



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:34 PM UTC

PDB ID : 5K70 / pdb_00005k70
Title : Sidekick-2 immunoglobulin domains 1-4 H18R/N22S mutant
Authors : Goodman, K.M.; Mannepalli, S.; Honig, B.; Shapiro, L.
Deposited on : 2016-05-25
Resolution : 2.70 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
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

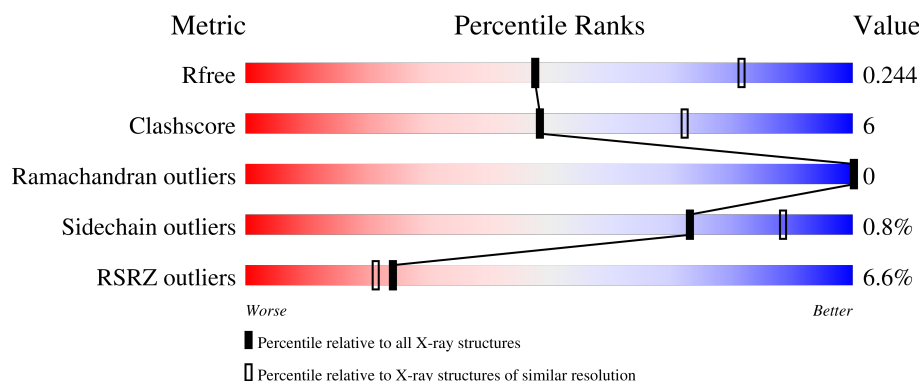
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	384	9% 85% 14% ..
1	B	384	4% 87% 11% .
1	C	384	4% 83% 13% ..
1	D	384	9% 80% 14% . 5%
2	E	3	33% 67%

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Mol	Chain	Length	Quality of chain
3	F	2	 100%
3	G	2	 50% 50%
3	H	2	 50% 50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11602 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.

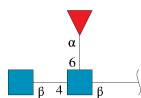
- Molecule 1 is a protein called Protein sidekick-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	381	Total	C	N	O	S	0	1	0
			2891	1826	499	553	13			
1	B	377	Total	C	N	O	S	0	0	0
			2887	1819	507	547	14			
1	C	374	Total	C	N	O	S	0	0	0
			2823	1779	496	536	12			
1	D	363	Total	C	N	O	S	0	0	0
			2717	1718	466	519	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q6V4S5
A	-3	PRO	-	expression tag	UNP Q6V4S5
A	18	ARG	HIS	engineered mutation	UNP Q6V4S5
A	22	SER	ASN	engineered mutation	UNP Q6V4S5
B	-4	GLY	-	expression tag	UNP Q6V4S5
B	-3	PRO	-	expression tag	UNP Q6V4S5
B	18	ARG	HIS	engineered mutation	UNP Q6V4S5
B	22	SER	ASN	engineered mutation	UNP Q6V4S5
C	-4	GLY	-	expression tag	UNP Q6V4S5
C	-3	PRO	-	expression tag	UNP Q6V4S5
C	18	ARG	HIS	engineered mutation	UNP Q6V4S5
C	22	SER	ASN	engineered mutation	UNP Q6V4S5
D	-4	GLY	-	expression tag	UNP Q6V4S5
D	-3	PRO	-	expression tag	UNP Q6V4S5
D	18	ARG	HIS	engineered mutation	UNP Q6V4S5
D	22	SER	ASN	engineered mutation	UNP Q6V4S5

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



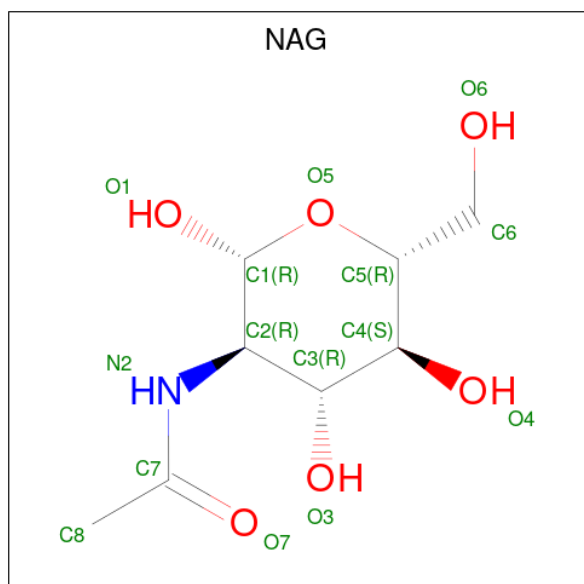
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 3 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



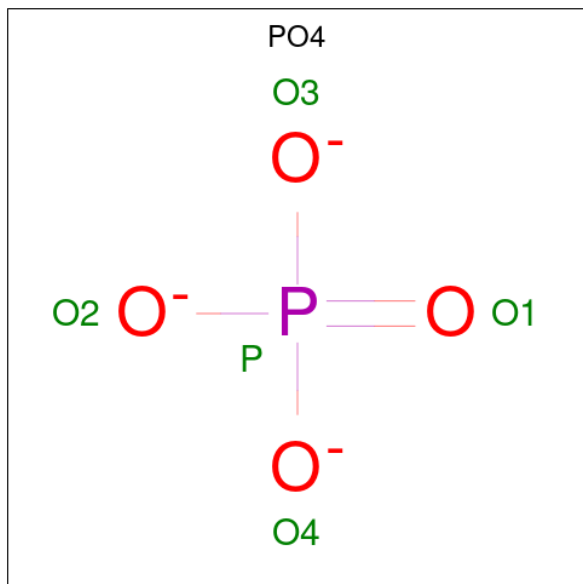
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	2	Total	C	N	O	0	0	0
			24	14	1	9			
3	G	2	Total	C	N	O	0	0	0
			24	14	1	9			
3	H	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			5	4	1		
5	C	1	Total	O	P	0	0
			5	4	1		
5	C	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		

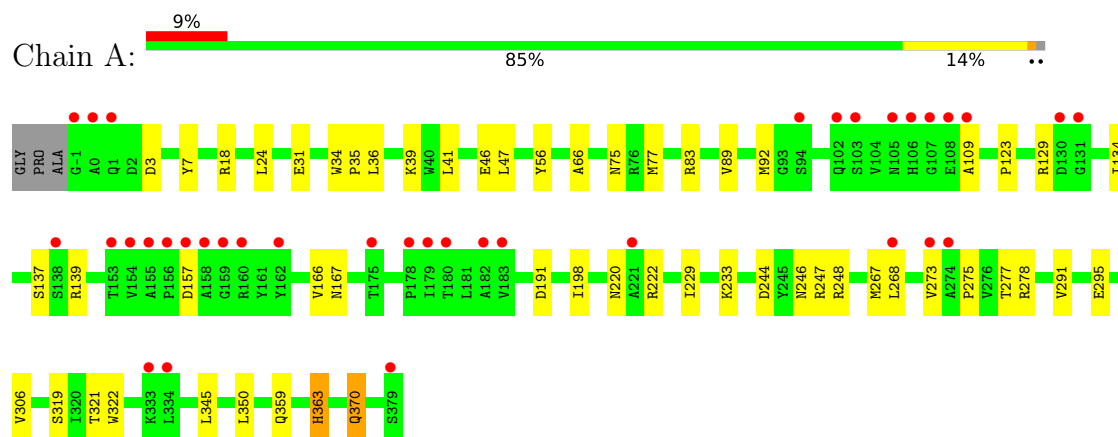
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	26	Total	O	0	0
			26	26		
6	B	17	Total	O	0	0
			17	17		
6	C	12	Total	O	0	0
			12	12		
6	D	7	Total	O	0	0
			7	7		

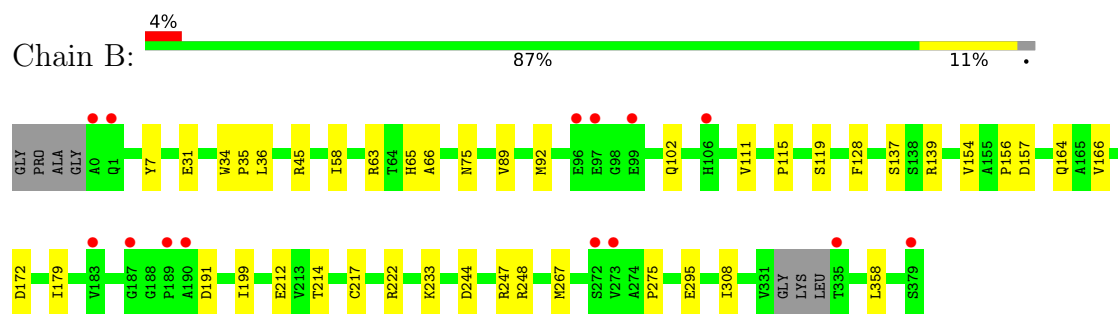
3 Residue-property plots [i](#)

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.

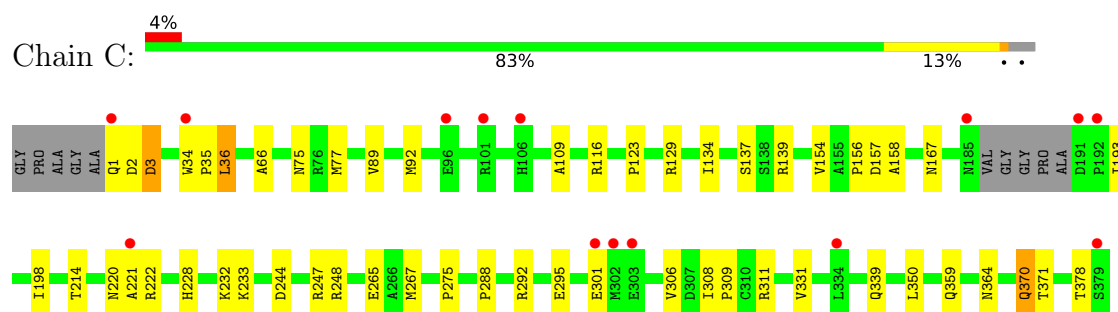
• Molecule 1: Protein sidekick-2



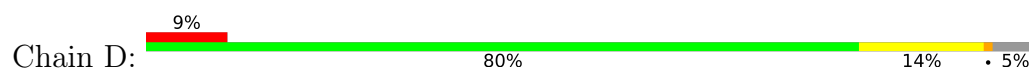
• Molecule 1: Protein sidekick-2

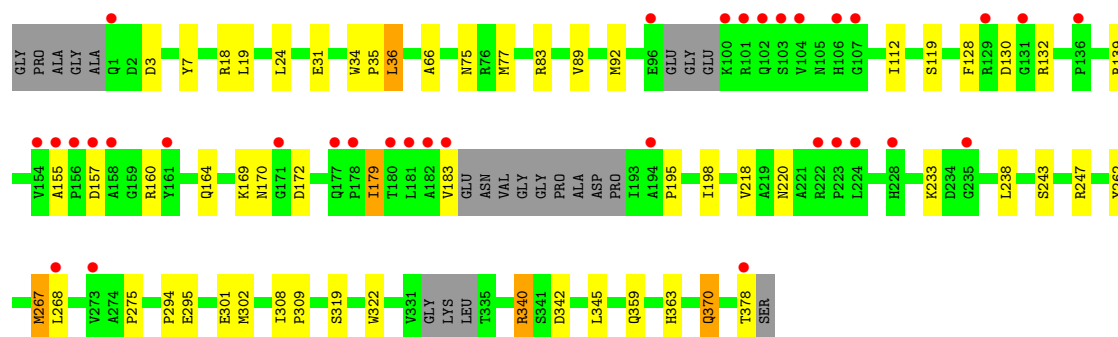


• Molecule 1: Protein sidekick-2



• Molecule 1: Protein sidekick-2





- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 33% 67%



- Molecule 3: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 100%



- Molecule 3: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 50% 50%



- Molecule 3: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	110.89Å 113.43Å 185.91Å 90.00° 103.69° 90.00°	Depositor
Resolution (Å)	39.52 – 2.70 39.52 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.52-2.70) 99.9 (39.52-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.206 , 0.243 0.209 , 0.244	Depositor DCC
R_{free} test set	3112 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11602	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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: FUC, NAG, PO4

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	0.35	0/2961	0.79	1/4044 (0.0%)
1	B	0.32	0/2952	0.78	0/4027
1	C	0.33	0/2886	0.82	2/3944 (0.1%)
1	D	0.36	0/2777	0.81	0/3798
All	All	0.34	0/11576	0.80	3/15813 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2	ASP	N-CA-C	7.92	119.70	111.14
1	C	3	ASP	N-CA-C	7.90	121.36	110.06
1	A	291	VAL	N-CA-C	-5.08	107.44	111.81

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	2891	0	2812	34	0
1	B	2887	0	2829	27	0
1	C	2823	0	2717	33	0
1	D	2717	0	2600	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	38	0	34	0	0
3	F	24	0	22	0	0
3	G	24	0	22	0	0
3	H	24	0	22	0	0
4	A	14	0	13	1	0
4	B	14	0	13	1	0
4	C	14	0	13	0	0
5	A	30	0	0	0	0
5	B	20	0	0	0	0
5	C	10	0	0	1	0
5	D	10	0	0	0	0
6	A	26	0	0	0	0
6	B	17	0	0	0	0
6	C	12	0	0	0	0
6	D	7	0	0	0	0
All	All	11602	0	11097	125	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 (125) 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:139:ARG:NH2	1:A:157:ASP:OD2	2.07	0.85
1:D:130:ASP:OD1	1:D:160:ARG:NH1	2.13	0.82
1:A:166:VAL:HG21	4:A:404:NAG:H82	1.63	0.80
1:C:92:MET:HE3	1:C:167:ASN:HB2	1.63	0.80
1:C:139:ARG:NH2	1:C:157:ASP:OD2	2.15	0.80
1:D:139:ARG:NH1	1:D:157:ASP:OD2	2.15	0.79
1:A:295:GLU:OE2	1:B:233:LYS:NZ	2.16	0.78
1:D:198:ILE:HD11	1:D:220:ASN:HB2	1.66	0.77
1:B:139:ARG:NH2	1:B:157:ASP:OD2	2.16	0.74
1:D:66:ALA:HB2	1:D:89:VAL:HG23	1.72	0.71
1:D:92:MET:HG3	1:D:119:SER:HB2	1.74	0.70
1:A:92:MET:HE3	1:A:167:ASN:HB2	1.73	0.70
1:B:191:ASP:O	1:B:222:ARG:NH1	2.25	0.69
1:C:233:LYS:NZ	1:D:295:GLU:OE2	2.19	0.68
1:B:137:SER:O	1:B:247:ARG:NH2	2.26	0.68
1:D:267:MET:HB3	1:D:275:PRO:HB3	1.76	0.68
1:B:92:MET:HG3	1:B:119:SER:HB2	1.75	0.67
1:A:267:MET:HB3	1:A:275:PRO:HB3	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:292:ARG:HH11	1:C:311:ARG:HH22	1.44	0.66
1:B:45:ARG:NH2	1:D:302:MET:SD	2.68	0.66
1:D:319:SER:HB2	1:D:363:HIS:CE1	2.32	0.65
1:C:36:LEU:HD12	1:C:75:ASN:HB3	1.78	0.64
1:C:267:MET:HB3	1:C:275:PRO:HB3	1.79	0.64
1:B:34:TRP:HZ2	1:D:34:TRP:HZ2	1.45	0.64
1:C:66:ALA:HB2	1:C:89:VAL:HG23	1.82	0.61
1:A:92:MET:HE1	1:A:123:PRO:HB3	1.82	0.61
1:D:359:GLN:HE21	1:D:370:GLN:HG3	1.67	0.60
1:C:154:VAL:HG23	1:C:156:PRO:HD2	1.84	0.60
1:C:295:GLU:OE1	1:D:233:LYS:NZ	2.35	0.59
1:C:198:ILE:HD11	1:C:220:ASN:HB2	1.85	0.59
1:D:83:ARG:HG2	1:D:83:ARG:HH11	1.68	0.59
1:D:340:ARG:NH2	1:D:342:ASP:OD2	2.36	0.58
1:D:218:VAL:HG22	1:D:247:ARG:HD3	1.85	0.58
1:C:306:VAL:HG12	1:C:350:LEU:HD11	1.85	0.58
1:A:83:ARG:HH11	1:A:83:ARG:HG2	1.69	0.58
1:A:359:GLN:HE21	1:A:370:GLN:HG3	1.68	0.57
1:C:109:ALA:HB2	1:C:220:ASN:HD22	1.71	0.56
1:C:129:ARG:HB2	1:C:134:ILE:HD11	1.86	0.56
1:D:160:ARG:N	1:D:160:ARG:HD3	2.20	0.56
1:D:301:GLU:HA	1:D:378:THR:HB	1.89	0.55
1:B:36:LEU:HD23	1:B:75:ASN:HB3	1.89	0.55
1:A:321:THR:HG1	1:A:363[A]:HIS:CE1	2.24	0.54
1:D:195:PRO:HD3	1:D:268:LEU:HD23	1.89	0.54
1:B:154:VAL:HG23	1:B:156:PRO:HD2	1.90	0.54
1:B:34:TRP:HZ2	1:D:34:TRP:CZ2	2.23	0.53
1:D:18:ARG:HE	1:D:24:LEU:HD13	1.73	0.53
1:C:193:ILE:H	1:C:222:ARG:HB2	1.73	0.53
1:D:294:PRO:HB3	1:D:309:PRO:HD2	1.90	0.53
1:D:233:LYS:HB2	1:D:238:LEU:HD11	1.89	0.53
1:A:36:LEU:HD23	1:A:75:ASN:HB3	1.89	0.52
1:A:18:ARG:HG3	1:A:24:LEU:HD13	1.91	0.51
1:D:128:PHE:HE2	1:D:164:GLN:HG2	1.75	0.51
1:B:63:ARG:HA	1:B:89:VAL:HG21	1.92	0.51
1:A:277:THR:O	1:A:278:ARG:NH1	2.39	0.51
1:D:34:TRP:CD1	1:D:35:PRO:HA	2.46	0.51
1:D:233:LYS:HE3	1:D:262:TYR:CZ	2.46	0.50
1:C:301:GLU:HA	1:C:378:THR:OG1	2.12	0.50
1:B:92:MET:HE2	1:B:172:ASP:HB3	1.94	0.50
1:C:359:GLN:HE21	1:C:370:GLN:HG3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:322:TRP:CE2	1:D:345:LEU:HB2	2.46	0.50
1:D:36:LEU:HD12	1:D:75:ASN:HB3	1.93	0.50
1:A:129:ARG:HB2	1:A:134:ILE:HD11	1.93	0.50
1:A:109:ALA:HB3	1:A:198:ILE:HD13	1.94	0.49
1:A:229:ILE:HB	1:A:246:ASN:HB3	1.95	0.49
1:B:34:TRP:CD1	1:B:35:PRO:HA	2.48	0.48
1:B:267:MET:HB3	1:B:275:PRO:HB3	1.95	0.48
1:A:268:LEU:HD12	1:A:273:VAL:HG21	1.95	0.48
1:B:66:ALA:HB2	1:B:89:VAL:HG23	1.94	0.48
1:A:3:ASP:HB2	1:A:77:MET:SD	2.54	0.48
1:C:214:THR:HG21	1:C:248:ARG:HD3	1.96	0.47
1:B:212:GLU:OE2	1:B:214:THR:OG1	2.29	0.47
1:C:370:GLN:HG2	1:C:371:THR:N	2.29	0.47
1:A:92:MET:CE	1:A:123:PRO:HB3	2.44	0.47
1:D:92:MET:HE2	1:D:172:ASP:HB3	1.96	0.47
1:A:322:TRP:CE2	1:A:345:LEU:HB2	2.50	0.47
1:C:244:ASP:HB3	1:C:248:ARG:HG3	1.97	0.47
1:C:34:TRP:CD1	1:C:35:PRO:HA	2.50	0.46
1:B:102:GLN:NE2	1:B:111:VAL:O	2.47	0.46
1:C:232:LYS:NZ	1:C:265:GLU:OE2	2.38	0.45
1:A:34:TRP:CD1	1:A:35:PRO:HA	2.51	0.45
1:A:233:LYS:NZ	1:B:295:GLU:OE2	2.48	0.45
1:B:199:ILE:O	1:B:217:CYS:HA	2.17	0.45
1:A:198:ILE:CD1	1:A:220:ASN:HB2	2.47	0.45
1:B:244:ASP:HB3	1:B:248:ARG:HG3	1.98	0.45
1:D:155:ALA:HA	1:D:183:VAL:HG21	1.99	0.45
1:C:109:ALA:HB2	1:C:220:ASN:ND2	2.33	0.44
1:C:288:PRO:HG3	1:C:364:ASN:HB2	1.99	0.44
1:D:112:ILE:HG21	1:D:179:ILE:HG21	1.98	0.44
1:A:191:ASP:O	1:A:222:ARG:HD2	2.17	0.44
1:D:130:ASP:C	1:D:132:ARG:H	2.25	0.43
1:D:233:LYS:HB3	1:D:238:LEU:HD21	1.98	0.43
1:A:306:VAL:HG12	1:A:350:LEU:HD11	2.01	0.43
1:B:166:VAL:HG21	4:B:403:NAG:H82	2.00	0.43
1:C:116:ARG:HG2	5:C:404:PO4:O4	2.19	0.43
1:D:3:ASP:HB2	1:D:77:MET:SD	2.58	0.43
1:A:137:SER:O	1:A:247:ARG:NH2	2.39	0.43
1:D:19:LEU:HD22	1:D:170:ASN:HB3	2.01	0.43
1:A:198:ILE:HD12	1:A:220:ASN:HB2	2.01	0.43
1:C:308:ILE:HA	1:C:309:PRO:HD3	1.86	0.42
1:D:308:ILE:HA	1:D:309:PRO:HD3	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:228:HIS:HD2	1:C:267:MET:HE2	1.84	0.42
1:D:19:LEU:HD21	1:D:169:LYS:O	2.19	0.42
1:B:7:TYR:CE1	1:B:31:GLU:HB3	2.54	0.42
1:C:92:MET:CE	1:C:123:PRO:HB3	2.49	0.42
1:A:244:ASP:HB3	1:A:248:ARG:HG3	2.02	0.42
1:B:58:ILE:HD13	1:B:65:HIS:HB3	2.00	0.42
1:C:129:ARG:NH1	1:C:158:ALA:O	2.52	0.42
1:B:128:PHE:HE2	1:B:164:GLN:HG2	1.85	0.42
1:A:47:LEU:HD13	1:A:56:TYR:CZ	2.55	0.42
1:A:92:MET:CE	1:A:167:ASN:HB2	2.46	0.42
1:A:359:GLN:NE2	1:A:370:GLN:HG3	2.33	0.42
1:C:331:VAL:HG11	1:C:339:GLN:HB2	2.02	0.41
1:A:41:LEU:CD2	1:A:46:GLU:HG2	2.50	0.41
1:B:34:TRP:CG	1:B:35:PRO:HA	2.55	0.41
1:A:319:SER:OG	1:A:363[A]:HIS:ND1	2.52	0.41
1:B:115:PRO:HG3	1:B:179:ILE:HD11	2.03	0.41
1:D:7:TYR:CZ	1:D:31:GLU:HB2	2.56	0.41
1:C:1:GLN:HA	1:D:243:SER:HB2	2.02	0.41
1:C:137:SER:O	1:C:247:ARG:NH2	2.35	0.41
1:C:220:ASN:OD1	1:C:221:ALA:N	2.54	0.41
1:A:66:ALA:HB2	1:A:89:VAL:HG23	2.01	0.41
1:A:7:TYR:CZ	1:A:31:GLU:HB3	2.55	0.41
1:B:308:ILE:HD13	1:B:358:LEU:HD13	2.03	0.41
1:D:160:ARG:HD3	1:D:160:ARG:H	1.86	0.41
1:C:3:ASP:HB2	1:C:77:MET:SD	2.61	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	380/384 (99%)	375 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	373/384 (97%)	367 (98%)	6 (2%)	0	100	100
1	C	370/384 (96%)	366 (99%)	4 (1%)	0	100	100
1	D	355/384 (92%)	350 (99%)	5 (1%)	0	100	100
All	All	1478/1536 (96%)	1458 (99%)	20 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	307/324 (95%)	303 (99%)	4 (1%)	61	83
1	B	309/324 (95%)	309 (100%)	0	100	100
1	C	294/324 (91%)	292 (99%)	2 (1%)	76	90
1	D	284/324 (88%)	279 (98%)	5 (2%)	51	78
All	All	1194/1296 (92%)	1183 (99%)	11 (1%)	73	87

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LYS
1	A	363[A]	HIS
1	A	363[B]	HIS
1	A	370	GLN
1	C	36	LEU
1	C	370	GLN
1	D	36	LEU
1	D	179	ILE
1	D	267	MET
1	D	340	ARG
1	D	370	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	B	228	HIS
1	B	289	GLN
1	C	228	HIS
1	C	253	ASN
1	C	370	GLN
1	D	220	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 ⓘ

9 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	0.35	0	17,19,21	0.54	0
2	NAG	E	2	2	14,14,15	0.61	1 (7%)	17,19,21	0.63	0
2	FUC	E	3	2	10,10,11	0.63	0	14,14,16	0.93	1 (7%)
3	NAG	F	1	3,1	14,14,15	0.61	1 (7%)	17,19,21	0.57	0
3	FUC	F	2	3	10,10,11	0.59	0	14,14,16	1.13	1 (7%)
3	NAG	G	1	3,1	14,14,15	0.78	1 (7%)	17,19,21	0.62	0
3	FUC	G	2	3	10,10,11	0.65	0	14,14,16	0.81	0
3	NAG	H	1	3,1	14,14,15	0.47	0	17,19,21	0.71	0
3	FUC	H	2	3	10,10,11	0.90	0	14,14,16	1.45	2 (14%)

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	-	4/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	FUC	E	3	2	-	-	0/1/1/1
3	NAG	F	1	3,1	-	4/6/23/26	0/1/1/1
3	FUC	F	2	3	-	-	0/1/1/1
3	NAG	G	1	3,1	-	2/6/23/26	0/1/1/1
3	FUC	G	2	3	-	-	0/1/1/1
3	NAG	H	1	3,1	-	4/6/23/26	0/1/1/1
3	FUC	H	2	3	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	1	NAG	C1-C2	2.18	1.55	1.52
2	E	2	NAG	C1-C2	2.09	1.55	1.52
3	F	1	NAG	C1-C2	2.08	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	2	FUC	O5-C5-C4	3.43	115.72	109.55
3	H	2	FUC	C1-O5-C5	2.73	119.41	112.97
3	F	2	FUC	C1-O5-C5	2.30	118.39	112.97
2	E	3	FUC	C1-O5-C5	2.05	117.80	112.97

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	1	NAG	O5-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
3	F	1	NAG	C8-C7-N2-C2
3	F	1	NAG	O7-C7-N2-C2
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2

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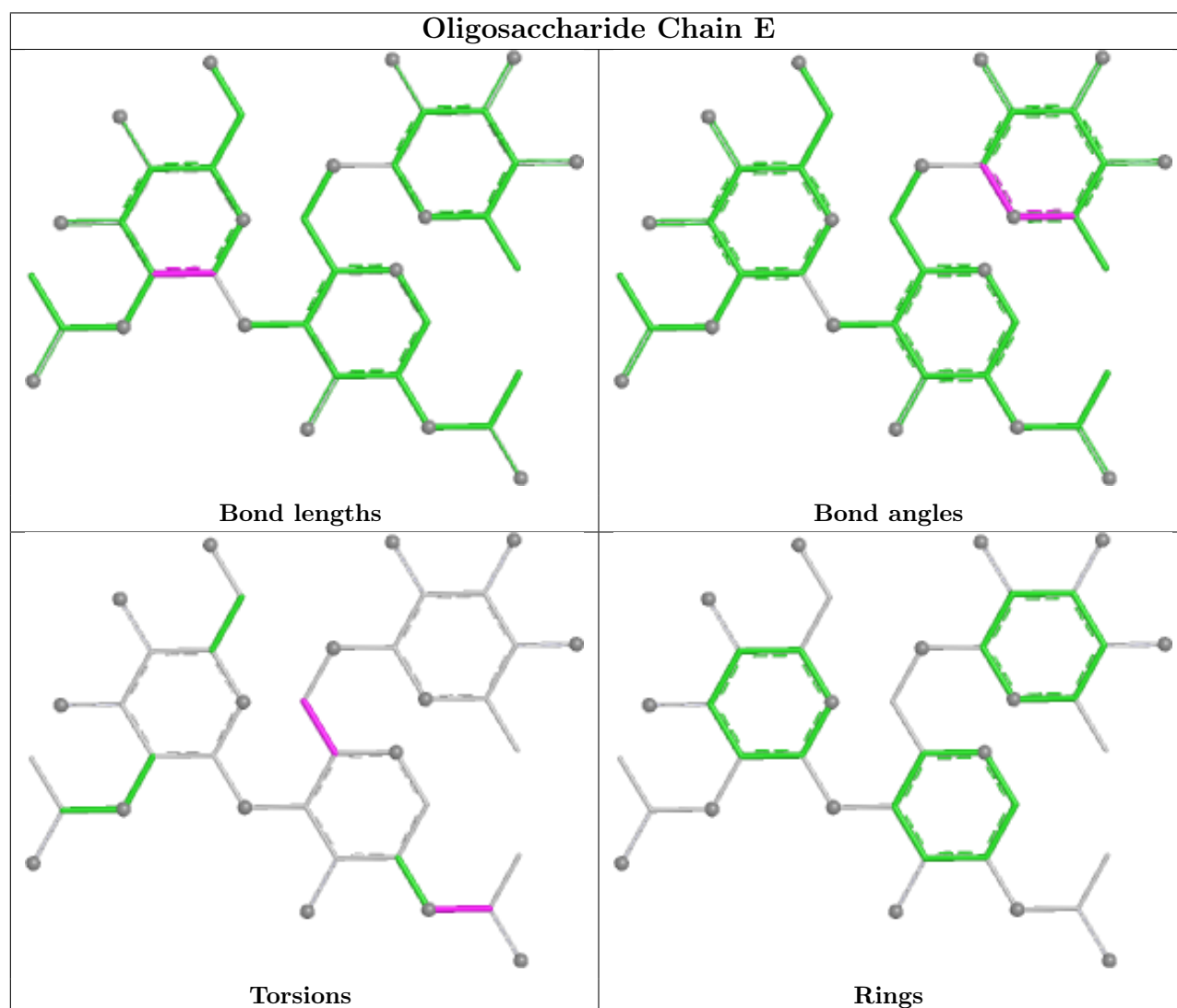
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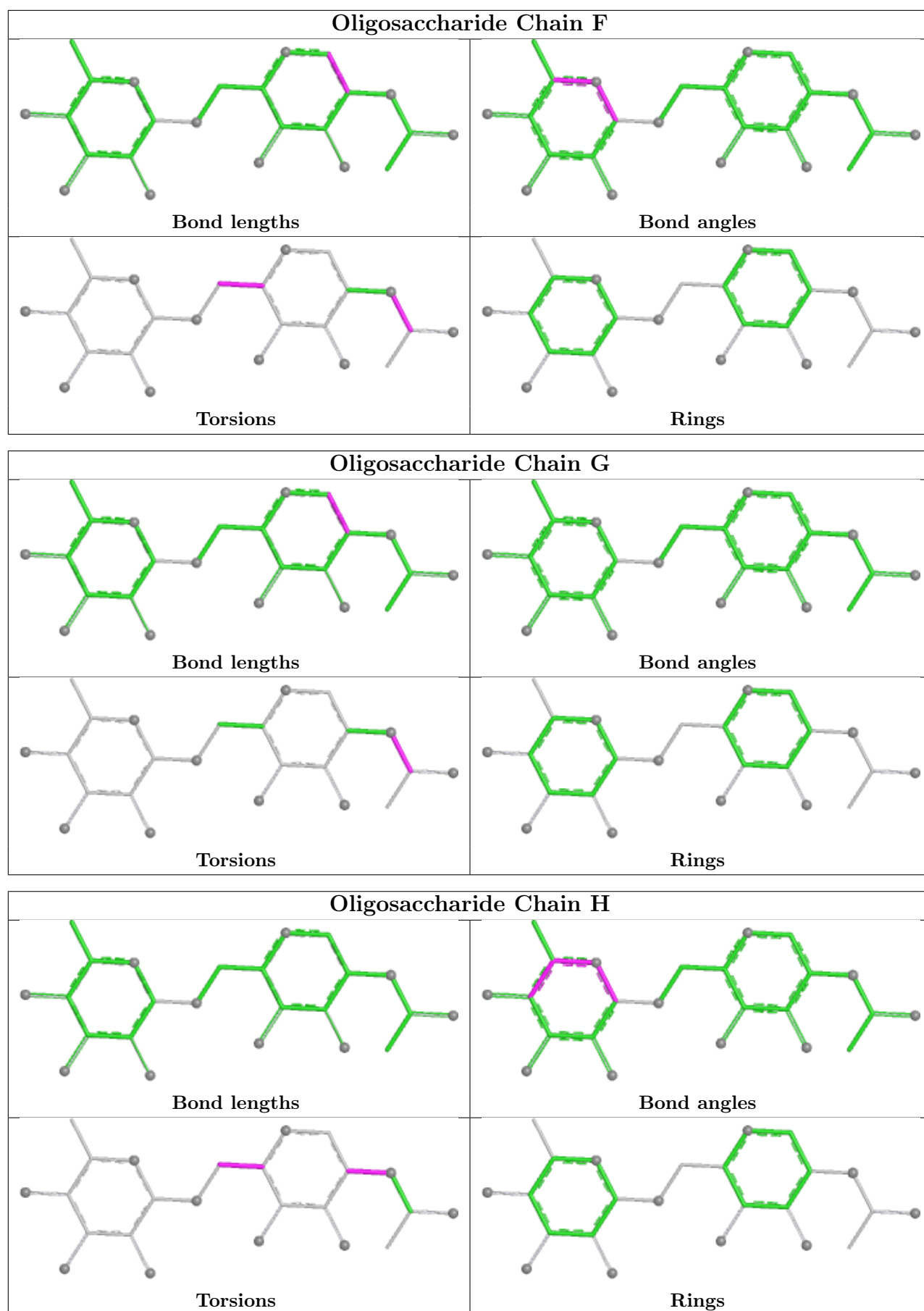
Mol	Chain	Res	Type	Atoms
2	E	1	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	H	1	NAG	C1-C2-N2-C7
3	F	1	NAG	C4-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C3-C2-N2-C7

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

17 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
5	PO4	B	404	-	4,4,4	0.93	0	6,6,6	0.51	0
5	PO4	A	410	-	4,4,4	0.95	0	6,6,6	0.43	0
5	PO4	D	404	-	4,4,4	0.97	0	6,6,6	0.43	0
5	PO4	A	405	-	4,4,4	1.00	0	6,6,6	0.44	0
5	PO4	A	407	-	4,4,4	0.98	0	6,6,6	0.44	0
4	NAG	C	403	1	14,14,15	0.30	0	17,19,21	0.72	0
5	PO4	A	406	-	4,4,4	0.95	0	6,6,6	0.44	0
5	PO4	A	409	-	4,4,4	0.95	0	6,6,6	0.45	0
5	PO4	B	405	-	4,4,4	0.96	0	6,6,6	0.52	0
5	PO4	C	405	-	4,4,4	0.96	0	6,6,6	0.46	0
5	PO4	A	408	-	4,4,4	0.92	0	6,6,6	0.47	0
4	NAG	A	404	1	14,14,15	0.40	0	17,19,21	0.81	1 (5%)
5	PO4	B	406	-	4,4,4	0.92	0	6,6,6	0.49	0
5	PO4	B	407	-	4,4,4	0.94	0	6,6,6	0.48	0
5	PO4	C	404	-	4,4,4	0.96	0	6,6,6	0.49	0
5	PO4	D	401	-	4,4,4	0.94	0	6,6,6	0.45	0
4	NAG	B	403	1	14,14,15	0.50	0	17,19,21	0.66	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
4	NAG	B	403	1	-	2/6/23/26	0/1/1/1
4	NAG	C	403	1	-	4/6/23/26	0/1/1/1
4	NAG	A	404	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	404	NAG	C1-O5-C5	2.73	115.85	112.19
4	B	403	NAG	C1-O5-C5	2.21	115.14	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	403	NAG	O5-C5-C6-O6
4	B	403	NAG	C4-C5-C6-O6
4	C	403	NAG	C4-C5-C6-O6
4	C	403	NAG	C3-C2-N2-C7
4	C	403	NAG	O5-C5-C6-O6
4	C	403	NAG	C1-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	NAG	1	0
5	C	404	PO4	1	0
4	B	403	NAG	1	0

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	381/384 (99%)	0.43	36 (9%)	14 12	25, 52, 85, 116	1 (0%)
1	B	377/384 (98%)	0.11	14 (3%)	45 41	27, 54, 89, 105	0
1	C	374/384 (97%)	0.21	14 (3%)	45 41	33, 60, 90, 109	0
1	D	363/384 (94%)	0.46	34 (9%)	14 12	29, 64, 129, 144	0
All	All	1495/1536 (97%)	0.30	98 (6%)	24 21	25, 57, 98, 144	1 (0%)

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	183	VAL	5.9
1	D	177	GLN	5.4
1	A	0	ALA	4.8
1	D	96	GLU	4.5
1	D	155	ALA	4.1
1	A	-1	GLY	4.0
1	B	96	GLU	3.8
1	A	379	SER	3.8
1	C	221	ALA	3.8
1	C	191	ASP	3.8
1	B	187	GLY	3.5
1	A	103	SER	3.4
1	C	379	SER	3.4
1	A	183	VAL	3.4
1	D	154	VAL	3.3
1	A	160	ARG	3.3
1	D	182	ALA	3.3
1	D	178	PRO	3.2
1	B	0	ALA	3.2
1	D	161	TYR	3.2
1	A	105	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	106	HIS	3.1
1	C	192	PRO	3.1
1	D	158	ALA	3.1
1	A	154	VAL	3.1
1	B	272	SER	3.1
1	A	106	HIS	3.0
1	A	157	ASP	3.0
1	A	159	GLY	3.0
1	A	155	ALA	3.0
1	D	106	HIS	3.0
1	B	189	PRO	3.0
1	D	1	GLN	2.9
1	A	156	PRO	2.9
1	D	100	LYS	2.9
1	A	108	GLU	2.8
1	A	94	SER	2.8
1	A	107	GLY	2.8
1	A	153	THR	2.8
1	D	101	ARG	2.8
1	D	268	LEU	2.7
1	D	103	SER	2.7
1	B	106	HIS	2.7
1	D	107	GLY	2.7
1	D	129	ARG	2.7
1	B	335	THR	2.7
1	A	178	PRO	2.7
1	A	180	THR	2.6
1	A	162	TYR	2.6
1	A	182	ALA	2.6
1	A	268	LEU	2.5
1	D	378	THR	2.5
1	A	334	LEU	2.5
1	C	301	GLU	2.5
1	C	1	GLN	2.5
1	D	273	VAL	2.5
1	A	138	SER	2.4
1	D	235	GLY	2.4
1	A	333	LYS	2.4
1	A	102	GLN	2.4
1	A	158	ALA	2.4
1	A	179	ILE	2.4
1	D	228	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	96	GLU	2.4
1	D	224	LEU	2.4
1	D	180	THR	2.4
1	C	34	TRP	2.4
1	B	99	GLU	2.3
1	B	1	GLN	2.3
1	D	222	ARG	2.3
1	B	273	VAL	2.3
1	D	104	VAL	2.3
1	B	190	ALA	2.3
1	D	181	LEU	2.3
1	D	157	ASP	2.2
1	A	273	VAL	2.2
1	C	302	MET	2.2
1	D	171	GLY	2.2
1	A	175	THR	2.2
1	A	221	ALA	2.2
1	C	334	LEU	2.2
1	B	97	GLU	2.1
1	A	1	GLN	2.1
1	B	183	VAL	2.1
1	C	303	GLU	2.1
1	D	223	PRO	2.1
1	A	274	ALA	2.1
1	D	194	ALA	2.1
1	D	136	PRO	2.1
1	C	185	ASN	2.1
1	A	131	GLY	2.1
1	A	130	ASP	2.0
1	D	102	GLN	2.0
1	D	131	GLY	2.0
1	C	101	ARG	2.0
1	A	109	ALA	2.0
1	B	379	SER	2.0
1	D	156	PRO	2.0

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

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

6.3 Carbohydrates

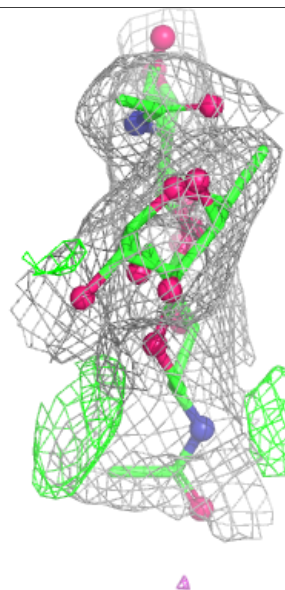
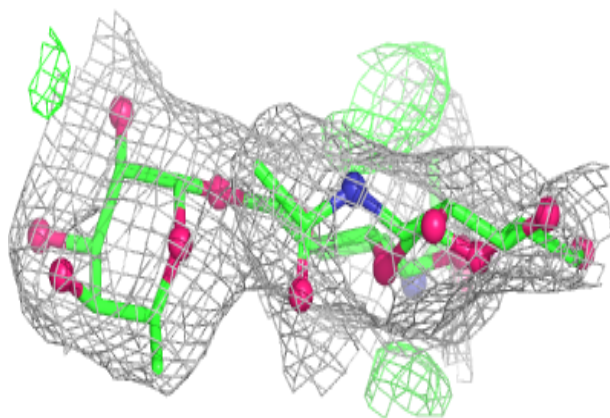
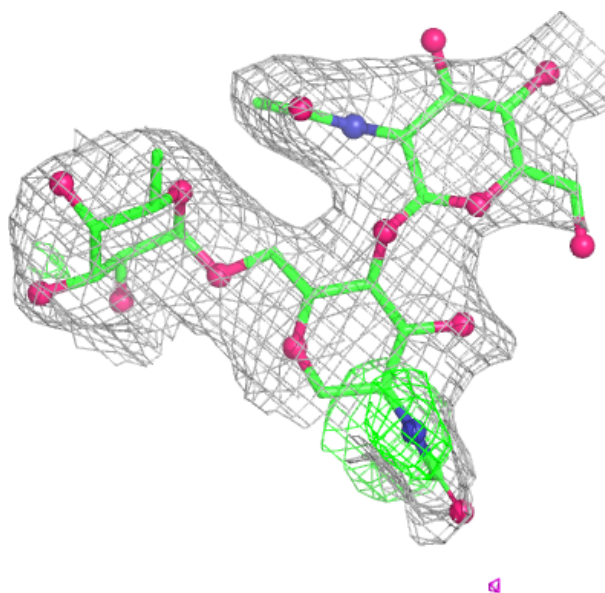
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	H	1	14/15	0.69	0.14	41,101,106,108	0
3	NAG	F	1	14/15	0.71	0.13	58,77,92,96	0
2	NAG	E	2	14/15	0.76	0.12	30,88,107,113	0
3	NAG	G	1	14/15	0.79	0.15	33,67,89,93	0
2	NAG	E	1	14/15	0.81	0.11	38,57,82,83	0
3	FUC	H	2	10/11	0.84	0.12	70,80,95,101	0
3	FUC	F	2	10/11	0.89	0.10	51,59,80,84	0
3	FUC	G	2	10/11	0.92	0.08	41,57,71,79	0
2	FUC	E	3	10/11	0.94	0.09	15,54,66,67	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.

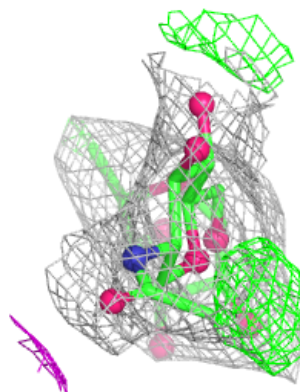
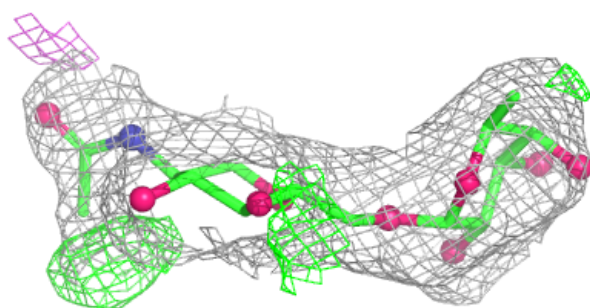
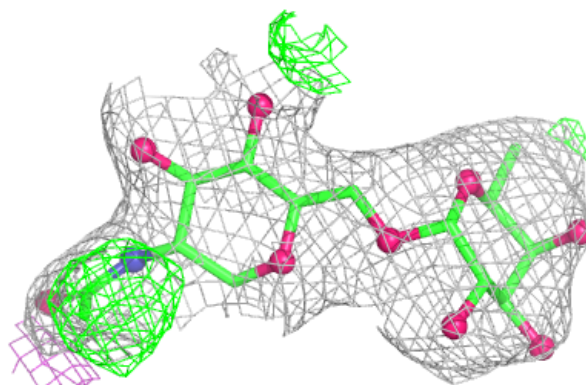
Electron density around Chain E:

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

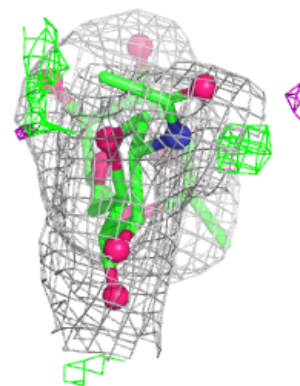
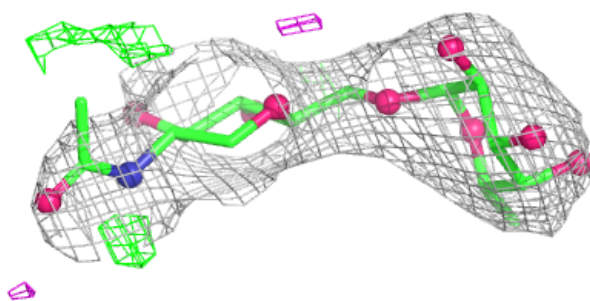
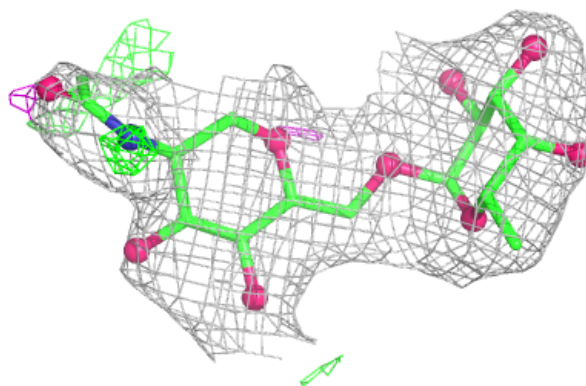


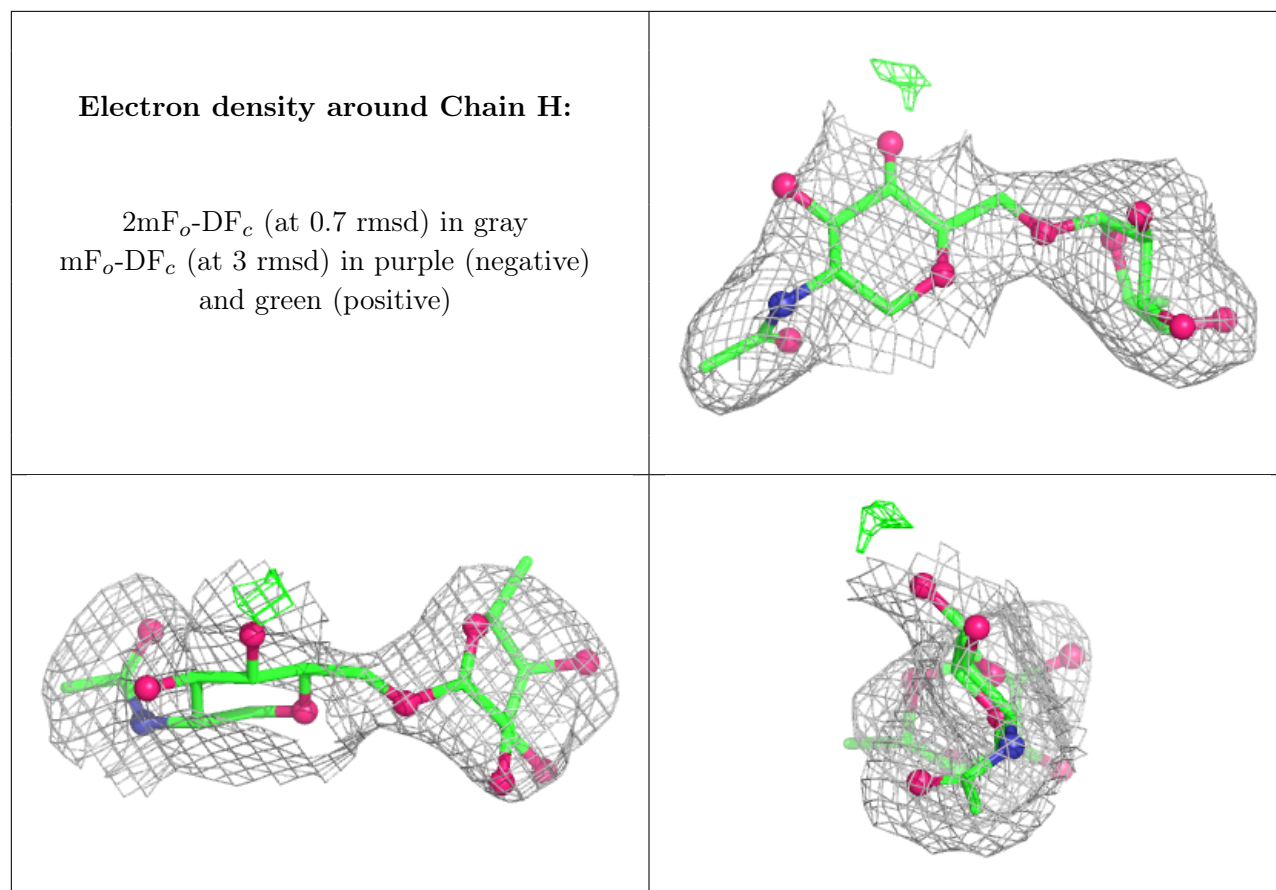
Electron density around Chain F:

$2mF_o - DF_c$ (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
5	PO4	D	404	5/5	0.61	0.14	124,130,140,142	0
4	NAG	B	403	14/15	0.63	0.14	46,99,122,128	0
5	PO4	C	404	5/5	0.67	0.14	90,109,112,117	0
5	PO4	C	405	5/5	0.70	0.13	115,126,136,137	0
5	PO4	B	404	5/5	0.71	0.14	76,93,118,133	0
5	PO4	B	406	5/5	0.75	0.15	87,108,115,120	0
4	NAG	A	404	14/15	0.77	0.13	42,75,95,98	0
4	NAG	C	403	14/15	0.82	0.14	71,101,120,126	0
5	PO4	B	405	5/5	0.82	0.15	102,103,110,112	0
5	PO4	B	407	5/5	0.83	0.16	118,120,120,126	0
5	PO4	A	409	5/5	0.84	0.18	63,66,110,132	0
5	PO4	A	408	5/5	0.85	0.13	56,76,115,129	0
5	PO4	A	407	5/5	0.86	0.21	74,85,105,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PO4	D	401	5/5	0.87	0.13	59,72,99,118	0
5	PO4	A	410	5/5	0.88	0.13	75,105,127,146	0
5	PO4	A	405	5/5	0.94	0.13	56,71,109,113	0
5	PO4	A	406	5/5	0.94	0.12	57,63,75,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.