



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 12:15 AM UTC

PDB ID : 5FIC / pdb_00005fic
Title : Open form of murine Acid Sphingomyelinase in presence of lipid
Authors : Gorelik, A.; Illes, K.; Heinz, L.X.; Superti-Furga, G.; Nagar, B.
Deposited on : 2015-12-22
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

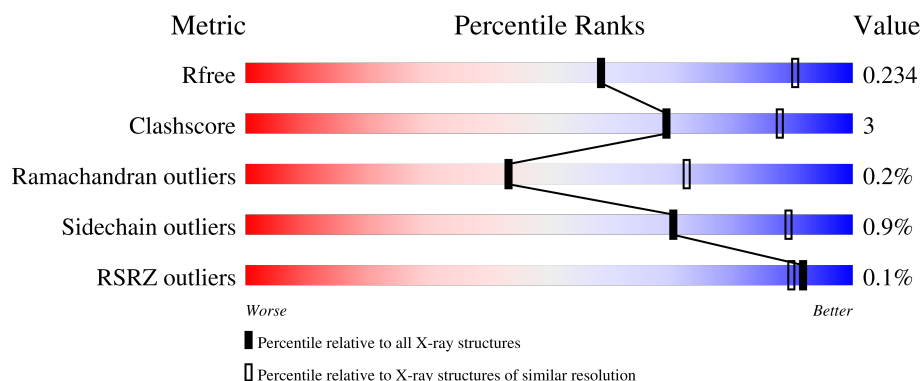
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

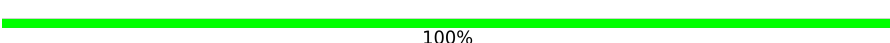
The reported resolution of this entry is 2.80 Å.

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.



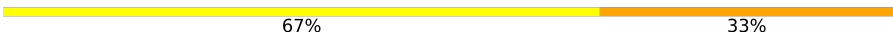
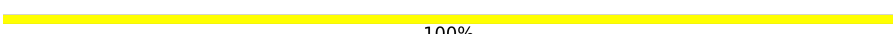
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	538	 87% 11% .
1	B	538	 87% 11% .
1	C	538	 88% 9% .
1	D	538	 90% 8% .
2	E	3	 100%

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Mol	Chain	Length	Quality of chain
2	I	3	 67% 33%
3	F	3	 67% 33%
3	J	3	 33% 67%
4	G	2	 50% 50%
4	H	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	PO4	A	710	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 33383 atoms, of which 16374 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 Spingomyelin phosphodiesterase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	527	Total	C	H	N	O	S	0	0	0
			8177	2678	4017	715	744	23			
1	B	527	Total	C	H	N	O	S	0	0	0
			8177	2678	4017	715	744	23			
1	C	527	Total	C	H	N	O	S	0	0	0
			8177	2678	4017	715	744	23			
1	D	527	Total	C	H	N	O	S	0	0	0
			8177	2678	4017	715	744	23			

There are 40 discrepancies between the modelled and reference sequences:

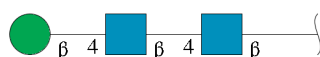
Chain	Residue	Modelled	Actual	Comment	Reference
A	74	ASP	-	expression tag	UNP Q04519
A	75	ARG	-	expression tag	UNP Q04519
A	76	HIS	-	expression tag	UNP Q04519
A	77	HIS	-	expression tag	UNP Q04519
A	78	HIS	-	expression tag	UNP Q04519
A	79	HIS	-	expression tag	UNP Q04519
A	80	HIS	-	expression tag	UNP Q04519
A	81	HIS	-	expression tag	UNP Q04519
A	82	LYS	-	expression tag	UNP Q04519
A	83	LEU	-	expression tag	UNP Q04519
B	74	ASP	-	expression tag	UNP Q04519
B	75	ARG	-	expression tag	UNP Q04519
B	76	HIS	-	expression tag	UNP Q04519
B	77	HIS	-	expression tag	UNP Q04519
B	78	HIS	-	expression tag	UNP Q04519
B	79	HIS	-	expression tag	UNP Q04519
B	80	HIS	-	expression tag	UNP Q04519
B	81	HIS	-	expression tag	UNP Q04519
B	82	LYS	-	expression tag	UNP Q04519
B	83	LEU	-	expression tag	UNP Q04519
C	74	ASP	-	expression tag	UNP Q04519

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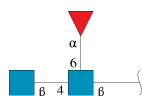
Chain	Residue	Modelled	Actual	Comment	Reference
C	75	ARG	-	expression tag	UNP Q04519
C	76	HIS	-	expression tag	UNP Q04519
C	77	HIS	-	expression tag	UNP Q04519
C	78	HIS	-	expression tag	UNP Q04519
C	79	HIS	-	expression tag	UNP Q04519
C	80	HIS	-	expression tag	UNP Q04519
C	81	HIS	-	expression tag	UNP Q04519
C	82	LYS	-	expression tag	UNP Q04519
C	83	LEU	-	expression tag	UNP Q04519
D	74	ASP	-	expression tag	UNP Q04519
D	75	ARG	-	expression tag	UNP Q04519
D	76	HIS	-	expression tag	UNP Q04519
D	77	HIS	-	expression tag	UNP Q04519
D	78	HIS	-	expression tag	UNP Q04519
D	79	HIS	-	expression tag	UNP Q04519
D	80	HIS	-	expression tag	UNP Q04519
D	81	HIS	-	expression tag	UNP Q04519
D	82	LYS	-	expression tag	UNP Q04519
D	83	LEU	-	expression tag	UNP Q04519

- Molecule 2 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
2	E	3	Total	C	H	N	O	0	0	0
			75	22	36	2	15			
2	I	3	Total	C	H	N	O	0	0	0
			76	22	37	2	15			

- Molecule 3 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
3	F	3	Total	C	H	N	O	0	0	0
			75	22	37	2	14			
3	J	3	Total	C	H	N	O	0	0	0
			74	22	36	2	14			

- 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	G	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
4	H	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Zn	0	0
			2	2		
5	B	2	Total	Zn	0	0
			2	2		
5	C	2	Total	Zn	0	0
			2	2		
5	D	2	Total	Zn	0	0
			2	2		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

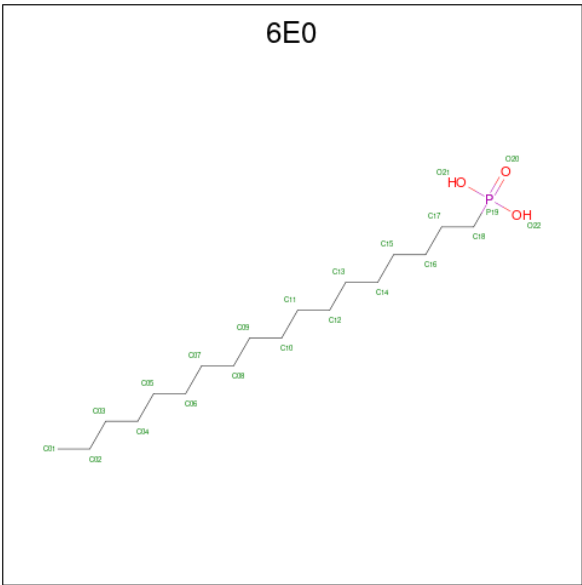


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		
6	A	1	Total	O	P	0	0
			5	4	1		
6	A	1	Total	O	P	0	0
			5	4	1		
6	B	1	Total	O	P	0	0
			5	4	1		
6	B	1	Total	O	P	0	0
			5	4	1		
6	C	1	Total	O	P	0	0
			5	4	1		
6	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

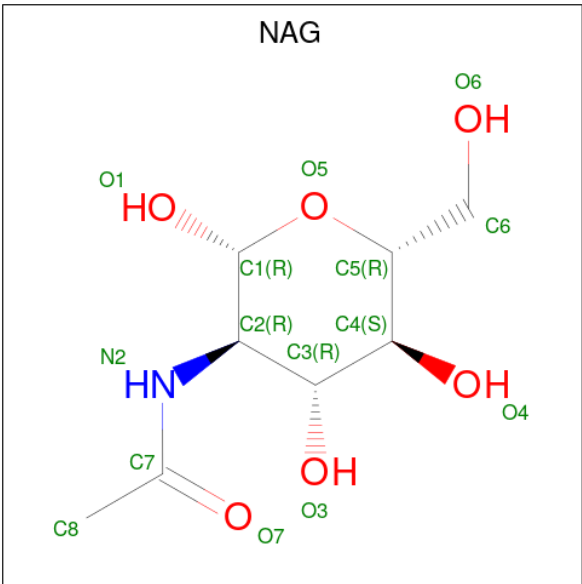
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	Cl	0	0
			2	2		
7	B	1	Total	Cl	0	0
			1	1		
7	C	1	Total	Cl	0	0
			1	1		
7	D	1	Total	Cl	0	0
			1	1		

- Molecule 8 is octadecylphosphonic acid (CCD ID: 6E0) (formula: C₁₈H₃₉O₃P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	H	O	P	0	0
			61	18	39	3	1		
8	D	1	Total	C	H	O	P	0	0
			61	18	39	3	1		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

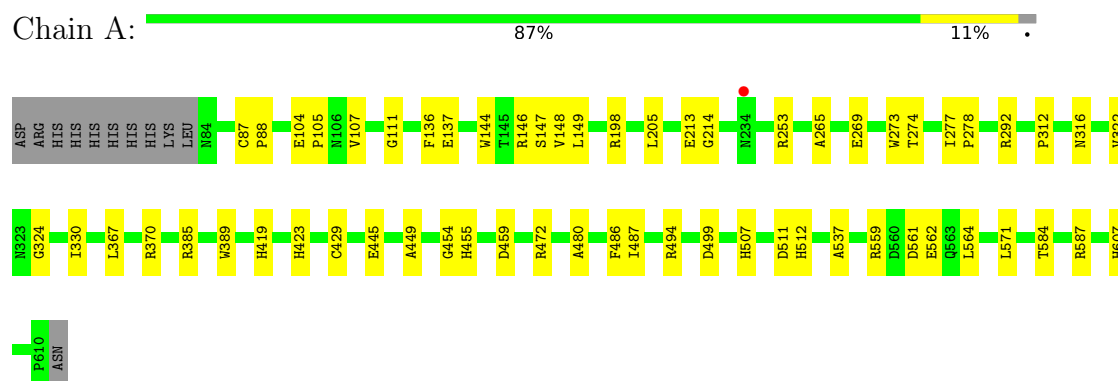
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	10	Total	O	0	0
			10	10		
10	B	11	Total	O	0	0
			11	11		
10	C	12	Total	O	0	0
			12	12		
10	D	6	Total	O	0	0
			6	6		

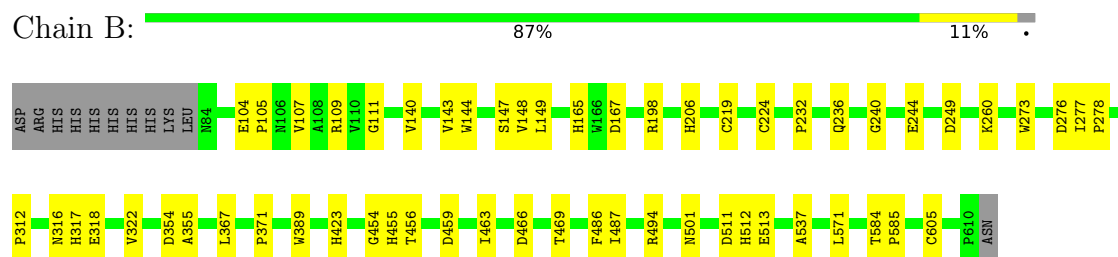
3 Residue-property plots

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.

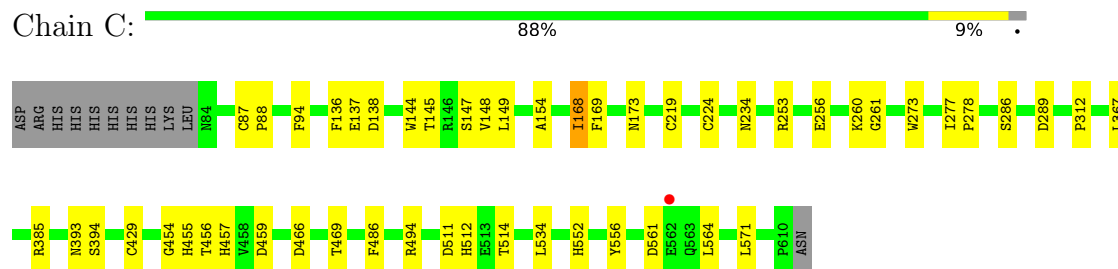
• Molecule 1: Spingomyelin phosphodiesterase



• Molecule 1: Spingomyelin phosphodiesterase

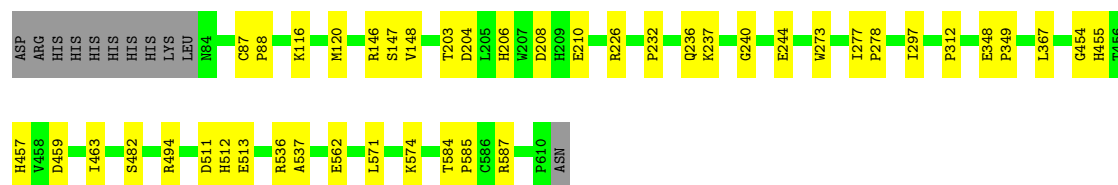


• Molecule 1: Spingomyelin phosphodiesterase



• Molecule 1: Spingomyelin phosphodiesterase





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

Chain E: 100%



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

Chain I: 67% 33%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 67% 33%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J: 33% 67%



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

Chain G: 50% 50%



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

Chain H: 100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	101.75Å 101.75Å 401.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.32 – 2.80 49.32 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.32-2.80) 100.0 (49.32-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.81Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.189 , 0.236 0.188 , 0.234	Depositor DCC
R_{free} test set	968 reflections (0.97%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.477 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	33383	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.25% 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: BMA, NAG, PO4, CL, 6E0, FUC, ZN

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	0.15	0/4304	0.31	0/5893
1	B	0.15	0/4304	0.31	0/5893
1	C	0.15	0/4304	0.31	0/5893
1	D	0.15	0/4304	0.31	0/5893
All	All	0.15	0/17216	0.31	0/23572

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4160	4017	4016	34	0
1	B	4160	4017	4016	31	0
1	C	4160	4017	4016	25	0
1	D	4160	4017	4016	22	0
2	E	39	36	34	0	0
2	I	39	37	34	0	0
3	F	38	37	34	1	0
3	J	38	36	34	0	0
4	G	28	27	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	28	27	25	1	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	15	0	0	2	0
6	B	10	0	0	2	0
6	C	5	0	0	0	0
6	D	5	0	0	0	0
7	A	2	0	0	2	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	22	39	0	0	0
8	D	22	39	0	0	0
9	B	14	14	13	0	0
9	C	14	14	13	2	0
10	A	10	0	0	3	0
10	B	11	0	0	5	0
10	C	12	0	0	2	0
10	D	6	0	0	1	0
All	All	17009	16374	16276	116	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 3.

All (116) 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:D:463:ILE:O	10:D:801:HOH:O	1.92	0.87
1:B:109:ARG:NH1	6:B:707:PO4:O2	2.10	0.85
1:D:562:GLU:OE1	1:D:587:ARG:NH2	2.14	0.80
9:C:705:NAG:O7	9:C:705:NAG:O3	2.04	0.76
1:A:449:ALA:O	10:A:801:HOH:O	2.05	0.74
1:C:394:SER:OG	10:C:801:HOH:O	2.04	0.74
1:A:459:ASP:OD1	1:A:494:ARG:NH2	2.22	0.72
1:A:480:ALA:O	10:A:802:HOH:O	2.08	0.70
1:C:511:ASP:OD1	1:C:512:HIS:N	2.23	0.70
1:A:253:ARG:NH2	7:A:713:CL:CL	2.63	0.68
1:A:511:ASP:OD1	1:A:512:HIS:N	2.26	0.68
1:B:459:ASP:OD1	1:B:494:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:511:ASP:OD1	1:B:512:HIS:N	2.30	0.64
1:B:466:ASP:OD2	1:B:469:THR:OG1	2.12	0.64
1:B:501:ASN:OD1	10:B:801:HOH:O	2.15	0.64
1:C:261:GLY:O	10:C:802:HOH:O	2.15	0.64
1:B:317:HIS:HE2	6:B:706:PO4:P	2.20	0.63
1:B:316:ASN:OD1	1:B:423:HIS:CD2	2.43	0.63
1:A:445:GLU:O	10:A:803:HOH:O	2.15	0.63
1:A:370:ARG:NH2	1:A:499:ASP:O	2.33	0.61
1:D:147:SER:OG	1:D:148:VAL:N	2.34	0.60
1:A:562:GLU:OE2	1:A:587:ARG:NH2	2.36	0.58
1:A:316:ASN:OD1	1:A:423:HIS:CD2	2.56	0.58
1:B:276:ASP:N	1:B:318:GLU:OE2	2.37	0.58
1:D:511:ASP:OD1	1:D:512:HIS:N	2.36	0.58
1:C:385:ARG:NH1	1:C:429:CYS:O	2.38	0.56
1:A:385:ARG:NH1	1:A:429:CYS:O	2.39	0.55
1:A:198:ARG:N	1:A:269:GLU:OE1	2.39	0.54
1:C:466:ASP:OD2	1:C:469:THR:OG1	2.25	0.53
1:B:605:CYS:O	10:B:802:HOH:O	2.19	0.53
1:D:459:ASP:OD1	1:D:494:ARG:NH2	2.43	0.52
1:C:561:ASP:OD2	1:C:564:LEU:N	2.36	0.52
1:A:147:SER:OG	1:A:148:VAL:N	2.43	0.52
1:C:514:THR:O	1:C:534:LEU:N	2.42	0.52
9:C:705:NAG:HO3	9:C:705:NAG:C7	2.17	0.52
1:B:317:HIS:HA	1:B:322:VAL:HG23	1.93	0.51
1:C:459:ASP:OD1	1:C:494:ARG:NH2	2.44	0.51
1:B:463:ILE:O	10:B:803:HOH:O	2.19	0.50
1:A:198:ARG:NE	1:A:265:ALA:O	2.42	0.50
1:A:198:ARG:NH1	6:A:710:PO4:O2	2.43	0.50
1:B:147:SER:OG	1:B:148:VAL:N	2.41	0.50
1:B:371:PRO:O	10:B:801:HOH:O	2.20	0.50
1:C:87:CYS:HB3	1:C:88:PRO:HD3	1.94	0.50
1:D:240:GLY:N	1:D:244:GLU:OE1	2.42	0.50
1:B:104:GLU:N	1:B:105:PRO:HD2	2.27	0.50
1:A:87:CYS:HB3	1:A:88:PRO:HD3	1.95	0.49
1:A:274:THR:O	1:A:423:HIS:ND1	2.47	0.48
1:C:273:TRP:O	1:C:312:PRO:HA	2.14	0.48
1:B:456:THR:OG1	10:B:804:HOH:O	2.20	0.47
1:C:144:TRP:O	1:C:149:LEU:N	2.44	0.47
1:B:240:GLY:N	1:B:244:GLU:OE1	2.43	0.47
1:A:277:ILE:HB	1:A:278:PRO:HD3	1.97	0.46
1:C:147:SER:OG	1:C:148:VAL:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:208:ASP:OD1	1:D:226:ARG:NH1	2.49	0.46
1:C:277:ILE:HB	1:C:278:PRO:HD3	1.98	0.46
1:D:206:HIS:HA	1:D:277:ILE:O	2.16	0.46
4:G:1:NAG:H62	4:G:2:NAG:O5	2.17	0.45
1:B:143:VAL:HG12	1:B:389:TRP:CE3	2.52	0.45
1:A:584:THR:OG1	1:C:234:ASN:ND2	2.48	0.45
1:A:472:ARG:NE	7:A:712:CL:CL	2.86	0.45
1:B:219:CYS:N	1:B:224:CYS:SG	2.89	0.45
1:B:232:PRO:HB2	1:B:236:GLN:HB2	1.98	0.45
1:C:168:ILE:HG22	1:C:169:PHE:N	2.31	0.45
1:D:116:LYS:O	1:D:120:MET:HG2	2.17	0.45
1:B:165:HIS:NE2	1:B:167:ASP:OD2	2.51	0.44
1:A:107:VAL:O	1:A:111:GLY:N	2.41	0.43
1:B:198:ARG:NH2	1:B:513:GLU:OE1	2.51	0.43
1:C:219:CYS:N	1:C:224:CYS:SG	2.90	0.43
1:C:456:THR:O	1:C:457:HIS:HB2	2.18	0.43
1:A:330:ILE:HD13	1:A:389:TRP:CE3	2.53	0.43
1:A:419:HIS:NE2	1:A:507:HIS:O	2.46	0.43
1:D:210:GLU:HB2	1:D:226:ARG:NH1	2.34	0.43
1:A:454:GLY:O	1:A:455:HIS:HB3	2.19	0.43
4:H:1:NAG:O4	4:H:2:NAG:O7	2.37	0.43
1:B:144:TRP:HB3	1:B:149:LEU:HD13	2.01	0.42
1:B:486:PHE:HA	1:B:487:ILE:HA	1.85	0.42
1:C:256:GLU:HG2	1:C:260:LYS:HE3	2.00	0.42
1:A:273:TRP:O	1:A:312:PRO:HA	2.18	0.42
1:B:140:VAL:O	1:B:143:VAL:HG22	2.20	0.42
1:B:277:ILE:HB	1:B:278:PRO:HD3	2.01	0.42
1:B:354:ASP:OD2	1:B:355:ALA:N	2.52	0.42
1:D:87:CYS:HB3	1:D:88:PRO:HD3	2.02	0.42
1:D:203:THR:HG23	1:D:482:SER:HA	2.02	0.42
1:D:273:TRP:O	1:D:312:PRO:HA	2.20	0.42
1:C:454:GLY:O	1:C:455:HIS:HB3	2.20	0.42
1:A:144:TRP:HB3	1:A:149:LEU:HD13	2.02	0.42
1:A:561:ASP:OD2	1:A:564:LEU:N	2.40	0.42
1:D:482:SER:O	1:D:574:LYS:NZ	2.48	0.42
1:B:107:VAL:O	1:B:111:GLY:N	2.39	0.42
1:C:286:SER:OG	1:C:289:ASP:OD1	2.33	0.42
1:D:454:GLY:O	1:D:455:HIS:HB3	2.20	0.41
1:A:486:PHE:HA	1:A:487:ILE:HA	1.87	0.41
1:A:559:ARG:NH1	1:A:607:HIS:O	2.53	0.41
1:C:136:PHE:O	1:C:137:GLU:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:GLU:N	1:A:105:PRO:CD	2.84	0.41
1:A:136:PHE:O	1:A:137:GLU:C	2.63	0.41
1:A:205:LEU:N	1:A:205:LEU:HD12	2.36	0.41
1:D:584:THR:N	1:D:585:PRO:HD2	2.36	0.41
1:B:273:TRP:O	1:B:312:PRO:HA	2.20	0.41
1:C:145:THR:HA	1:C:149:LEU:HB2	2.03	0.41
1:D:277:ILE:HB	1:D:278:PRO:HD3	2.03	0.41
1:B:206:HIS:O	1:B:249:ASP:HB3	2.21	0.41
1:B:584:THR:N	1:B:585:PRO:HD2	2.36	0.40
1:C:94:PHE:CZ	1:C:154:ALA:HB1	2.56	0.40
1:C:552:HIS:CE1	1:C:556:TYR:HE2	2.39	0.40
1:C:138:ASP:OD1	1:C:138:ASP:N	2.55	0.40
1:D:277:ILE:CG2	1:D:297:ILE:HG13	2.52	0.40
1:D:232:PRO:HB2	1:D:236:GLN:HB2	2.04	0.40
1:D:513:GLU:HG3	1:D:536:ARG:HG3	2.03	0.40
1:A:213:GLU:HG2	1:A:214:GLY:N	2.37	0.40
1:D:204:ASP:CG	1:D:457:HIS:CD2	3.00	0.40
1:D:348:GLU:N	1:D:349:PRO:CD	2.85	0.40
3:F:1:NAG:O4	3:F:2:NAG:O7	2.39	0.40
1:A:198:ARG:HG2	6:A:710:PO4:O1	2.20	0.40
1:A:322:VAL:C	1:A:324:GLY:H	2.30	0.40
1:B:454:GLY:O	1:B:455:HIS:HB3	2.21	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	525/538 (98%)	492 (94%)	32 (6%)	1 (0%)	43	72
1	B	525/538 (98%)	492 (94%)	32 (6%)	1 (0%)	43	72
1	C	525/538 (98%)	492 (94%)	32 (6%)	1 (0%)	43	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	525/538 (98%)	494 (94%)	30 (6%)	1 (0%)	43	72
All	All	2100/2152 (98%)	1970 (94%)	126 (6%)	4 (0%)	43	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	537	ALA
1	B	537	ALA
1	C	486	PHE
1	D	537	ALA

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	449/460 (98%)	445 (99%)	4 (1%)	70	89
1	B	449/460 (98%)	446 (99%)	3 (1%)	76	91
1	C	449/460 (98%)	443 (99%)	6 (1%)	61	86
1	D	449/460 (98%)	445 (99%)	4 (1%)	70	89
All	All	1796/1840 (98%)	1779 (99%)	17 (1%)	70	89

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	ARG
1	A	292	ARG
1	A	367	LEU
1	A	571	LEU
1	B	260	LYS
1	B	367	LEU
1	B	571	LEU
1	C	168	ILE
1	C	173	ASN
1	C	253	ARG

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Mol	Chain	Res	Type
1	C	367	LEU
1	C	393	ASN
1	C	571	LEU
1	D	146	ARG
1	D	237	LYS
1	D	367	LEU
1	D	571	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	165	HIS
1	A	173	ASN
1	A	334	GLN
1	A	409	GLN
1	A	451	GLN
1	A	497	GLN
1	A	566	GLN
1	B	334	GLN
1	B	409	GLN
1	B	576	HIS
1	B	607	HIS
1	C	334	GLN
1	C	357	HIS
1	C	521	GLN
1	D	106	ASN
1	D	409	GLN
1	D	436	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 ⓘ

16 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	0.47	0	17,19,21	0.47	0
2	NAG	E	2	2	14,14,15	0.49	0	17,19,21	0.43	0
2	BMA	E	3	2	11,11,12	0.77	0	15,15,17	0.64	0
3	NAG	F	1	1,3	14,14,15	0.59	0	17,19,21	0.88	1 (5%)
3	NAG	F	2	3	14,14,15	0.32	0	17,19,21	0.39	0
3	FUC	F	3	3	10,10,11	1.19	1 (10%)	14,14,16	1.78	4 (28%)
4	NAG	G	1	1,4	14,14,15	0.51	0	17,19,21	1.15	2 (11%)
4	NAG	G	2	4	14,14,15	0.54	0	17,19,21	0.43	0
4	NAG	H	1	1,4	14,14,15	0.29	0	17,19,21	0.45	0
4	NAG	H	2	4	14,14,15	0.29	0	17,19,21	0.41	0
2	NAG	I	1	1,2	14,14,15	0.35	0	17,19,21	0.41	0
2	NAG	I	2	2	14,14,15	1.20	1 (7%)	17,19,21	1.07	1 (5%)
2	BMA	I	3	2	11,11,12	0.66	0	15,15,17	0.75	0
3	NAG	J	1	1,3	14,14,15	0.97	1 (7%)	17,19,21	1.10	2 (11%)
3	NAG	J	2	3	14,14,15	0.42	0	17,19,21	0.46	0
3	FUC	J	3	3	10,10,11	0.99	1 (10%)	14,14,16	1.18	1 (7%)

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	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	BMA	E	3	2	-	2/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	FUC	F	3	3	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	NAG	H	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1
2	BMA	I	3	2	-	1/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	FUC	J	3	3	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	2	NAG	O5-C1	-3.91	1.37	1.43
3	J	1	NAG	O5-C1	-3.52	1.37	1.43
3	F	3	FUC	C1-C2	2.81	1.58	1.52
3	J	3	FUC	C1-C2	2.13	1.57	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	3	FUC	C1-O5-C5	3.78	121.88	112.97
3	F	3	FUC	C1-C2-C3	3.64	114.95	109.64
2	I	2	NAG	C4-C3-C2	2.90	115.27	111.02
3	J	3	FUC	C1-C2-C3	2.82	113.75	109.64
3	F	1	NAG	C1-O5-C5	2.73	115.84	112.19
4	G	1	NAG	O4-C4-C3	-2.69	104.04	110.38
3	F	3	FUC	O5-C5-C4	2.55	114.14	109.55
4	G	1	NAG	C1-O5-C5	2.41	115.42	112.19
3	J	1	NAG	C4-C3-C2	2.35	114.46	111.02
3	J	1	NAG	O4-C4-C3	-2.26	105.05	110.38
3	F	3	FUC	O5-C1-C2	2.25	116.15	110.79

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	NAG	O5-C5-C6-O6
4	G	2	NAG	C4-C5-C6-O6

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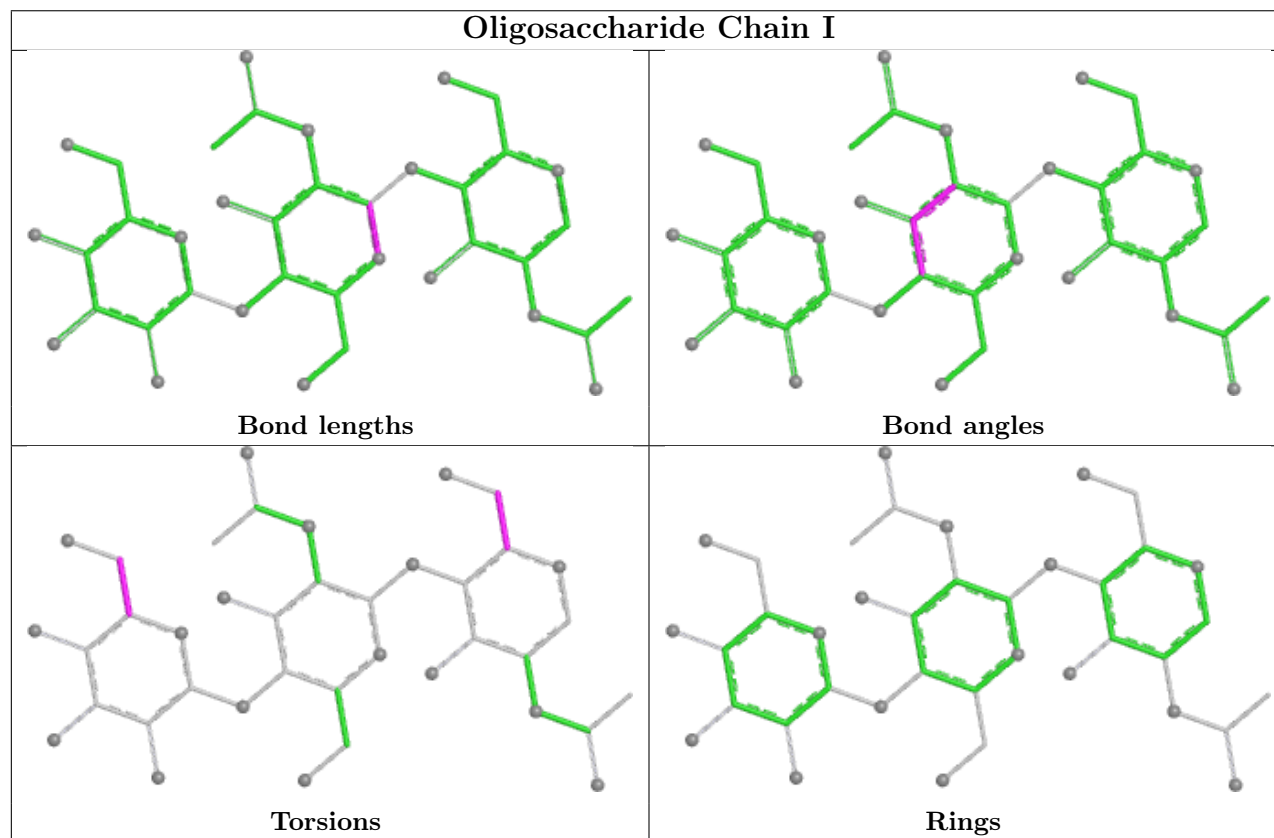
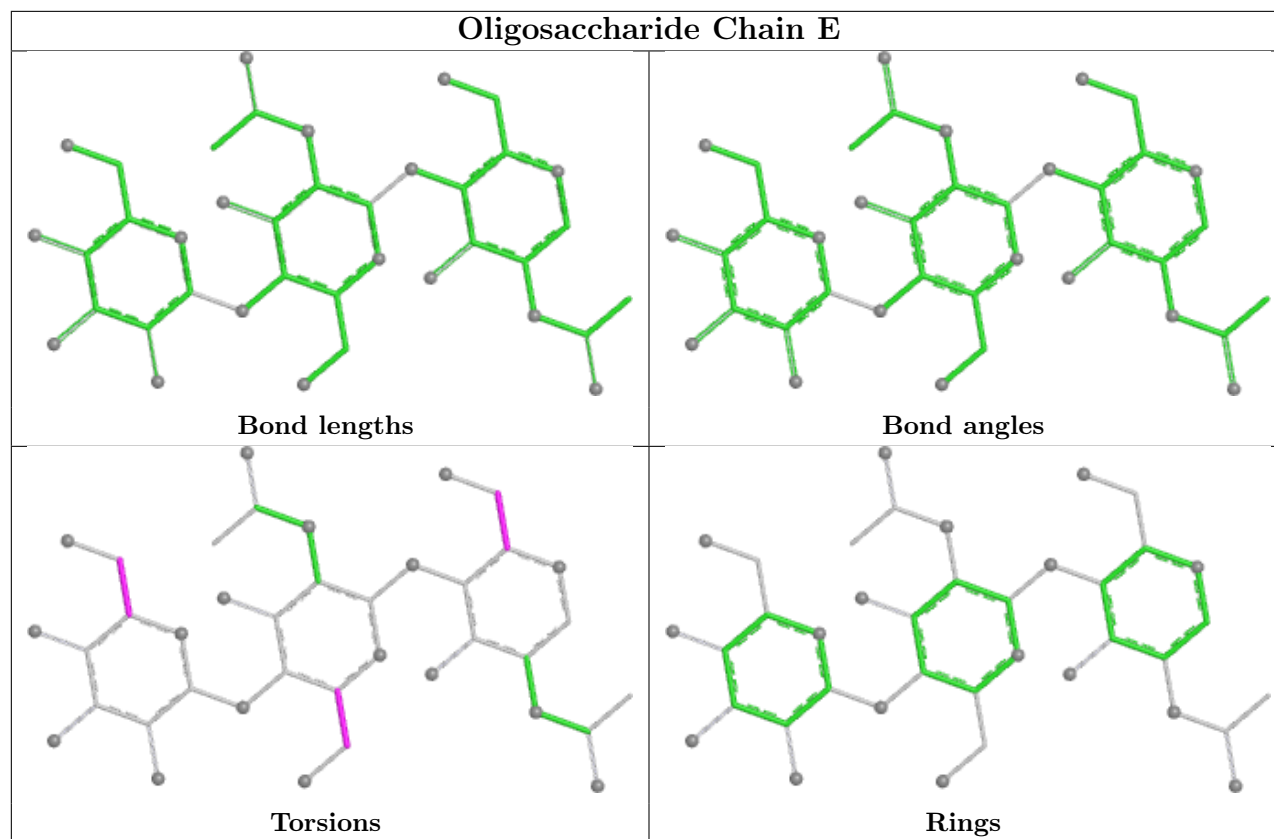
Mol	Chain	Res	Type	Atoms
3	F	1	NAG	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
4	H	2	NAG	O5-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
4	H	2	NAG	C4-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
2	E	3	BMA	C4-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
2	I	3	BMA	O5-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
2	I	1	NAG	C4-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
2	I	1	NAG	O5-C5-C6-O6

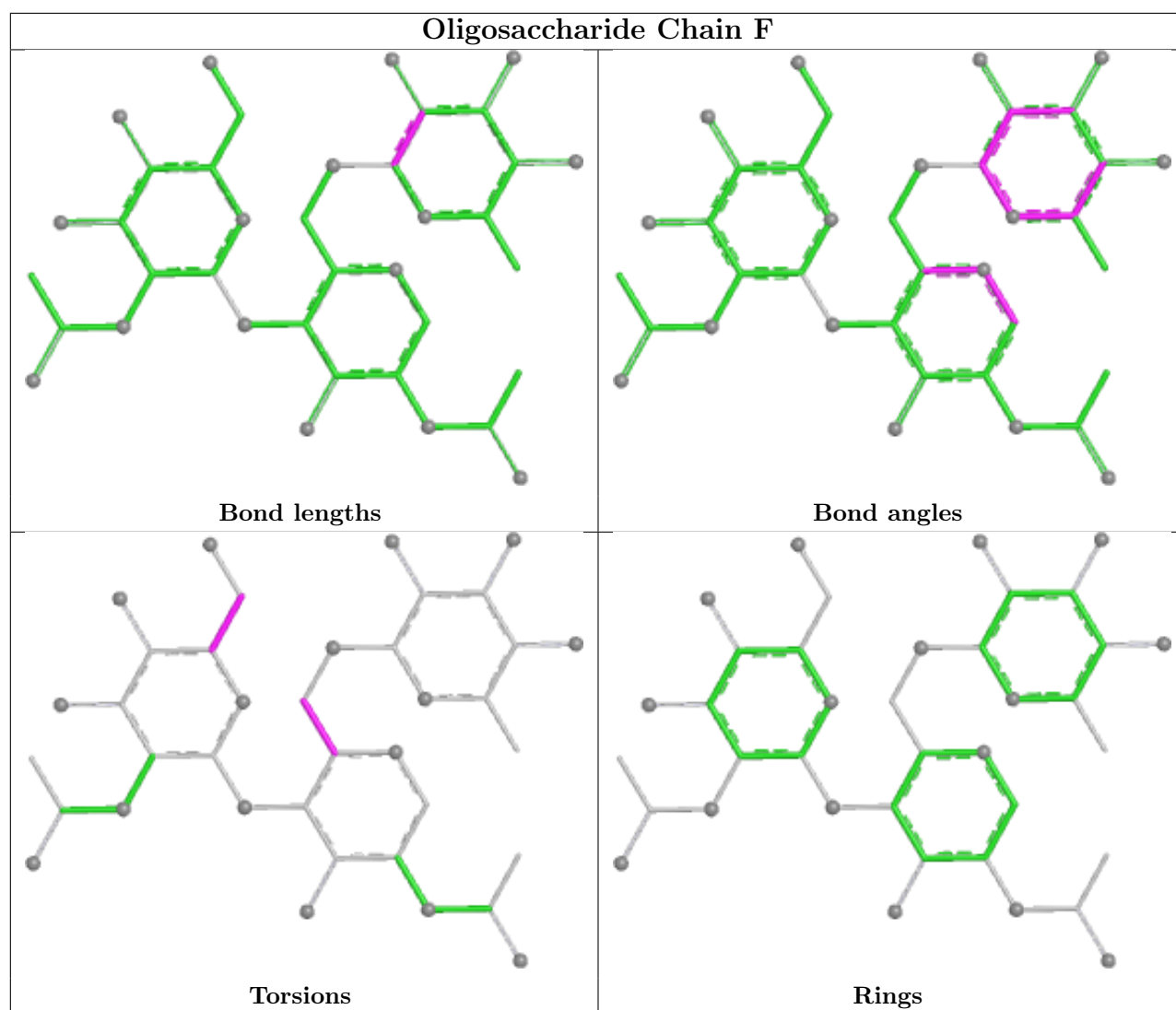
There are no ring outliers.

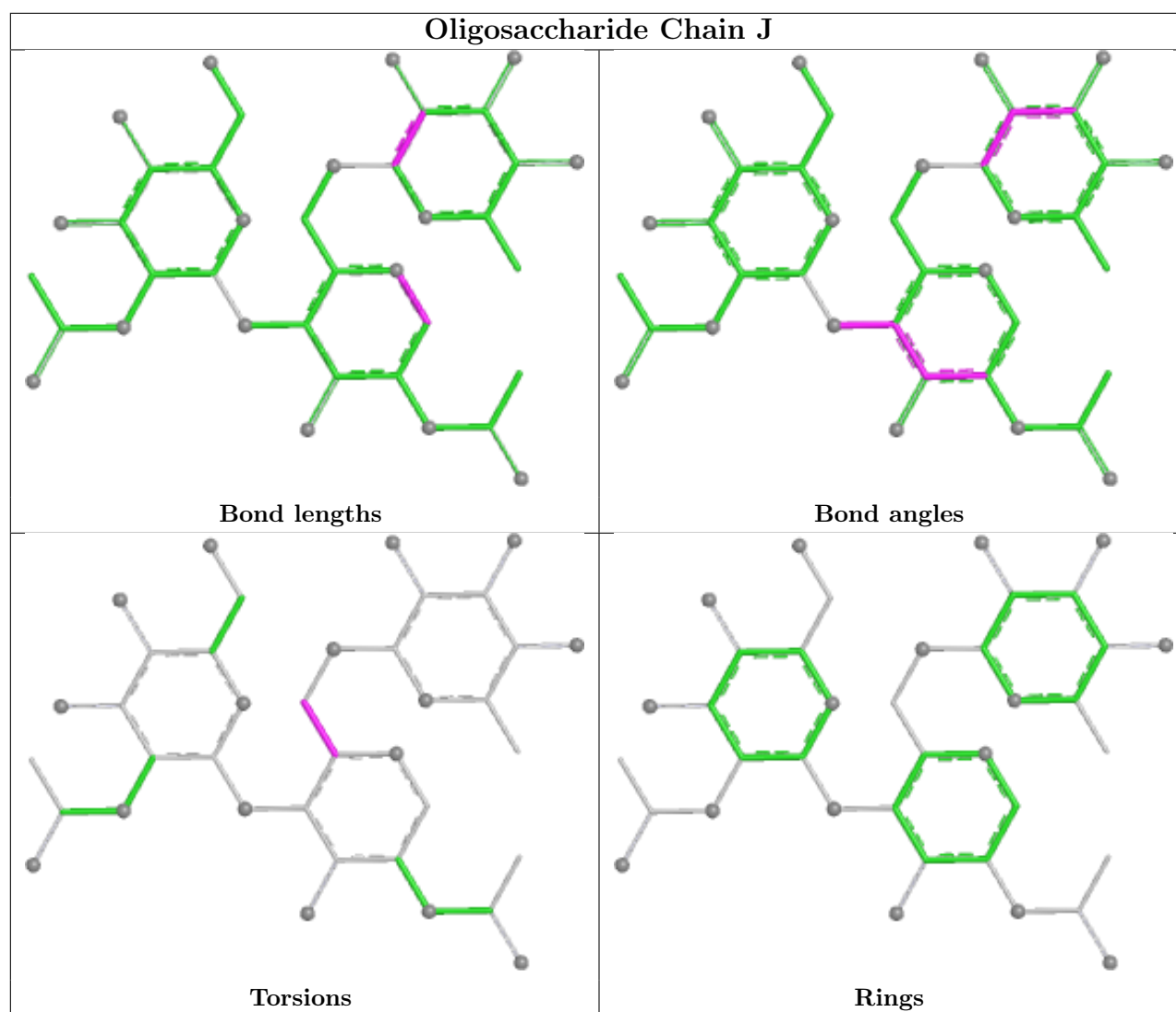
6 monomers are involved in 3 short contacts:

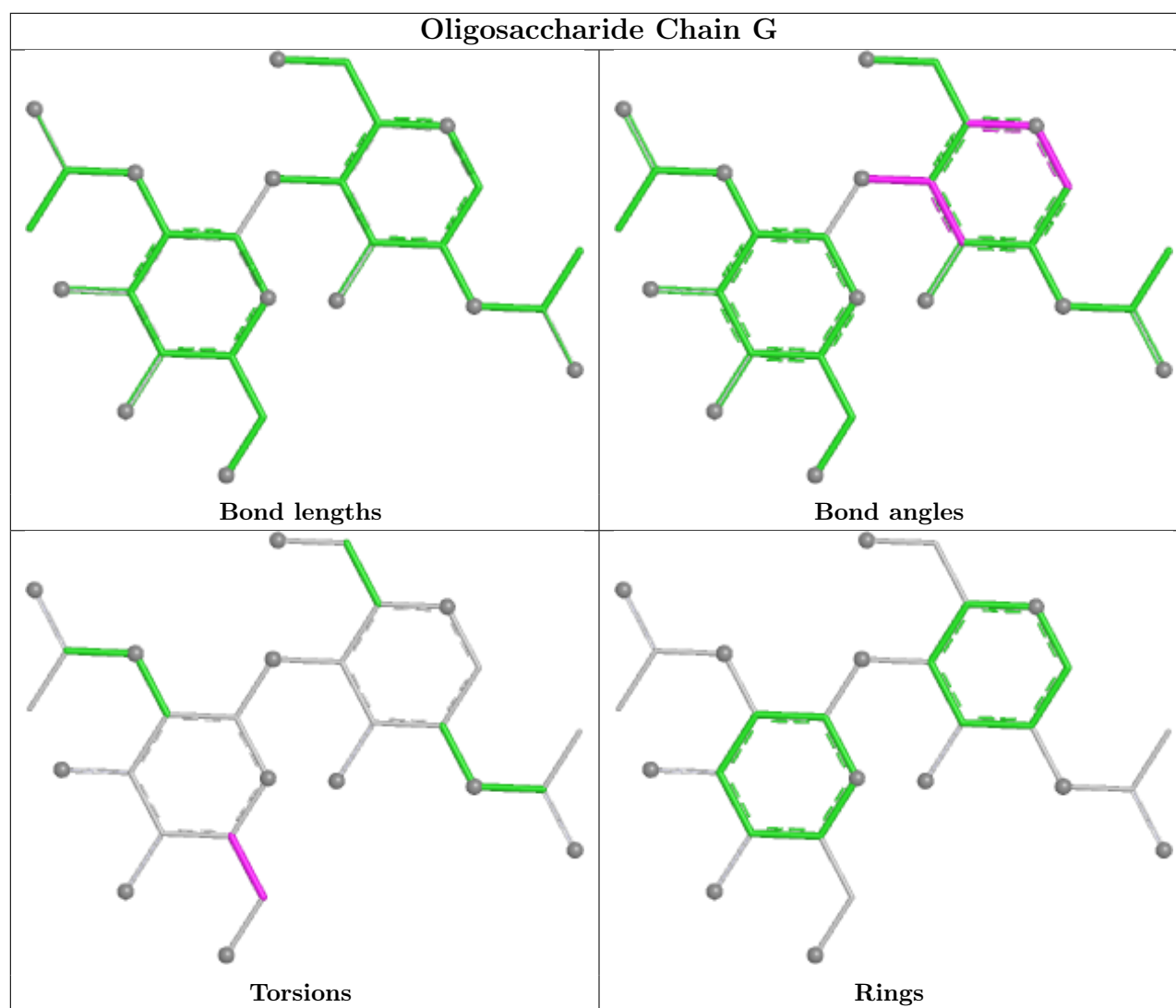
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	2	NAG	1	0
4	G	2	NAG	1	0
3	F	1	NAG	1	0
4	H	1	NAG	1	0
4	G	1	NAG	1	0
3	F	2	NAG	1	0

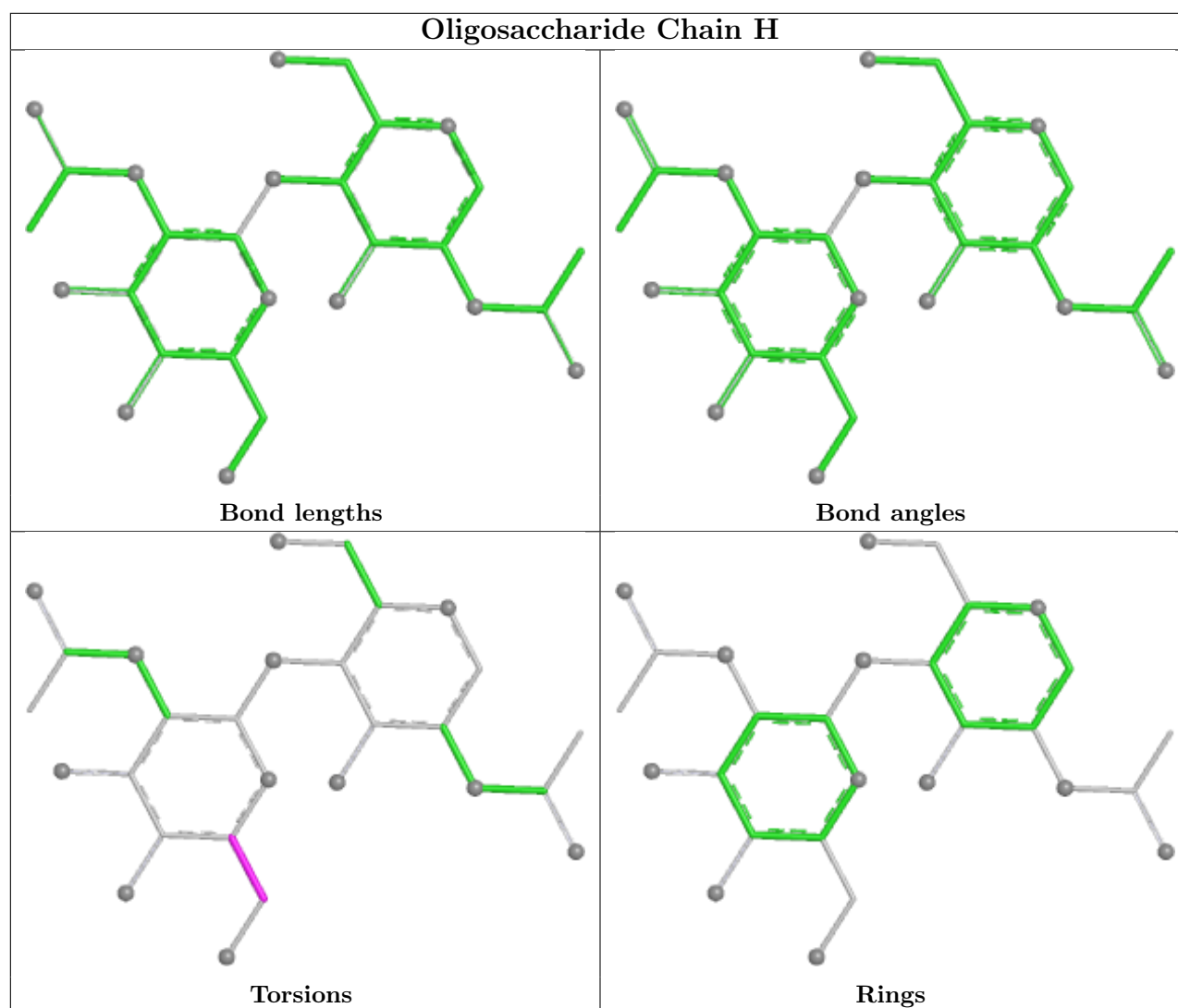
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 13 are monoatomic - leaving 11 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	PO4	C	706	5	4,4,4	0.93	0	6,6,6	0.62	0
9	NAG	C	705	1	14,14,15	0.52	0	17,19,21	0.44	0
6	PO4	A	709	5	4,4,4	0.99	0	6,6,6	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PO4	B	707	-	4,4,4	0.96	0	6,6,6	0.45	0
6	PO4	A	711	-	4,4,4	0.98	0	6,6,6	0.47	0
9	NAG	B	705	1	14,14,15	0.29	0	17,19,21	0.34	0
6	PO4	A	710	-	4,4,4	0.96	0	6,6,6	0.52	0
6	PO4	B	706	5	4,4,4	0.92	0	6,6,6	0.59	0
8	6E0	D	711	-	21,21,21	2.30	3 (14%)	23,23,23	0.77	1 (4%)
8	6E0	A	714	-	21,21,21	2.28	3 (14%)	23,23,23	0.98	1 (4%)
6	PO4	D	709	5	4,4,4	0.98	0	6,6,6	0.47	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
9	NAG	C	705	1	-	3/6/23/26	0/1/1/1
9	NAG	B	705	1	-	0/6/23/26	0/1/1/1
8	6E0	D	711	-	-	14/19/19/19	-
8	6E0	A	714	-	-	6/19/19/19	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	711	6E0	P19-C18	7.82	1.87	1.78
8	A	714	6E0	P19-C18	7.73	1.87	1.78
8	D	711	6E0	P19-O21	4.83	1.65	1.55
8	A	714	6E0	P19-O22	4.74	1.65	1.55
8	D	711	6E0	P19-O22	4.72	1.65	1.55
8	A	714	6E0	P19-O21	4.67	1.65	1.55

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	714	6E0	P19-C18-C17	-3.76	110.31	114.94
8	D	711	6E0	P19-C18-C17	-2.30	112.11	114.94

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	D	711	6E0	C17-C18-P19-O20
8	D	711	6E0	C17-C18-P19-O21
8	D	711	6E0	C17-C18-P19-O22
9	C	705	NAG	C4-C5-C6-O6
9	C	705	NAG	O5-C5-C6-O6
8	D	711	6E0	C12-C13-C14-C15
8	A	714	6E0	C10-C11-C12-C13
8	D	711	6E0	C10-C11-C12-C13
8	D	711	6E0	C08-C09-C10-C11
8	D	711	6E0	C16-C17-C18-P19
8	A	714	6E0	C07-C08-C09-C10
8	A	714	6E0	C05-C06-C07-C08
8	A	714	6E0	C11-C12-C13-C14
8	D	711	6E0	C09-C10-C11-C12
9	C	705	NAG	C3-C2-N2-C7
8	D	711	6E0	C11-C12-C13-C14
8	D	711	6E0	C01-C02-C03-C04
8	D	711	6E0	C02-C03-C04-C05
8	A	714	6E0	C01-C02-C03-C04
8	A	714	6E0	C03-C04-C05-C06
8	D	711	6E0	C14-C15-C16-C17
8	D	711	6E0	C04-C05-C06-C07
8	D	711	6E0	C06-C07-C08-C09

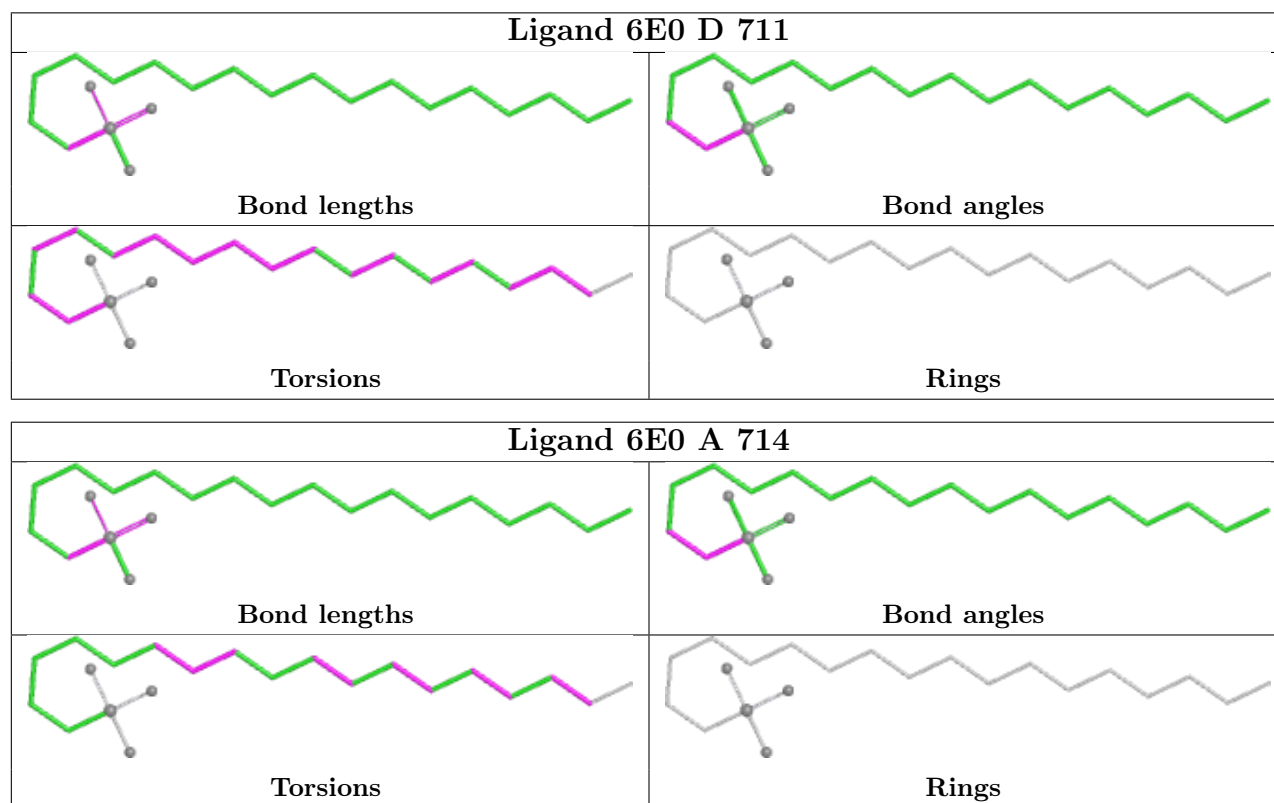
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	C	705	NAG	2	0
6	B	707	PO4	1	0
6	A	710	PO4	2	0
6	B	706	PO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	527/538 (97%)	-1.56	1 (0%) 91 88	27, 58, 92, 156	0
1	B	527/538 (97%)	-1.54	0 100 100	29, 62, 97, 125	0
1	C	527/538 (97%)	-1.53	1 (0%) 91 88	24, 60, 103, 152	0
1	D	527/538 (97%)	-1.53	0 100 100	29, 61, 99, 139	0
All	All	2108/2152 (97%)	-1.54	2 (0%) 92 90	24, 61, 98, 156	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	562	GLU	3.9
1	A	234	ASN	2.3

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.

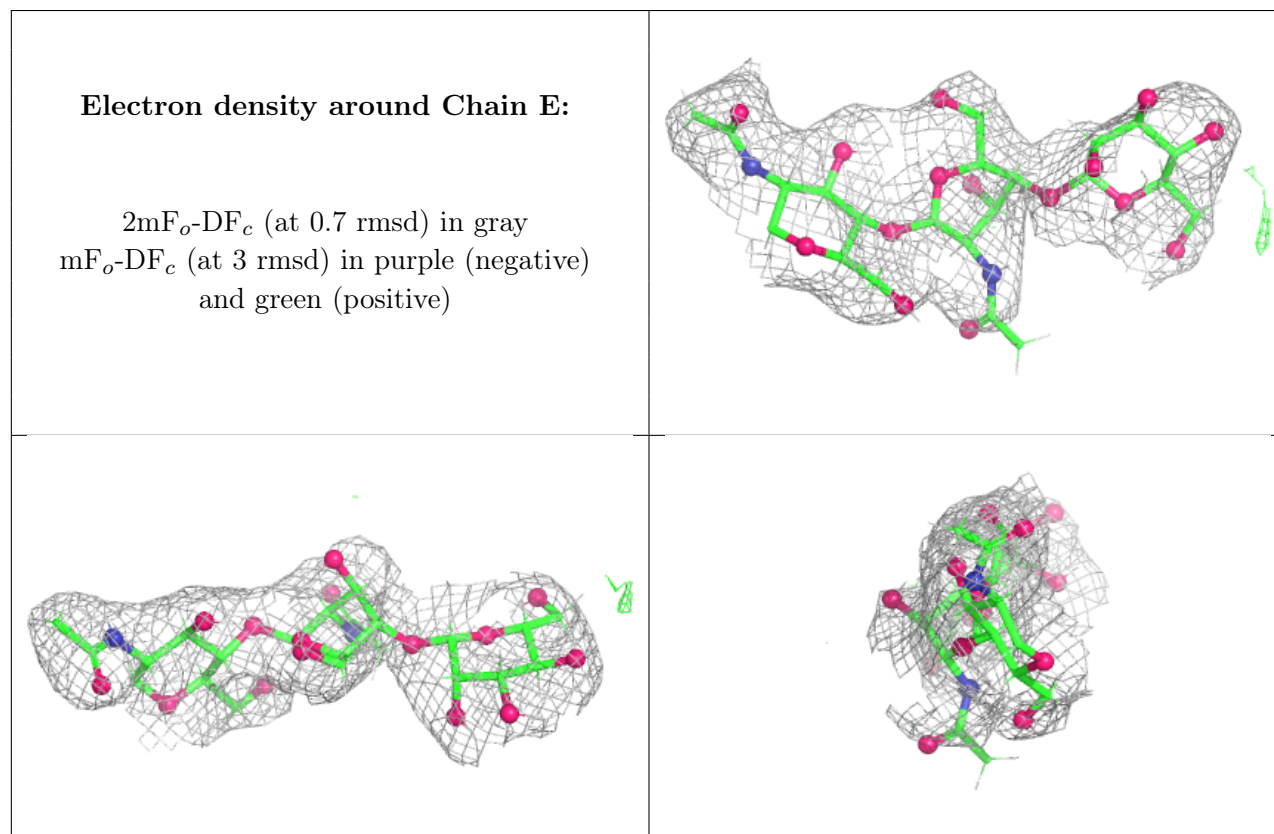
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BMA	E	3	11/12	0.98	0.04	80,98,119,123	0
4	NAG	G	2	14/15	0.98	0.04	66,92,115,121	0
4	NAG	H	2	14/15	0.98	0.05	61,93,113,124	0
2	NAG	I	2	14/15	0.99	0.03	39,69,88,102	0
2	BMA	I	3	11/12	0.99	0.04	69,93,112,117	0

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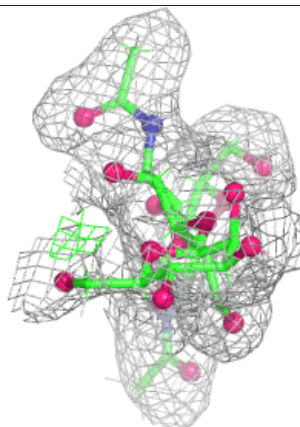
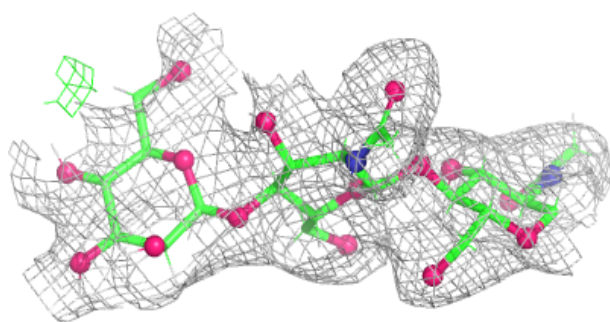
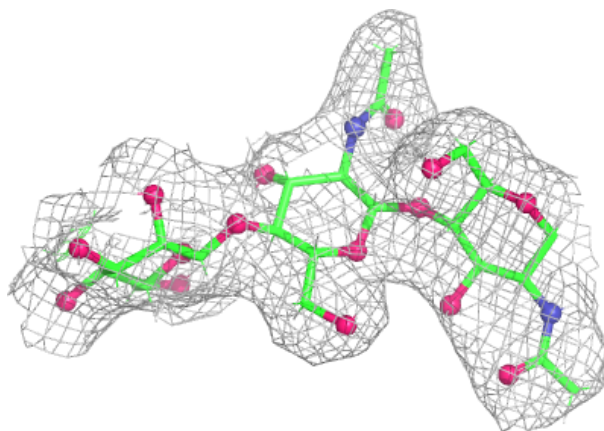
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	F	1	14/15	0.99	0.03	81,99,119,129	0
3	NAG	F	2	14/15	0.99	0.06	78,97,117,123	0
3	FUC	F	3	10/11	0.99	0.04	67,92,106,115	0
3	NAG	J	1	14/15	0.99	0.03	72,87,98,108	0
3	NAG	J	2	14/15	0.99	0.04	71,91,112,124	0
3	FUC	J	3	10/11	0.99	0.03	73,84,95,100	0
4	NAG	G	1	14/15	0.99	0.03	41,69,87,90	0
2	NAG	E	2	14/15	0.99	0.05	80,92,108,112	0
4	NAG	H	1	14/15	0.99	0.03	58,81,102,105	0
2	NAG	I	1	14/15	0.99	0.04	47,60,72,80	0
2	NAG	E	1	14/15	1.00	0.03	44,66,85,95	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.



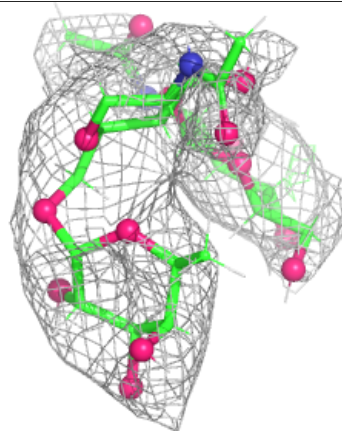
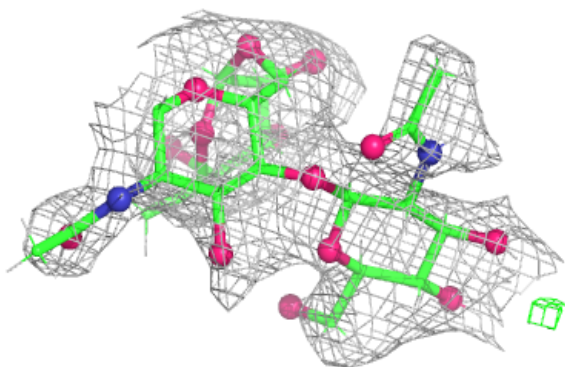
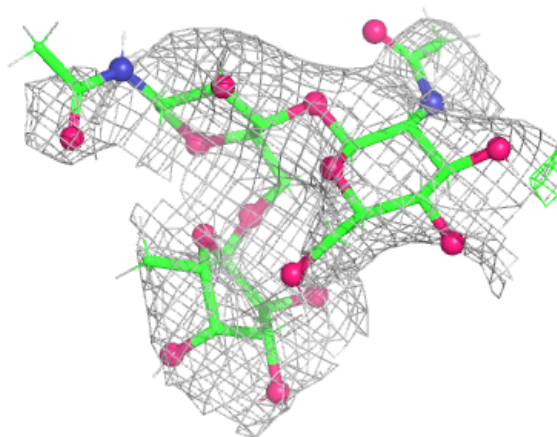
Electron density around Chain I:

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



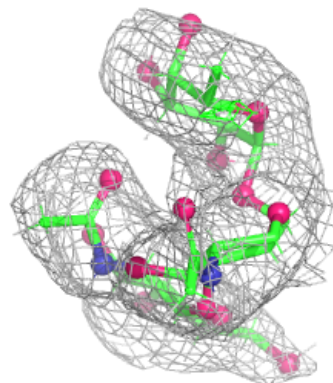
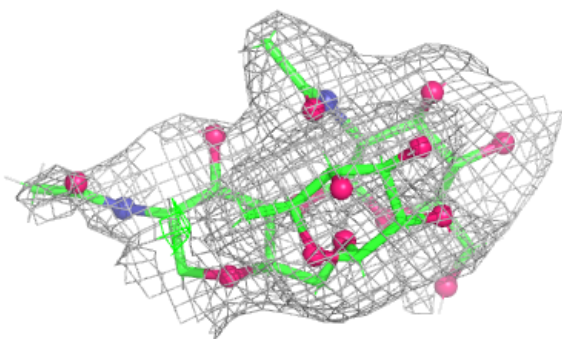
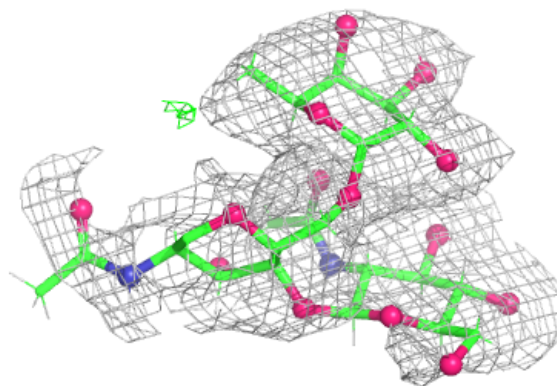
Electron density around Chain F:

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

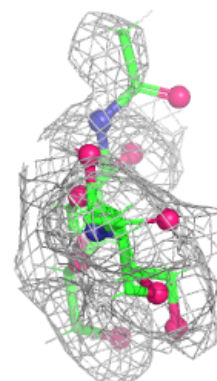
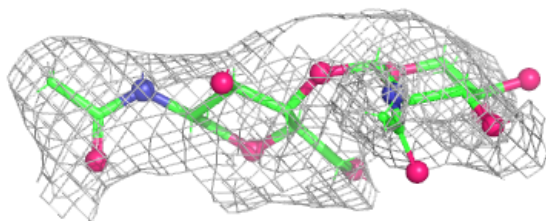
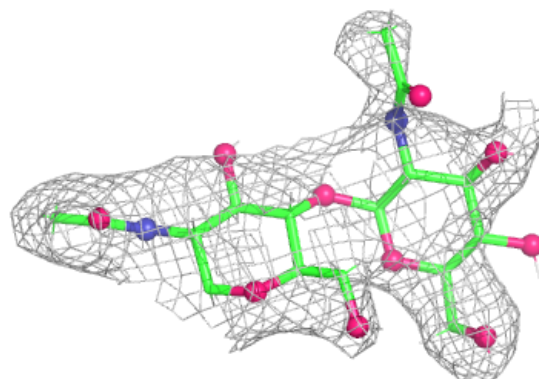


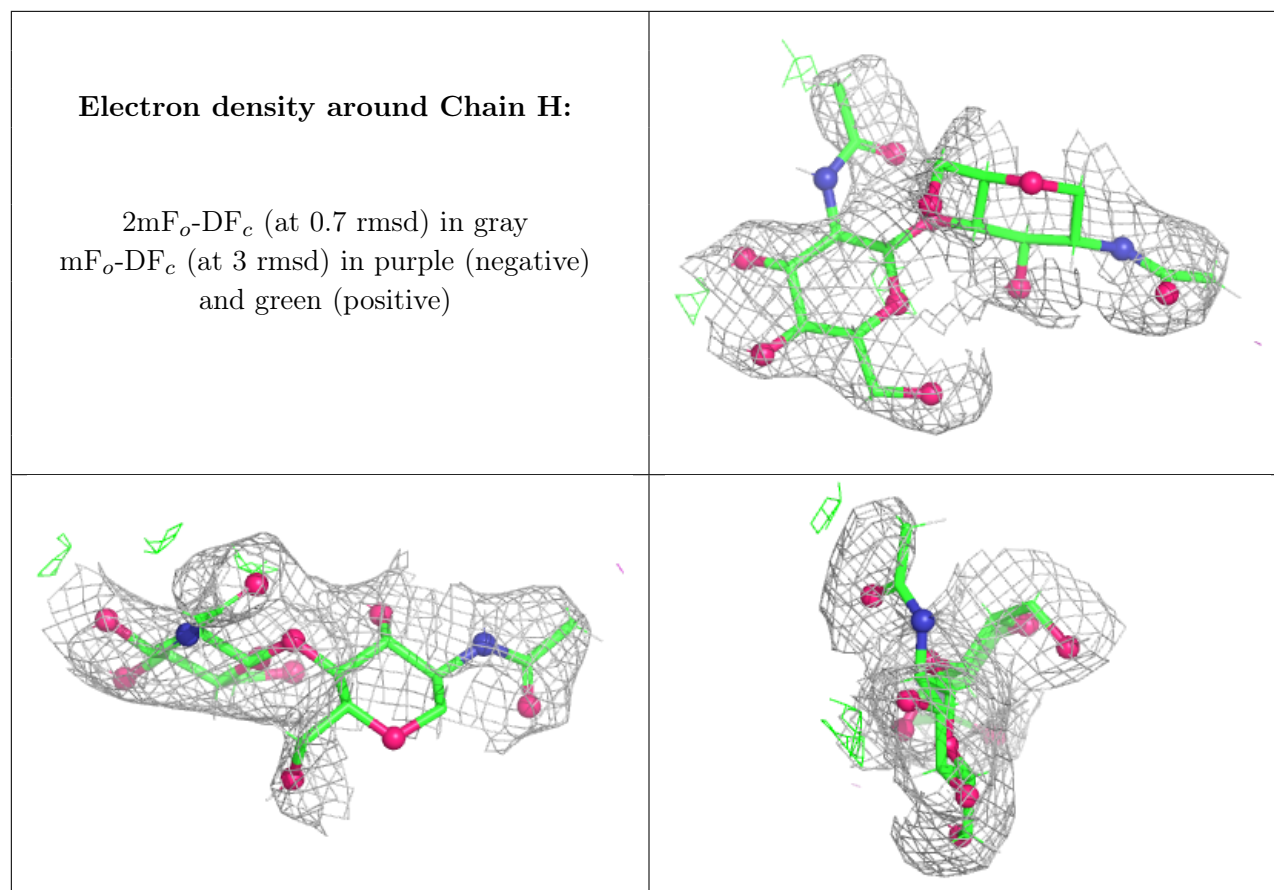
Electron density around Chain J:

$2mF_o-DF_c$ (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
9	NAG	C	705	14/15	0.97	0.05	73,100,119,123	0
6	PO4	A	710	5/5	0.99	0.04	55,64,82,86	0
6	PO4	B	707	5/5	0.99	0.03	63,74,92,102	0
7	CL	A	712	1/1	0.99	0.05	58,58,58,58	0
8	6E0	A	714	22/22	0.99	0.06	52,71,87,133	0
8	6E0	D	711	22/22	0.99	0.06	42,68,90,127	0
9	NAG	B	705	14/15	0.99	0.03	54,82,92,100	0
6	PO4	A	709	5/5	0.99	0.05	46,51,59,60	0
5	ZN	A	701	1/1	1.00	0.01	37,37,37,37	0
5	ZN	A	702	1/1	1.00	0.02	45,45,45,45	0
6	PO4	A	711	5/5	1.00	0.03	21,50,69,71	0
6	PO4	B	706	5/5	1.00	0.05	47,50,74,87	0
5	ZN	B	701	1/1	1.00	0.01	56,56,56,56	0

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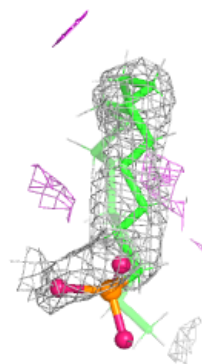
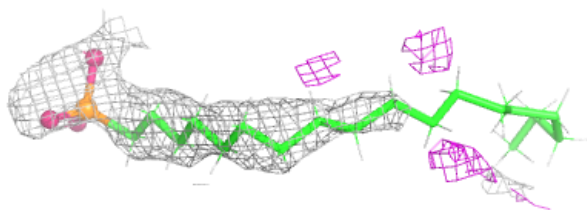
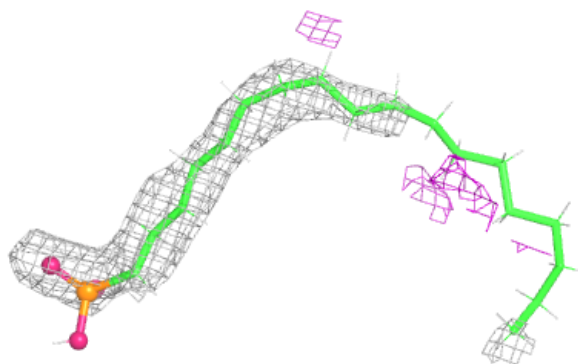
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	PO4	C	706	5/5	1.00	0.03	24,32,39,40	0
6	PO4	D	709	5/5	1.00	0.04	36,45,56,56	0
5	ZN	B	702	1/1	1.00	0.01	42,42,42,42	0
7	CL	A	713	1/1	1.00	0.04	55,55,55,55	0
7	CL	B	708	1/1	1.00	0.07	50,50,50,50	0
7	CL	C	707	1/1	1.00	0.03	44,44,44,44	0
7	CL	D	710	1/1	1.00	0.02	26,26,26,26	0
5	ZN	C	701	1/1	1.00	0.01	26,26,26,26	0
5	ZN	C	702	1/1	1.00	0.01	44,44,44,44	0
5	ZN	D	701	1/1	1.00	0.01	42,42,42,42	0
5	ZN	D	702	1/1	1.00	0.01	35,35,35,35	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.

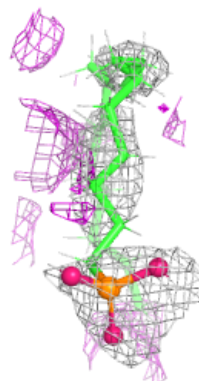
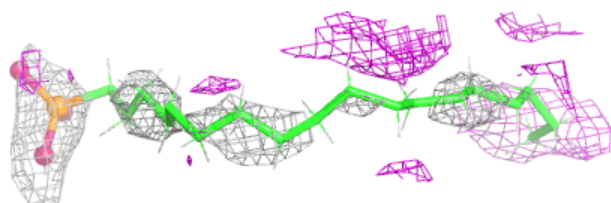
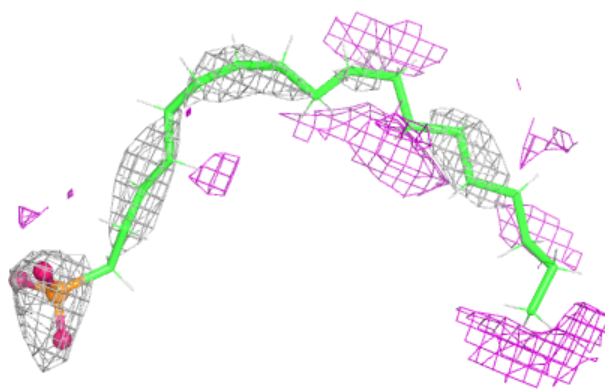
Electron density around 6E0 A 714:

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 6E0 D 711:

$2mF_o - DF_c$ (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.