HE22	4:D:237:ILE:HD11	1.84	0.43
1:A:296:ARG:HA	1:A:297:HIS:HA	1.80	0.42
4:D:13:LYS:HG3	4:D:19:VAL:HG22	2.01	0.42
4:D:205:GLN:HA	4:D:245:ARG:O	2.19	0.42
1:A:73:TYR:CD1	7:A:307:AGH:HAE2	2.55	0.42
1:A:298:HIS:O	1:A:299:HIS:CB	2.68	0.41
4:D:38:ASP:O	4:D:39:PRO:C	2.63	0.41
2:B:73:THR:HG22	2:B:74:GLU:N	2.36	0.41
1:A:14:GLN:HB3	1:A:100:LEU:HB2	2.03	0.41
1:A:51:LYS:NZ	1:A:243:GLU:OE2	2.53	0.41
4:D:133:PRO:HD3	4:D:146:LEU:HG	2.02	0.41
1:A:265:VAL:HB	1:A:275:ILE:HB	2.03	0.41
1:A:219:TRP:HZ2	1:A:228:GLU:OE2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:GLU:HA	1:A:261:LEU:HD12	2.02	0.40
2:B:12:ARG:HB2	2:B:22:ILE:HB	2.03	0.40
3:C:115:ILE:HB	3:C:146:SER:HB3	2.03	0.40
3:C:95:ARG:HB2	3:C:100:GLY:HA2	2.03	0.40
4:D:133:PRO:HB2	4:D:138:ILE:HD11	2.03	0.40
3:C:35:PHE:CD1	3:C:43:LEU:HB3	2.57	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	273/302 (90%)	264 (97%)	8 (3%)	1 (0%)	30	60
2	B	93/99 (94%)	90 (97%)	3 (3%)	0	100	100
3	C	191/207 (92%)	185 (97%)	6 (3%)	0	100	100
4	D	236/242 (98%)	227 (96%)	8 (3%)	1 (0%)	30	60
All	All	793/850 (93%)	766 (97%)	25 (3%)	2 (0%)	36	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	GLY
4	D	39	PRO

5.3.2 Protein sidechains [i](#)

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	245/264 (93%)	234 (96%)	11 (4%)	24	58
2	B	91/93 (98%)	87 (96%)	4 (4%)	25	59
3	C	176/186 (95%)	170 (97%)	6 (3%)	32	68
4	D	213/215 (99%)	202 (95%)	11 (5%)	21	53
All	All	725/758 (96%)	693 (96%)	32 (4%)	25	59

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	THR
1	A	51	LYS
1	A	61	GLN
1	A	75	VAL
1	A	96	ILE
1	A	100	LEU
1	A	113	GLU
1	A	150	LEU
1	A	170	LEU
1	A	279	TRP
1	A	282	LEU
2	B	4	THR
2	B	12	ARG
2	B	21	ASN
2	B	35	ILE
3	C	60	ARG
3	C	95	ARG
3	C	118	ILE
3	C	138	VAL
3	C	152	GLN
3	C	156	SER
4	D	9	ARG
4	D	15	MET
4	D	26	ASP
4	D	62	LYS
4	D	67	VAL
4	D	97	THR
4	D	174	CYS
4	D	180	LEU
4	D	208	ARG

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Mol	Chain	Res	Type
4	D	223	ASN
4	D	227	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	230	GLN
1	A	299	HIS
2	B	8	GLN
2	B	21	ASN
2	B	29	GLN
3	C	30	ASN
3	C	52	GLN
3	C	76	HIS
3	C	105	HIS
3	C	152	GLN
4	D	183	GLN
4	D	216	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

2 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
5	NAG	E	1	1,5	14,14,15	0.67	0	17,19,21	1.59	5 (29%)
5	NAG	E	2	5	14,14,15	0.67	0	17,19,21	1.35	2 (11%)

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
5	NAG	E	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	2	NAG	C1-O5-C5	-3.93	106.92	112.19
5	E	1	NAG	O4-C4-C3	-3.48	102.16	110.38
5	E	1	NAG	C4-C3-C2	3.05	115.48	111.02
5	E	2	NAG	C4-C3-C2	2.63	114.87	111.02
5	E	1	NAG	O5-C1-C2	-2.50	107.42	111.29
5	E	1	NAG	C8-C7-N2	2.12	119.64	116.12
5	E	1	NAG	C1-O5-C5	2.00	114.87	112.19

There are no chirality outliers.

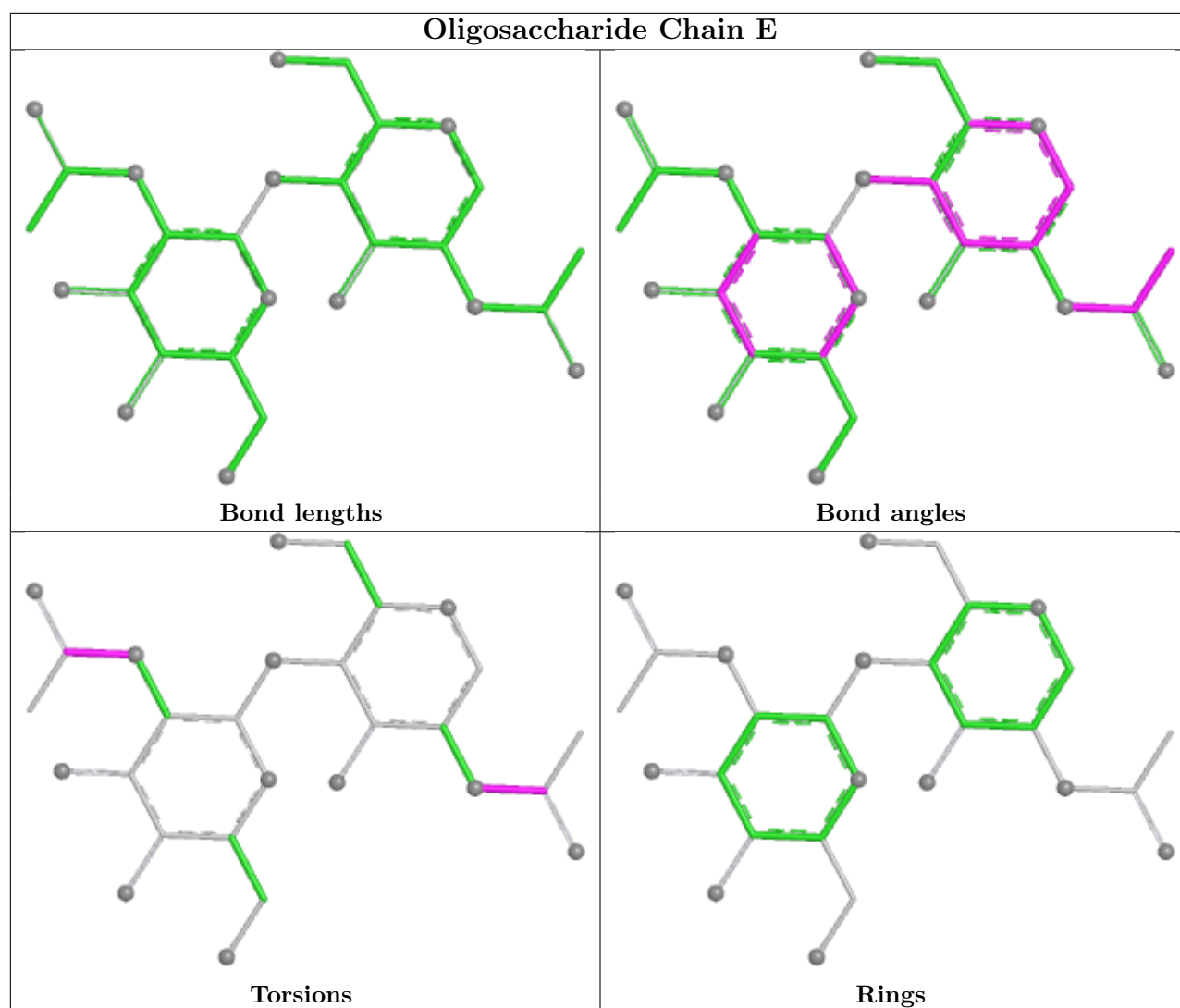
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	2	NAG	C8-C7-N2-C2
5	E	2	NAG	O7-C7-N2-C2
5	E	1	NAG	C8-C7-N2-C2
5	E	1	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

3 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	$\# Z > 2$
7	AGH	A	307	-	60,60,60	0.42	1 (1%)	66,69,69	0.63	0
6	NAG	A	304	1	14,14,15	0.46	0	17,19,21	1.03	1 (5%)
6	NAG	A	303	1	14,14,15	0.42	0	17,19,21	1.81	1 (5%)

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	AGH	A	307	-	-	27/58/78/78	0/1/1/1
6	NAG	A	304	1	-	4/6/23/26	0/1/1/1
6	NAG	A	303	1	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	307	AGH	O1A-C1A	2.03	1.43	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	303	NAG	C1-O5-C5	6.57	120.99	112.19
6	A	304	NAG	C1-O5-C5	2.94	116.12	112.19

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	303	NAG	C8-C7-N2-C2
6	A	303	NAG	O7-C7-N2-C2
7	A	307	AGH	CAA-CAB-CAC-CAD
6	A	303	NAG	O5-C5-C6-O6
6	A	304	NAG	O5-C5-C6-O6
6	A	303	NAG	C4-C5-C6-O6
6	A	304	NAG	C4-C5-C6-O6
6	A	304	NAG	C8-C7-N2-C2
6	A	304	NAG	O7-C7-N2-C2
7	A	307	AGH	CAI-CAJ-CAK-CAL
7	A	307	AGH	CAC-CAD-CAE-CAF
7	A	307	AGH	CAR-CAS-CAT-CAU
7	A	307	AGH	CAQ-CAR-CAS-CAT
7	A	307	AGH	CAL-CAM-CAN-CAO
7	A	307	AGH	CAN-CAO-CAP-CAQ
7	A	307	AGH	C12-C13-C14-C15
7	A	307	AGH	C3-C2-N2-CAA
7	A	307	AGH	CAB-CAC-CAD-CAE

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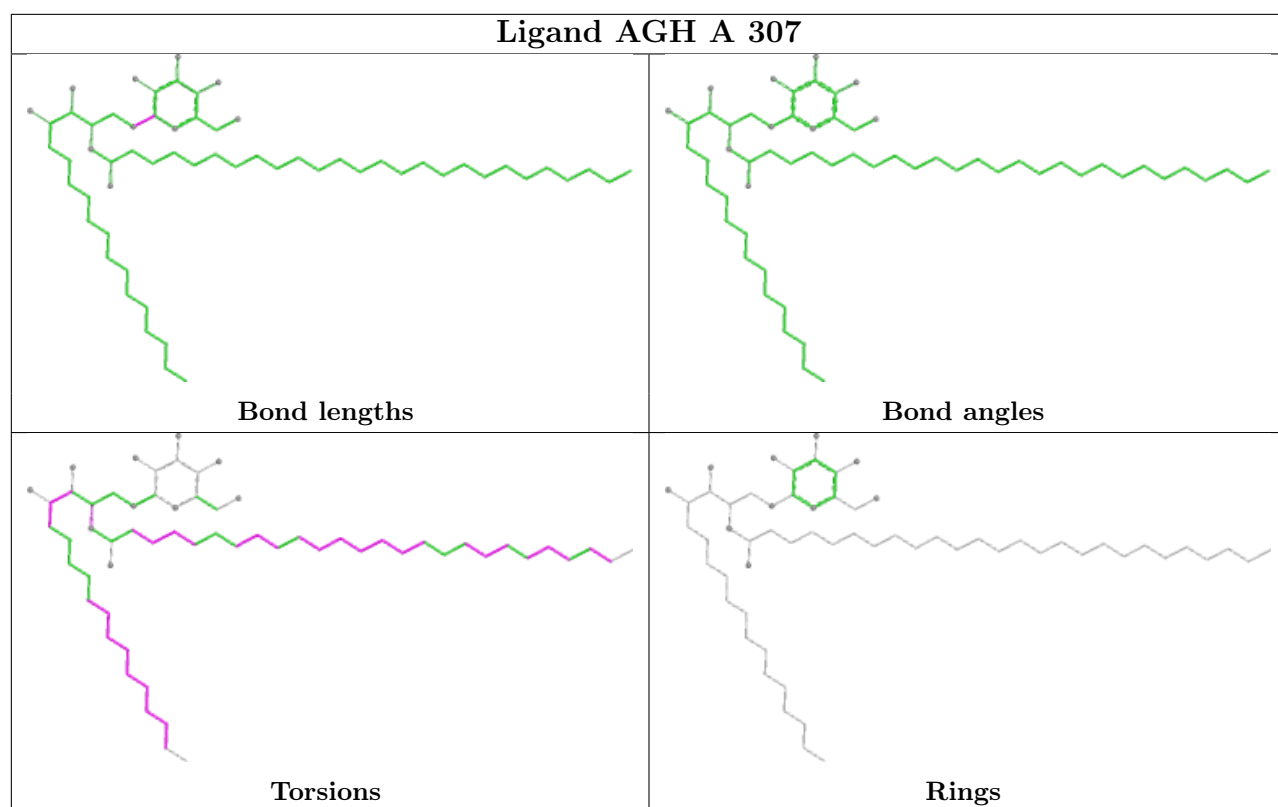
Mol	Chain	Res	Type	Atoms
7	A	307	AGH	C11-C12-C13-C14
7	A	307	AGH	CAM-CAN-CAO-CAP
7	A	307	AGH	C14-C15-C16-C17
7	A	307	AGH	C13-C14-C15-C16
7	A	307	AGH	CAG-CAH-CAI-CAJ
7	A	307	AGH	C15-C16-C17-C18
7	A	307	AGH	C9-C10-C11-C12
7	A	307	AGH	CAT-CAU-CAV-CAW
7	A	307	AGH	C11-C10-C9-C8
7	A	307	AGH	CAU-CAV-CAW-CAX
7	A	307	AGH	C2-C3-C4-C5
7	A	307	AGH	O4-C4-C5-C6
7	A	307	AGH	C10-C11-C12-C13
7	A	307	AGH	CAF-CAG-CAH-CAI
7	A	307	AGH	CAW-CAX-CAY-CAZ
7	A	307	AGH	CAK-CAL-CAM-CAN
7	A	307	AGH	CAJ-CAK-CAL-CAM

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	307	AGH	3	0

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



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	281/302 (93%)	0.47	12 (4%) 40 31	23, 43, 48, 57	1 (0%)
2	B	97/99 (97%)	0.45	0 100 100	39, 44, 49, 52	0
3	C	197/207 (95%)	0.46	6 (3%) 52 42	31, 44, 48, 50	2 (1%)
4	D	240/242 (99%)	0.50	12 (5%) 34 26	27, 44, 49, 56	1 (0%)
All	All	815/850 (95%)	0.47	30 (3%) 45 36	23, 44, 49, 57	4 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	173	ARG	7.0
3	C	154	LYS	5.2
4	D	26	ASP	4.1
1	A	280	GLY	4.0
4	D	14	ARG	3.9
4	D	247	ASP	3.9
1	A	112	SER	3.6
3	C	55	LYS	3.5
1	A	111	ALA	3.4
1	A	107	TYR	3.3
1	A	106	MET	3.3
4	D	2	MET	2.7
3	C	135	ASP	2.7
3	C	188	ALA	2.6
4	D	97	THR	2.6
1	A	241	ALA	2.5
3	C	164	CYS	2.5
4	D	188	ASP	2.4
4	D	7	MET	2.4
4	D	41	LEU	2.4
1	A	105	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
4	D	227	THR	2.3
1	A	282	LEU	2.2
4	D	225	GLU	2.2
4	D	22	GLU	2.2
4	D	118	GLU	2.2
1	A	177	GLU	2.1
1	A	279	TRP	2.1
3	C	185	SER	2.1
1	A	181	SER	2.0

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

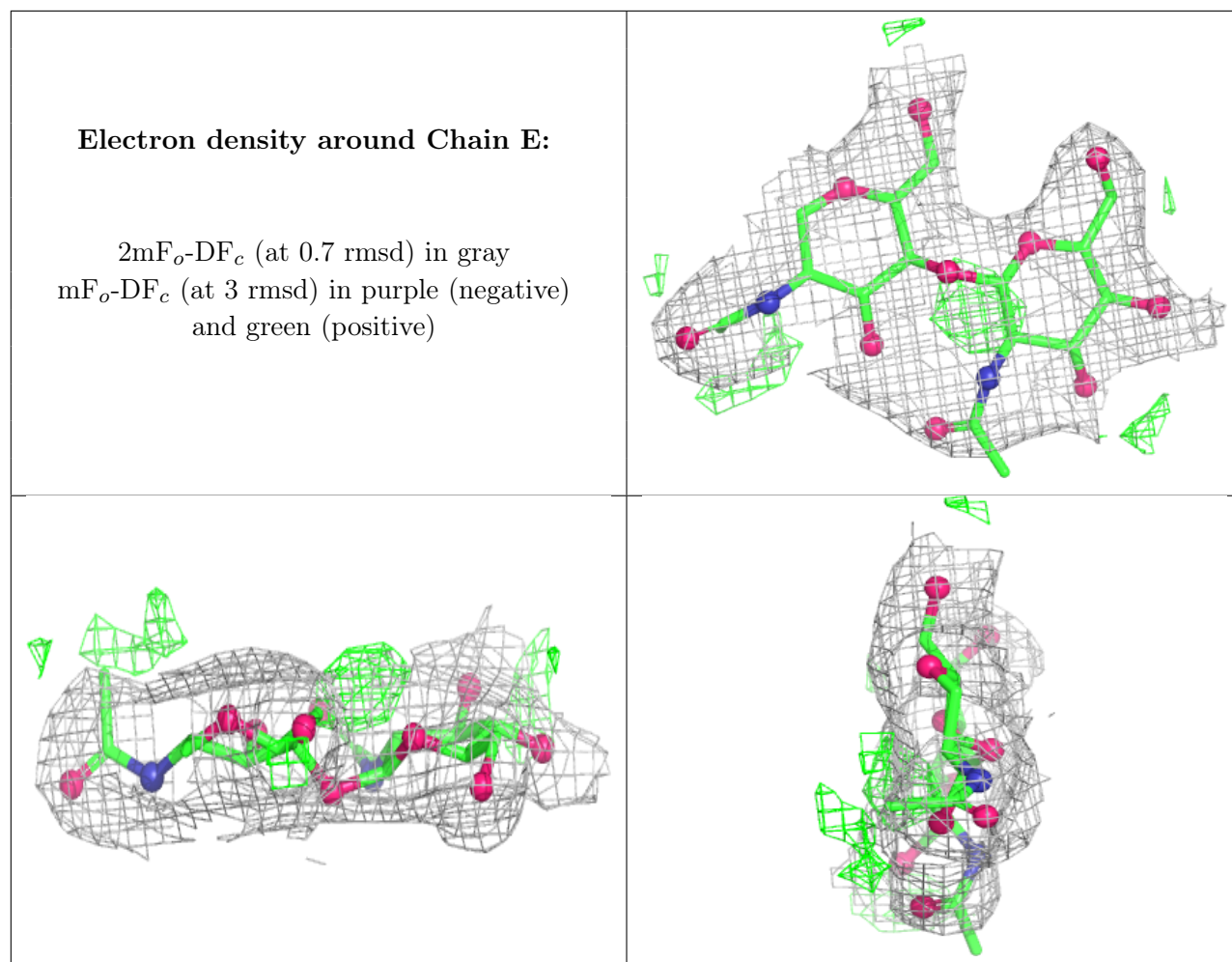
There are no non-standard protein/DNA/RNA residues in this entry.

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
5	NAG	E	2	14/15	0.77	0.14	48,49,50,50	0
5	NAG	E	1	14/15	0.79	0.13	44,45,46,47	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.



6.4 Ligands ⓘ

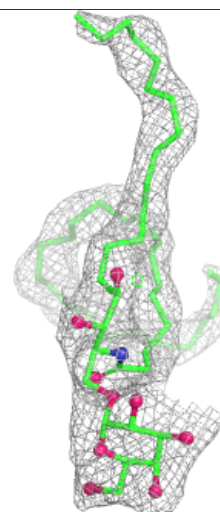
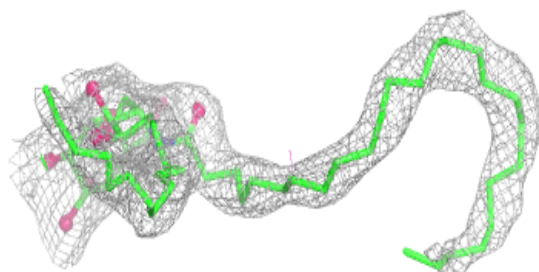
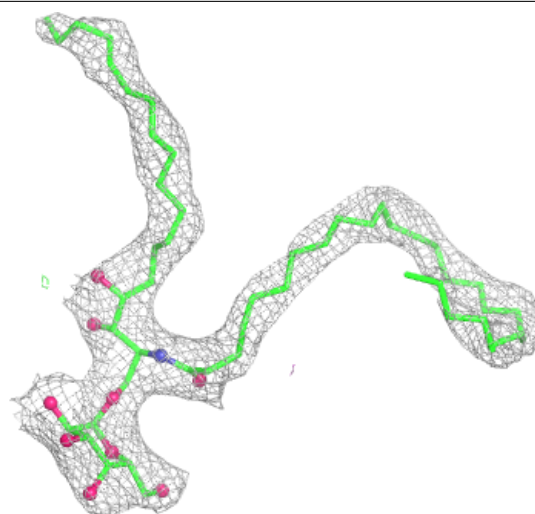
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	A	304	14/15	0.74	0.14	48,49,50,50	0
6	NAG	A	303	14/15	0.79	0.14	45,45,47,47	0
7	AGH	A	307	60/60	0.95	0.12	35,48,60,61	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 AGH A 307:

$2mF_o-DF_c$ (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.