



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:39 PM UTC

PDB ID : 8V07 / pdb_00008v07
Title : Crystal structure of mouse PLD3 co-crystallized with 5'Pi-ssDNA for 30 days
Authors : Yuan, M.; Wilson, I.A.
Deposited on : 2023-11-17
Resolution : 1.99 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

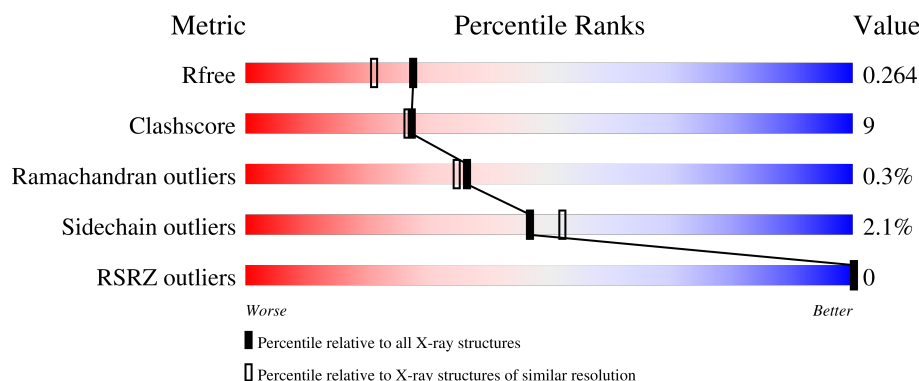
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	467	
1	B	467	
1	C	467	
1	D	467	
2	E	7	

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Mol	Chain	Length	Quality of chain
2	H	7	 71%29%
3	F	2	 100%
3	G	2	 100%
3	J	2	 100%
3	K	2	 50%50%
4	I	4	 75%25%

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
8	PO4	D	503	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 13786 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 5'-3' exonuclease PLD3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	408	Total	C	N	O	S	0	0	0
			3194	2020	556	601	17			
1	A	408	Total	C	N	O	S	0	2	0
			3217	2034	562	604	17			
1	C	408	Total	C	N	O	S	0	0	0
			3197	2022	559	599	17			
1	D	407	Total	C	N	O	S	0	2	0
			3206	2028	561	600	17			

There are 164 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	22	HIS	-	expression tag	UNP O35405
B	23	HIS	-	expression tag	UNP O35405
B	24	HIS	-	expression tag	UNP O35405
B	25	HIS	-	expression tag	UNP O35405
B	26	HIS	-	expression tag	UNP O35405
B	27	HIS	-	expression tag	UNP O35405
B	28	GLY	-	expression tag	UNP O35405
B	29	PRO	-	expression tag	UNP O35405
B	30	LEU	-	expression tag	UNP O35405
B	31	VAL	-	expression tag	UNP O35405
B	32	ASP	-	expression tag	UNP O35405
B	33	VAL	-	expression tag	UNP O35405
B	34	ALA	-	expression tag	UNP O35405
B	35	SER	-	expression tag	UNP O35405
B	36	ASN	-	expression tag	UNP O35405
B	37	GLU	-	expression tag	UNP O35405
B	38	GLN	-	expression tag	UNP O35405
B	39	LYS	-	expression tag	UNP O35405
B	40	LEU	-	expression tag	UNP O35405
B	41	ILE	-	expression tag	UNP O35405
B	42	SER	-	expression tag	UNP O35405

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Chain	Residue	Modelled	Actual	Comment	Reference
B	43	GLU	-	expression tag	UNP O35405
B	44	GLU	-	expression tag	UNP O35405
B	45	ASP	-	expression tag	UNP O35405
B	46	LEU	-	expression tag	UNP O35405
B	47	ALA	-	expression tag	UNP O35405
B	48	SER	-	expression tag	UNP O35405
B	49	MET	-	expression tag	UNP O35405
B	50	THR	-	expression tag	UNP O35405
B	51	GLY	-	expression tag	UNP O35405
B	52	GLY	-	expression tag	UNP O35405
B	53	GLN	-	expression tag	UNP O35405
B	54	GLN	-	expression tag	UNP O35405
B	55	MET	-	expression tag	UNP O35405
B	56	GLY	-	expression tag	UNP O35405
B	57	ARG	-	expression tag	UNP O35405
B	58	ASP	-	expression tag	UNP O35405
B	59	ILE	-	expression tag	UNP O35405
B	60	GLU	-	expression tag	UNP O35405
B	61	GLY	-	expression tag	UNP O35405
B	62	ARG	-	expression tag	UNP O35405
A	22	HIS	-	expression tag	UNP O35405
A	23	HIS	-	expression tag	UNP O35405
A	24	HIS	-	expression tag	UNP O35405
A	25	HIS	-	expression tag	UNP O35405
A	26	HIS	-	expression tag	UNP O35405
A	27	HIS	-	expression tag	UNP O35405
A	28	GLY	-	expression tag	UNP O35405
A	29	PRO	-	expression tag	UNP O35405
A	30	LEU	-	expression tag	UNP O35405
A	31	VAL	-	expression tag	UNP O35405
A	32	ASP	-	expression tag	UNP O35405
A	33	VAL	-	expression tag	UNP O35405
A	34	ALA	-	expression tag	UNP O35405
A	35	SER	-	expression tag	UNP O35405
A	36	ASN	-	expression tag	UNP O35405
A	37	GLU	-	expression tag	UNP O35405
A	38	GLN	-	expression tag	UNP O35405
A	39	LYS	-	expression tag	UNP O35405
A	40	LEU	-	expression tag	UNP O35405
A	41	ILE	-	expression tag	UNP O35405
A	42	SER	-	expression tag	UNP O35405
A	43	GLU	-	expression tag	UNP O35405

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Chain	Residue	Modelled	Actual	Comment	Reference
A	44	GLU	-	expression tag	UNP O35405
A	45	ASP	-	expression tag	UNP O35405
A	46	LEU	-	expression tag	UNP O35405
A	47	ALA	-	expression tag	UNP O35405
A	48	SER	-	expression tag	UNP O35405
A	49	MET	-	expression tag	UNP O35405
A	50	THR	-	expression tag	UNP O35405
A	51	GLY	-	expression tag	UNP O35405
A	52	GLY	-	expression tag	UNP O35405
A	53	GLN	-	expression tag	UNP O35405
A	54	GLN	-	expression tag	UNP O35405
A	55	MET	-	expression tag	UNP O35405
A	56	GLY	-	expression tag	UNP O35405
A	57	ARG	-	expression tag	UNP O35405
A	58	ASP	-	expression tag	UNP O35405
A	59	ILE	-	expression tag	UNP O35405
A	60	GLU	-	expression tag	UNP O35405
A	61	GLY	-	expression tag	UNP O35405
A	62	ARG	-	expression tag	UNP O35405
C	22	HIS	-	expression tag	UNP O35405
C	23	HIS	-	expression tag	UNP O35405
C	24	HIS	-	expression tag	UNP O35405
C	25	HIS	-	expression tag	UNP O35405
C	26	HIS	-	expression tag	UNP O35405
C	27	HIS	-	expression tag	UNP O35405
C	28	GLY	-	expression tag	UNP O35405
C	29	PRO	-	expression tag	UNP O35405
C	30	LEU	-	expression tag	UNP O35405
C	31	VAL	-	expression tag	UNP O35405
C	32	ASP	-	expression tag	UNP O35405
C	33	VAL	-	expression tag	UNP O35405
C	34	ALA	-	expression tag	UNP O35405
C	35	SER	-	expression tag	UNP O35405
C	36	ASN	-	expression tag	UNP O35405
C	37	GLU	-	expression tag	UNP O35405
C	38	GLN	-	expression tag	UNP O35405
C	39	LYS	-	expression tag	UNP O35405
C	40	LEU	-	expression tag	UNP O35405
C	41	ILE	-	expression tag	UNP O35405
C	42	SER	-	expression tag	UNP O35405
C	43	GLU	-	expression tag	UNP O35405
C	44	GLU	-	expression tag	UNP O35405

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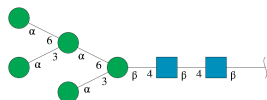
Chain	Residue	Modelled	Actual	Comment	Reference
C	45	ASP	-	expression tag	UNP O35405
C	46	LEU	-	expression tag	UNP O35405
C	47	ALA	-	expression tag	UNP O35405
C	48	SER	-	expression tag	UNP O35405
C	49	MET	-	expression tag	UNP O35405
C	50	THR	-	expression tag	UNP O35405
C	51	GLY	-	expression tag	UNP O35405
C	52	GLY	-	expression tag	UNP O35405
C	53	GLN	-	expression tag	UNP O35405
C	54	GLN	-	expression tag	UNP O35405
C	55	MET	-	expression tag	UNP O35405
C	56	GLY	-	expression tag	UNP O35405
C	57	ARG	-	expression tag	UNP O35405
C	58	ASP	-	expression tag	UNP O35405
C	59	ILE	-	expression tag	UNP O35405
C	60	GLU	-	expression tag	UNP O35405
C	61	GLY	-	expression tag	UNP O35405
C	62	ARG	-	expression tag	UNP O35405
D	22	HIS	-	expression tag	UNP O35405
D	23	HIS	-	expression tag	UNP O35405
D	24	HIS	-	expression tag	UNP O35405
D	25	HIS	-	expression tag	UNP O35405
D	26	HIS	-	expression tag	UNP O35405
D	27	HIS	-	expression tag	UNP O35405
D	28	GLY	-	expression tag	UNP O35405
D	29	PRO	-	expression tag	UNP O35405
D	30	LEU	-	expression tag	UNP O35405
D	31	VAL	-	expression tag	UNP O35405
D	32	ASP	-	expression tag	UNP O35405
D	33	VAL	-	expression tag	UNP O35405
D	34	ALA	-	expression tag	UNP O35405
D	35	SER	-	expression tag	UNP O35405
D	36	ASN	-	expression tag	UNP O35405
D	37	GLU	-	expression tag	UNP O35405
D	38	GLN	-	expression tag	UNP O35405
D	39	LYS	-	expression tag	UNP O35405
D	40	LEU	-	expression tag	UNP O35405
D	41	ILE	-	expression tag	UNP O35405
D	42	SER	-	expression tag	UNP O35405
D	43	GLU	-	expression tag	UNP O35405
D	44	GLU	-	expression tag	UNP O35405
D	45	ASP	-	expression tag	UNP O35405

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Chain	Residue	Modelled	Actual	Comment	Reference
D	46	LEU	-	expression tag	UNP O35405
D	47	ALA	-	expression tag	UNP O35405
D	48	SER	-	expression tag	UNP O35405
D	49	MET	-	expression tag	UNP O35405
D	50	THR	-	expression tag	UNP O35405
D	51	GLY	-	expression tag	UNP O35405
D	52	GLY	-	expression tag	UNP O35405
D	53	GLN	-	expression tag	UNP O35405
D	54	GLN	-	expression tag	UNP O35405
D	55	MET	-	expression tag	UNP O35405
D	56	GLY	-	expression tag	UNP O35405
D	57	ARG	-	expression tag	UNP O35405
D	58	ASP	-	expression tag	UNP O35405
D	59	ILE	-	expression tag	UNP O35405
D	60	GLU	-	expression tag	UNP O35405
D	61	GLY	-	expression tag	UNP O35405
D	62	ARG	-	expression tag	UNP O35405

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]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	7	Total	C	N	O	0	0	0
			83	46	2	35			
2	H	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



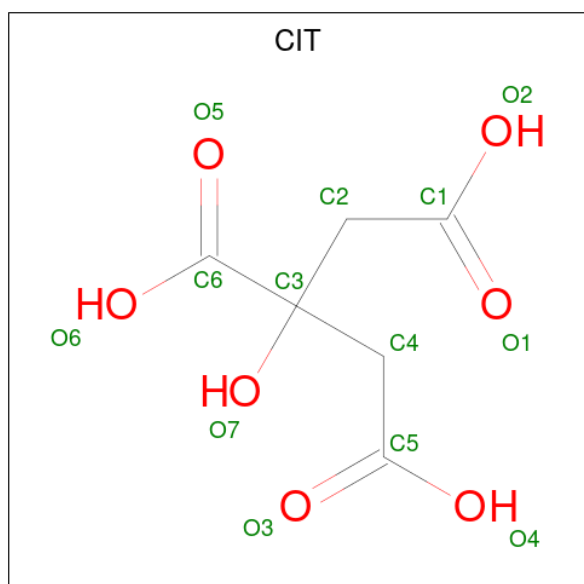
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	K	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



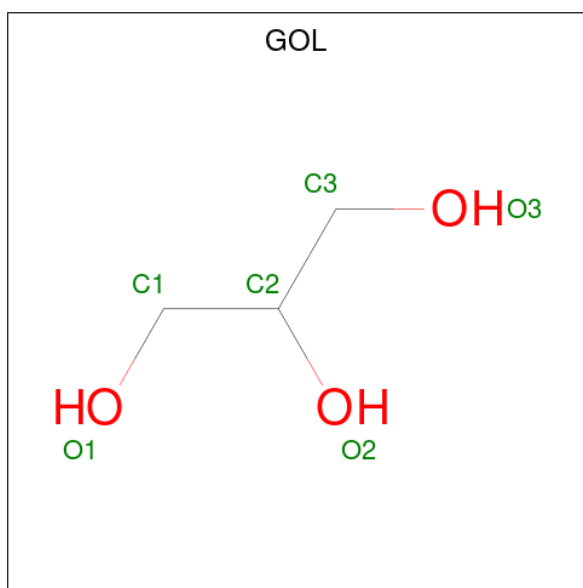
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).



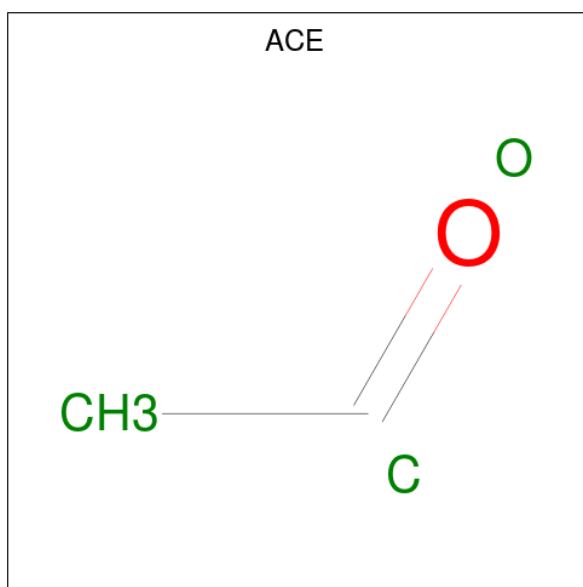
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



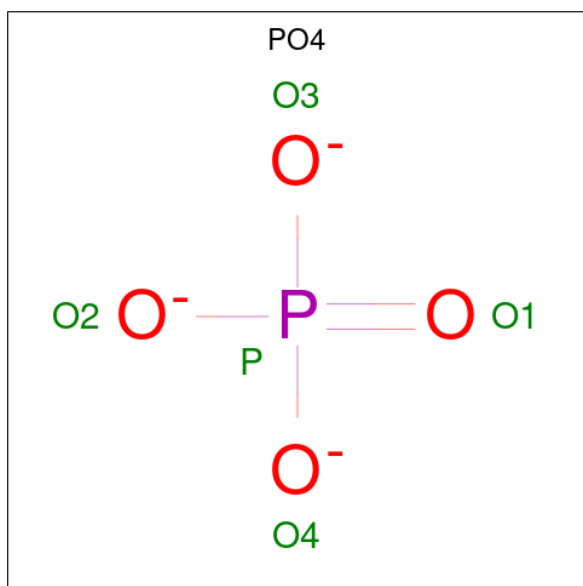
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is ACETYL GROUP (CCD ID: ACE) (formula: C_2H_4O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			3	2	1		

- Molecule 8 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



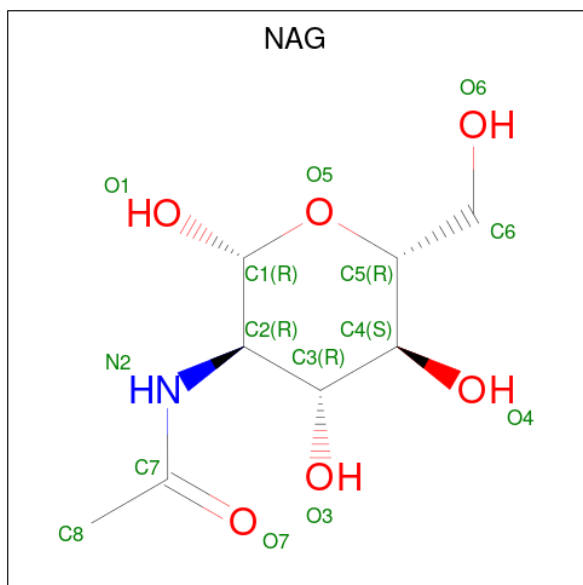
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	O	P	0	0
			5	4	1		
8	A	1	Total	O	P	0	0
			5	4	1		
8	C	1	Total	O	P	0	0
			5	4	1		

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

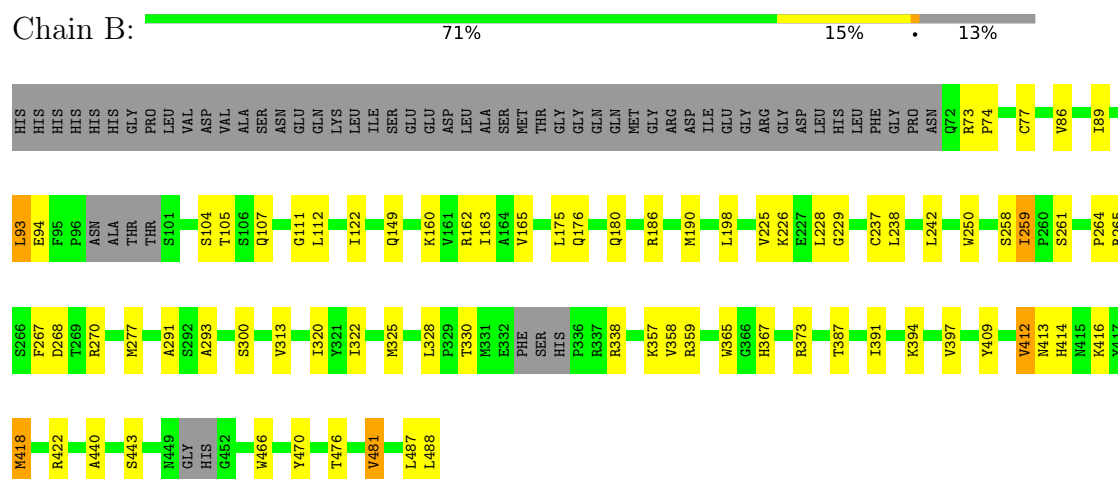
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	172	Total	O	0	0
			172	172		
10	A	135	Total	O	0	0
			135	135		
10	C	149	Total	O	0	0
			149	149		
10	D	102	Total	O	0	0
			102	102		

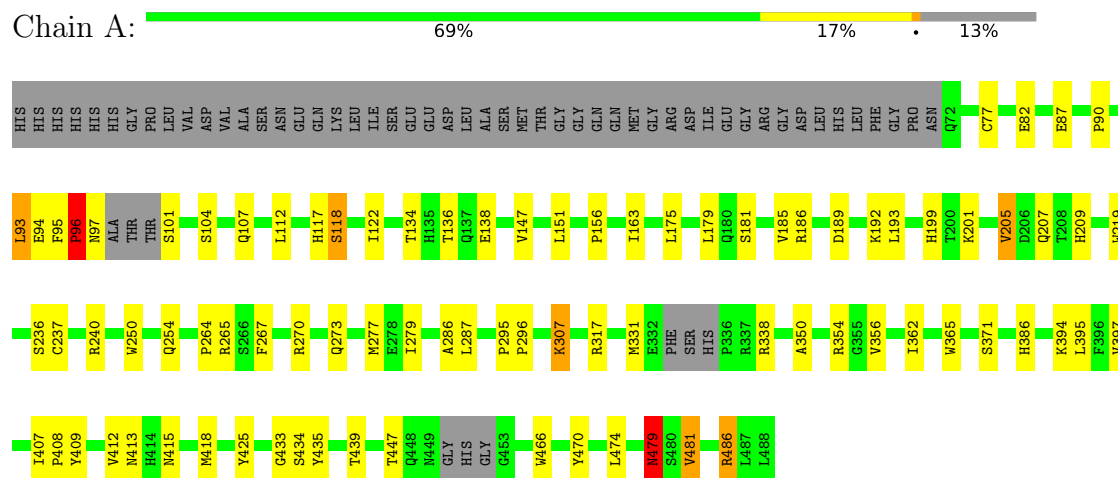
3 Residue-property plots

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.

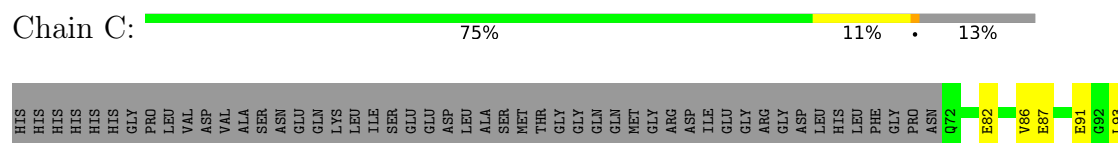
• Molecule 1: 5'-3' exonuclease PLD3

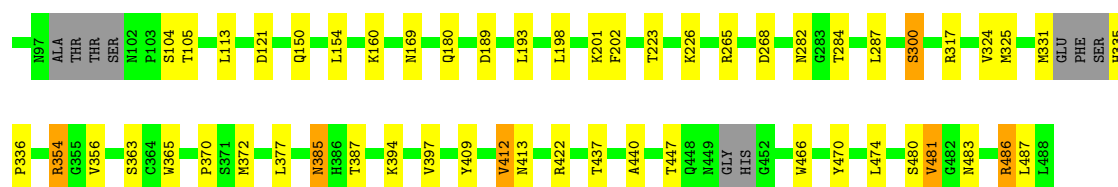


• Molecule 1: 5'-3' exonuclease PLD3



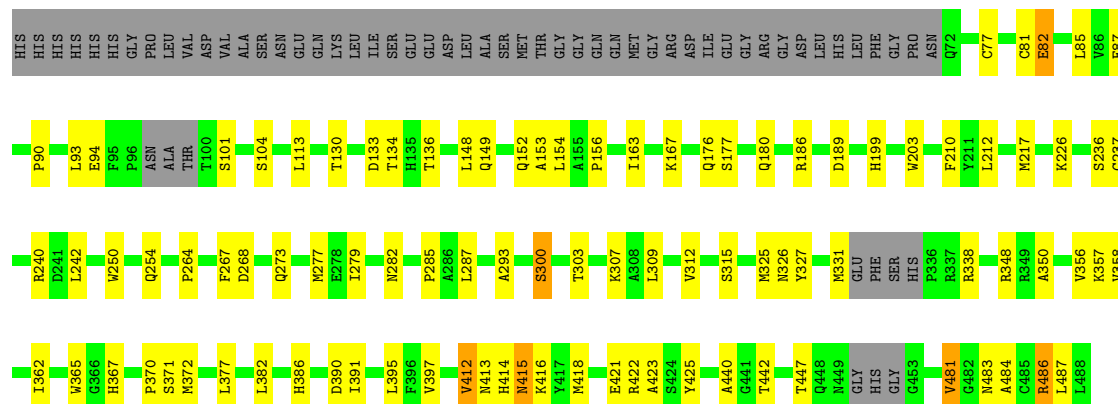
• Molecule 1: 5'-3' exonuclease PLD3





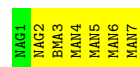
- Molecule 1: 5'-3' exonuclease PLD3

Chain D: 66% 19% 13%



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

Chain E: 14% 86%



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

Chain H: 71% 29%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 50%

MAG1
MAG2

- Molecule 4: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  75% 25%

MAG1
MAG2
BMA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.52Å 54.79Å 203.57Å 83.65° 89.10° 89.90°	Depositor
Resolution (Å)	37.12 – 1.99 37.12 – 1.99	Depositor EDS
% Data completeness (in resolution range)	82.2 (37.12-1.99) 82.3 (37.12-1.99)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.224 , 0.264 0.225 , 0.264	Depositor DCC
R_{free} test set	6474 reflections (4.03%)	wwPDB-VP
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.343	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.150 for h,-k,-l 0.077 for -h,k,k-l 0.076 for -h,-k,-k+l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13786	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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: ACE, PO4, GOL, MAN, NAG, BMA, CIT

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	0.65	0/3299	0.79	5/4494 (0.1%)
1	B	0.67	1/3275 (0.0%)	0.75	0/4462
1	C	0.65	0/3279	0.73	0/4469
1	D	0.61	0/3291	0.75	1/4484 (0.0%)
All	All	0.65	1/13144 (0.0%)	0.76	6/17909 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
1	C	0	2
1	D	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	418	MET	SD-CE	-6.12	1.64	1.79

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	96	PRO	N-CA-CB	-7.25	95.64	103.25
1	A	479	ASN	N-CA-C	6.27	124.15	110.80
1	A	479	ASN	N-CA-CB	6.15	120.88	110.49
1	D	285	PRO	CA-N-CD	-5.25	104.66	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	GLU	CA-C-N	-5.05	117.12	122.28
1	A	94	GLU	C-N-CA	-5.05	117.12	122.28

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	479	ASN	Mainchain
1	A	486	ARG	Sidechain
1	B	73	ARG	Sidechain
1	C	354	ARG	Sidechain
1	C	486	ARG	Sidechain
1	D	486	ARG	Sidechain

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	3217	0	3127	67	0
1	B	3194	0	3106	63	0
1	C	3197	0	3107	39	0
1	D	3206	0	3123	72	0
2	E	83	0	70	0	0
2	H	83	0	70	1	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
3	J	28	0	25	1	0
3	K	28	0	25	0	0
4	I	50	0	43	0	0
5	B	13	0	5	4	0
6	A	6	0	8	1	0
6	B	12	0	15	4	0
6	C	6	0	7	1	0
6	D	12	0	16	1	0
7	B	3	0	3	0	0
8	A	5	0	0	0	0
8	B	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	5	0	0	0	0
8	D	5	0	0	3	0
9	A	14	0	13	1	0
10	A	135	0	0	5	0
10	B	172	0	0	7	0
10	C	149	0	0	5	0
10	D	102	0	0	6	0
All	All	13786	0	12813	238	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 9.

All (238) 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:B:112:LEU:HA	6:B:504:GOL:H31	1.48	0.93
1:D:82:GLU:OE2	1:D:282:ASN:HA	1.72	0.90
1:C:397:VAL:HG11	1:C:481:VAL:HG13	1.56	0.87
1:C:372:MET:HE3	1:C:487:LEU:HD11	1.60	0.83
1:A:270:ARG:HA	1:A:270:ARG:NH1	1.97	0.79
1:D:421:GLU:HG2	1:D:422[A]:ARG:HG3	1.66	0.77
1:B:320:ILE:HG23	1:B:418:MET:HE2	1.67	0.76
1:C:202:PHE:HB3	10:C:602:HOH:O	1.86	0.76
1:D:397:VAL:HG21	1:D:481:VAL:HG13	1.68	0.76
1:A:386:HIS:ND1	10:A:601:HOH:O	2.20	0.74
1:C:397:VAL:HG11	1:C:481:VAL:CG1	2.18	0.74
1:C:409:TYR:H	6:C:501:GOL:H11	1.53	0.72
1:D:149:GLN:HA	1:D:152:GLN:HE21	1.51	0.72
1:D:350:ALA:HB1	1:D:356:VAL:HG21	1.72	0.71
1:D:236:SER:O	1:D:240:ARG:HG3	1.91	0.70
1:D:397:VAL:HG23	10:D:667:HOH:O	1.92	0.70
1:B:89:ILE:HD12	1:B:89:ILE:O	1.92	0.70
1:A:186:ARG:HD2	1:A:250:TRP:CE3	2.27	0.69
1:B:409:TYR:N	6:B:502:GOL:O2	2.21	0.69
1:A:186:ARG:HD2	1:A:250:TRP:CZ3	2.27	0.69
1:B:94:GLU:OE2	10:B:601:HOH:O	2.11	0.68
1:D:358:VAL:HB	1:D:391:ILE:HD13	1.75	0.67
1:A:270:ARG:HA	1:A:270:ARG:HH11	1.60	0.67
1:A:179:LEU:HD21	1:A:185:VAL:CG1	2.26	0.66
1:D:423:ALA:HB3	10:D:601:HOH:O	1.94	0.66
1:B:104:SER:OG	1:B:107:GLN:HG3	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:265:ARG:H	1:B:265:ARG:HD3	1.61	0.65
1:A:331:MET:HE3	1:A:331:MET:HA	1.78	0.65
1:C:82:GLU:OE2	1:C:282:ASN:HA	1.97	0.65
1:D:148:LEU:O	1:D:152:GLN:HG3	1.97	0.65
1:A:354:ARG:NH2	10:A:603:HOH:O	2.23	0.65
1:B:264:PRO:HG2	1:B:267:PHE:CE1	2.32	0.65
1:A:95:PHE:O	1:A:96:PRO:C	2.40	0.64
1:D:273:GLN:HE22	1:D:307:LYS:HE2	1.62	0.63
1:B:270:ARG:NH2	10:B:602:HOH:O	2.25	0.63
1:B:338:ARG:NH2	10:B:604:HOH:O	2.30	0.62
1:C:268:ASP:OD2	1:C:300:SER:OG	2.17	0.62
1:C:335:HIS:HB3	1:C:336:PRO:HD2	1.80	0.62
1:B:357:LYS:HE3	10:B:663:HOH:O	2.00	0.62
1:A:273:GLN:HE22	1:A:307[B]:LYS:HD3	1.65	0.61
1:A:395:LEU:HD21	1:A:474:LEU:HD23	1.82	0.61
1:B:397:VAL:HG11	1:B:481:VAL:HG13	1.82	0.61
1:A:254:GLN:NE2	10:A:602:HOH:O	2.21	0.60
1:C:370:PRO:HB2	1:D:386:HIS:ND1	2.17	0.60
1:D:414:HIS:CE1	8:D:503:PO4:O3	2.54	0.60
1:B:265:ARG:H	1:B:265:ARG:CD	2.16	0.59
1:A:179:LEU:HD21	1:A:185:VAL:HG12	1.84	0.59
1:D:90:PRO:HD2	1:D:93:LEU:HD22	1.85	0.59
1:A:95:PHE:O	1:A:97:ASN:OD1	2.21	0.58
1:B:122:ILE:HB	1:B:163:ILE:HD12	1.83	0.58
1:B:322:ILE:CG1	1:B:418:MET:HE3	2.33	0.57
1:A:179:LEU:N	1:A:179:LEU:HD23	2.19	0.57
1:B:160:LYS:HE2	1:B:162:ARG:HD3	1.85	0.57
1:A:394:LYS:HE3	1:A:466:TRP:CZ2	2.38	0.57
1:A:156:PRO:HD3	1:A:181:SER:O	2.05	0.57
1:D:357:LYS:HZ3	1:D:390:ASP:CG	2.11	0.57
1:D:415:ASN:C	1:D:415:ASN:HD22	2.13	0.57
1:C:387:THR:HG22	1:D:371:SER:HB2	1.86	0.56
1:A:331:MET:HE1	1:A:434:SER:N	2.20	0.56
1:D:176:GLN:O	1:D:180:GLN:HG2	2.04	0.56
1:A:175:LEU:HD13	1:A:185:VAL:HG21	1.87	0.56
1:C:180:GLN:NE2	10:C:604:HOH:O	2.30	0.56
1:B:250:TRP:NE1	5:B:501:CIT:H21	2.20	0.56
1:B:250:TRP:CD1	5:B:501:CIT:H21	2.41	0.56
1:B:250:TRP:HE1	5:B:501:CIT:H21	1.71	0.56
1:A:90:PRO:HD2	1:A:93:LEU:HD12	1.88	0.56
1:D:217:MET:HE3	10:D:652:HOH:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:377:LEU:HD23	1:C:474:LEU:HD13	1.88	0.55
1:B:322:ILE:HG12	1:B:418:MET:HE3	1.87	0.55
1:D:81:CYS:O	1:D:82:GLU:HG2	2.07	0.54
1:A:236:SER:O	1:A:240:ARG:HG3	2.08	0.54
1:D:357:LYS:NZ	1:D:390:ASP:CG	2.65	0.54
1:A:394:LYS:HG2	1:A:466:TRP:CZ3	2.43	0.54
1:A:77:CYS:SG	10:A:681:HOH:O	2.58	0.54
1:B:226:LYS:HB3	1:B:413:ASN:HA	1.90	0.54
1:A:394:LYS:HG2	1:A:466:TRP:CH2	2.43	0.54
1:C:121:ASP:OD2	10:C:601:HOH:O	2.18	0.53
1:C:201:LYS:O	10:C:602:HOH:O	2.19	0.53
1:D:331:MET:HG3	1:D:338:ARG:HB2	1.90	0.53
1:B:149:GLN:NE2	1:C:150:GLN:OE1	2.41	0.53
1:C:317:ARG:HG2	1:C:317:ARG:HH11	1.74	0.53
1:A:207:GLN:HB3	1:A:240:ARG:NH1	2.24	0.53
1:C:87:GLU:O	1:C:104:SER:HA	2.09	0.53
1:B:77:CYS:HB2	10:B:740:HOH:O	2.09	0.53
1:C:226:LYS:HB3	1:C:413:ASN:HA	1.90	0.53
1:D:130:THR:HG22	1:D:133:ASP:OD2	2.09	0.52
1:A:350:ALA:HB1	1:A:356:VAL:HG21	1.90	0.52
1:A:413:ASN:HD21	1:A:415:ASN:ND2	2.07	0.52
1:D:315:SER:O	1:D:422[A]:ARG:NH1	2.41	0.52
1:B:186:ARG:NH2	5:B:501:CIT:H42	2.25	0.52
1:C:287:LEU:HB2	1:C:447:THR:OG1	2.10	0.52
1:D:365:TRP:CE2	1:D:367:HIS:HB2	2.44	0.52
1:B:74:PRO:HB3	1:B:270:ARG:HG3	1.92	0.52
1:D:325:MET:HE2	1:D:416:LYS:HZ1	1.76	0.51
1:A:237:CYS:C	1:A:277:MET:HE1	2.36	0.51
1:B:358:VAL:CG1	1:B:391:ILE:HG12	2.40	0.51
1:D:264:PRO:HG2	1:D:267:PHE:CE1	2.47	0.50
1:B:237:CYS:C	1:B:277:MET:HE1	2.37	0.50
1:B:397:VAL:HG11	1:B:481:VAL:CG1	2.40	0.50
1:D:483:ASN:OD1	1:D:484:ALA:N	2.45	0.50
1:A:93:LEU:HD22	1:A:470:TYR:CE2	2.47	0.50
1:A:192:LYS:HG3	1:A:193:LEU:N	2.26	0.50
1:C:113:LEU:HD22	1:C:154:LEU:HD11	1.94	0.50
1:B:228:LEU:HG	1:B:229:GLY:N	2.26	0.49
1:A:122:ILE:HB	1:A:163:ILE:HD13	1.94	0.49
1:C:481:VAL:HG12	1:C:483:ASN:O	2.11	0.49
1:B:414:HIS:HD2	8:B:505:PO4:O2	1.96	0.49
1:D:236:SER:OG	1:D:240:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:THR:HG22	1:A:371:SER:HB2	1.95	0.49
1:A:397:VAL:HG11	1:A:481:VAL:CG1	2.44	0.48
1:D:130:THR:HG22	1:D:133:ASP:CG	2.37	0.48
1:D:203:TRP:CZ2	1:D:217:MET:HE1	2.49	0.48
1:B:112:LEU:HA	6:B:504:GOL:C3	2.33	0.48
1:B:359:ARG:HD3	1:B:466:TRP:CE2	2.48	0.48
1:A:331:MET:HG2	1:A:338:ARG:HB2	1.95	0.48
1:B:328:LEU:C	1:B:328:LEU:HD13	2.39	0.48
1:D:186:ARG:NH1	1:D:254:GLN:HG3	2.28	0.48
1:A:147:VAL:O	1:A:151:LEU:HD13	2.14	0.47
1:A:199:HIS:O	1:A:201:LYS:HD2	2.13	0.47
1:D:303:THR:HA	6:D:502:GOL:H2	1.97	0.47
1:D:414:HIS:HE1	8:D:503:PO4:O3	1.97	0.47
1:C:365:TRP:HB3	1:C:412:VAL:HG13	1.97	0.47
1:B:86:VAL:CG1	1:B:105:THR:HA	2.44	0.47
1:A:87:GLU:O	1:A:104:SER:HA	2.15	0.47
1:A:273:GLN:HE22	1:A:307[B]:LYS:CD	2.27	0.47
1:C:370:PRO:HB2	1:D:386:HIS:CE1	2.50	0.47
1:D:226:LYS:HB3	1:D:413:ASN:HA	1.97	0.47
1:C:317:ARG:HG2	1:C:317:ARG:NH1	2.30	0.47
1:B:258:SER:O	1:B:258:SER:OG	2.29	0.47
1:B:265:ARG:HD3	1:B:265:ARG:N	2.26	0.47
1:B:268:ASP:OD2	1:B:300:SER:HB3	2.15	0.47
1:A:273:GLN:HE22	1:A:307[A]:LYS:HG3	1.79	0.47
1:B:373:ARG:HB2	1:B:487:LEU:HD12	1.96	0.46
1:D:153:ALA:O	1:D:156:PRO:HD2	2.14	0.46
1:D:268:ASP:OD2	1:D:300:SER:OG	2.33	0.46
1:B:258:SER:O	1:B:259:ILE:HB	2.15	0.46
1:B:313:VAL:HG22	1:B:418:MET:HE1	1.97	0.46
1:D:326:ASN:ND2	10:D:612:HOH:O	2.48	0.46
1:D:312:VAL:HG13	10:D:601:HOH:O	2.14	0.46
1:B:365:TRP:CE2	1:B:367:HIS:HB2	2.51	0.46
1:C:422:ARG:CZ	1:C:422:ARG:HB2	2.46	0.46
1:B:293:ALA:O	1:B:440:ALA:HA	2.16	0.46
1:D:237:CYS:C	1:D:277:MET:HE1	2.41	0.46
1:D:365:TRP:HB3	1:D:412:VAL:HG13	1.97	0.46
1:C:91:GLU:HG2	1:C:223:THR:O	2.16	0.46
1:A:205:VAL:HG13	1:A:209:HIS:HB2	1.98	0.45
1:D:370:PRO:HD3	1:D:486:ARG:HD3	1.98	0.45
1:B:190:MET:HE3	1:B:190:MET:HB3	1.76	0.45
1:D:203:TRP:HZ2	1:D:217:MET:HE1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:MET:HB3	1:A:425:TYR:HB3	1.98	0.45
1:C:325:MET:HA	1:C:363:SER:HB2	1.98	0.45
1:B:225:VAL:HG11	1:B:414:HIS:ND1	2.32	0.45
1:A:138:GLU:CD	1:A:407:ILE:HD11	2.42	0.45
1:D:134:THR:O	1:D:136:THR:HG23	2.16	0.45
10:D:666:HOH:O	3:J:1:NAG:H83	2.16	0.45
1:A:189:ASP:HB3	1:A:192:LYS:HE2	1.98	0.45
1:B:176:GLN:O	1:B:180:GLN:HG3	2.17	0.45
1:D:152:GLN:OE1	1:D:177:SER:OG	2.35	0.45
1:A:265:ARG:H	1:A:265:ARG:NE	2.13	0.45
1:A:435:TYR:HA	1:A:439:THR:HB	1.98	0.45
1:C:385:ASN:ND2	1:C:385:ASN:H	2.13	0.45
1:B:93:LEU:HD22	1:B:470:TYR:CZ	2.51	0.44
1:D:421:GLU:HG2	1:D:422[B]:ARG:HG3	1.98	0.44
1:D:362:ILE:O	1:D:395:LEU:HA	2.17	0.44
1:D:199:HIS:NE2	8:D:503:PO4:O1	2.49	0.44
1:A:205:VAL:CG1	1:A:209:HIS:HB2	2.48	0.44
1:B:358:VAL:HG13	1:B:391:ILE:HG23	1.99	0.44
1:A:134:THR:O	1:A:136:THR:HG23	2.17	0.44
1:C:189:ASP:O	1:C:193:LEU:HG	2.16	0.44
1:A:265:ARG:H	1:A:265:ARG:CD	2.30	0.44
1:D:113:LEU:HD22	1:D:154:LEU:HD11	1.99	0.44
1:A:77:CYS:HB3	1:A:279:ILE:HG22	1.99	0.43
1:A:82:GLU:OE1	9:A:501:NAG:N2	2.48	0.43
1:D:293:ALA:O	1:D:440:ALA:HA	2.17	0.43
1:C:160:LYS:HG2	10:C:610:HOH:O	2.18	0.43
1:D:167:LYS:HG2	1:D:189:ASP:HA	1.99	0.43
1:B:320:ILE:HG23	1:B:418:MET:CE	2.43	0.43
1:C:354:ARG:HB2	1:C:356:VAL:HG23	1.99	0.43
1:A:117[A]:HIS:ND1	1:A:118:SER:HB2	2.33	0.43
1:D:154:LEU:HD23	1:D:154:LEU:HA	1.87	0.43
1:A:331:MET:HE1	1:A:433:GLY:C	2.44	0.43
1:C:265:ARG:NE	1:C:265:ARG:H	2.17	0.43
1:B:111:GLY:O	6:B:504:GOL:H12	2.19	0.43
1:D:418:MET:HB3	1:D:425:TYR:HB3	2.00	0.42
1:A:112:LEU:HD22	1:A:205:VAL:HG11	2.02	0.42
1:A:362:ILE:O	1:A:395:LEU:HA	2.19	0.42
1:A:107:GLN:HE21	1:A:107:GLN:HB3	1.60	0.42
1:A:365:TRP:CH2	1:A:409:TYR:HD1	2.38	0.42
1:D:212:LEU:HD11	1:D:442:THR:OG1	2.20	0.42
1:B:325:MET:HE2	1:B:416:LYS:NZ	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:93:LEU:C	1:D:94:GLU:HG2	2.44	0.42
1:A:287:LEU:HB2	1:A:447:THR:OG1	2.18	0.42
1:B:414:HIS:HE1	10:B:651:HOH:O	2.02	0.42
1:A:219:TRP:HB2	10:A:654:HOH:O	2.18	0.42
1:D:130:THR:HG23	1:D:133:ASP:H	1.84	0.42
2:H:2:NAG:H83	2:H:5:MAN:H2	2.02	0.42
1:C:169:ASN:HD22	1:C:169:ASN:HA	1.59	0.42
1:C:198:LEU:HD22	1:C:440:ALA:CB	2.50	0.42
1:D:203:TRP:O	1:D:210:PHE:HA	2.20	0.42
1:A:331:MET:HE1	1:A:434:SER:CA	2.50	0.42
1:C:86:VAL:CG1	1:C:105:THR:HA	2.50	0.42
1:D:87:GLU:O	1:D:104:SER:HA	2.20	0.42
1:D:163:ILE:O	1:D:250:TRP:HZ3	2.02	0.41
1:D:273:GLN:NE2	1:D:307:LYS:HE2	2.31	0.41
1:B:328:LEU:CD1	1:B:330:THR:OG1	2.68	0.41
1:D:264:PRO:HG2	1:D:267:PHE:CD1	2.56	0.41
1:A:295:PRO:HB2	1:A:296:PRO:HD3	2.01	0.41
1:B:165:VAL:C	1:B:198:LEU:HD23	2.45	0.41
1:A:397:VAL:HG11	1:A:481:VAL:HG12	2.02	0.41
1:C:335:HIS:HB3	1:C:336:PRO:CD	2.46	0.41
1:D:85:LEU:HD23	1:D:85:LEU:HA	1.91	0.41
1:D:350:ALA:C	1:D:356:VAL:HG22	2.45	0.41
1:B:476:THR:O	1:B:488:LEU:HD22	2.20	0.41
1:C:93:LEU:HD22	1:C:470:TYR:CZ	2.56	0.41
1:D:331:MET:HE3	1:D:331:MET:HB3	1.87	0.41
1:A:408:PRO:HA	6:A:502:GOL:H31	2.03	0.41
1:D:77:CYS:HB3	1:D:279:ILE:HG22	2.03	0.41
1:B:394:LYS:HG3	1:B:466:TRP:CH2	2.56	0.41
1:C:394:LYS:HG3	1:C:466:TRP:CH2	2.56	0.41
1:B:264:PRO:HG2	1:B:267:PHE:CD1	2.55	0.41
1:B:291:ALA:HB3	1:B:443:SER:OG	2.21	0.41
1:B:365:TRP:CE3	1:B:412:VAL:HG22	2.56	0.41
1:A:264:PRO:HG2	1:A:267:PHE:HE1	1.86	0.41
1:C:331:MET:HE1	1:C:437:THR:HG21	2.02	0.41
1:D:81:CYS:C	1:D:82:GLU:HG2	2.45	0.41
1:D:397:VAL:CG2	1:D:481:VAL:HG13	2.44	0.41
1:B:328:LEU:HD11	1:B:330:THR:OG1	2.20	0.41
1:A:365:TRP:N	1:A:365:TRP:CD1	2.89	0.41
1:D:287:LEU:HB2	1:D:447:THR:OG1	2.21	0.41
1:D:377:LEU:HD23	1:D:377:LEU:HA	1.81	0.41
1:A:279:ILE:CD1	1:A:286:ALA:HB3	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:327:TYR:O	1:D:372:MET:HG2	2.20	0.40
1:B:175:LEU:HD23	1:B:175:LEU:HA	1.86	0.40
1:A:192:LYS:HG3	1:A:193:LEU:HG	2.04	0.40
1:B:238:LEU:HA	1:B:238:LEU:HD12	1.80	0.40
1:B:422:ARG:NH2	10:B:617:HOH:O	2.54	0.40
1:D:348:ARG:NH1	1:D:382:LEU:HD11	2.37	0.40
1:A:317:ARG:HA	1:A:317:ARG:HH11	1.86	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	402/467 (86%)	390 (97%)	10 (2%)	2 (0%)	24	21
1	B	400/467 (86%)	390 (98%)	9 (2%)	1 (0%)	36	35
1	C	400/467 (86%)	390 (98%)	10 (2%)	0	100	100
1	D	401/467 (86%)	390 (97%)	10 (2%)	1 (0%)	43	42
All	All	1603/1868 (86%)	1560 (97%)	39 (2%)	4 (0%)	36	42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	PRO
1	D	101	SER
1	A	479	ASN
1	B	259	ILE

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	353/398 (89%)	343 (97%)	10 (3%)	38	41
1	B	350/398 (88%)	345 (99%)	5 (1%)	59	66
1	C	350/398 (88%)	342 (98%)	8 (2%)	44	49
1	D	352/398 (88%)	344 (98%)	8 (2%)	44	49
All	All	1405/1592 (88%)	1374 (98%)	31 (2%)	47	50

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	93	LEU
1	B	242	LEU
1	B	261	SER
1	B	412	VAL
1	B	481	VAL
1	A	93	LEU
1	A	96	PRO
1	A	101	SER
1	A	118	SER
1	A	205	VAL
1	A	307[A]	LYS
1	A	307[B]	LYS
1	A	412	VAL
1	A	481	VAL
1	A	486	ARG
1	C	284	THR
1	C	300	SER
1	C	324	VAL
1	C	385	ASN
1	C	412	VAL
1	C	480	SER
1	C	481	VAL
1	C	486	ARG
1	D	82	GLU

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Mol	Chain	Res	Type
1	D	242	LEU
1	D	300	SER
1	D	309	LEU
1	D	412	VAL
1	D	415	ASN
1	D	481	VAL
1	D	487	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	117	HIS
1	B	143	GLN
1	B	149	GLN
1	B	184	GLN
1	B	254	GLN
1	B	326	ASN
1	B	414	HIS
1	B	415	ASN
1	B	448	GLN
1	A	184	GLN
1	A	195	HIS
1	A	273	GLN
1	A	326	ASN
1	A	385	ASN
1	A	386	HIS
1	A	415	ASN
1	C	97	ASN
1	C	143	GLN
1	C	169	ASN
1	C	383	HIS
1	C	385	ASN
1	C	415	ASN
1	D	273	GLN
1	D	326	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 ⓘ

26 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	0.31	0	17,19,21	0.79	0
2	NAG	E	2	2	14,14,15	0.87	1 (7%)	17,19,21	0.82	2 (11%)
2	BMA	E	3	2	11,11,12	1.00	1 (9%)	15,15,17	0.86	1 (6%)
2	MAN	E	4	2	11,11,12	1.56	2 (18%)	15,15,17	1.10	1 (6%)
2	MAN	E	5	2	11,11,12	1.37	2 (18%)	15,15,17	1.19	1 (6%)
2	MAN	E	6	2	11,11,12	0.89	0	15,15,17	0.90	1 (6%)
2	MAN	E	7	2	11,11,12	1.04	1 (9%)	15,15,17	1.24	2 (13%)
3	NAG	F	1	1,3	14,14,15	0.32	0	17,19,21	0.67	0
3	NAG	F	2	3	14,14,15	0.39	0	17,19,21	0.69	0
3	NAG	G	1	1,3	14,14,15	0.46	0	17,19,21	0.47	0
3	NAG	G	2	3	14,14,15	0.31	0	17,19,21	0.69	0
2	NAG	H	1	1,2	14,14,15	0.69	1 (7%)	17,19,21	0.72	0
2	NAG	H	2	2	14,14,15	0.69	0	17,19,21	0.85	1 (5%)
2	BMA	H	3	2	11,11,12	1.17	1 (9%)	15,15,17	1.17	1 (6%)
2	MAN	H	4	2	11,11,12	0.83	0	15,15,17	1.36	2 (13%)
2	MAN	H	5	2	11,11,12	1.55	2 (18%)	15,15,17	1.53	3 (20%)
2	MAN	H	6	2	11,11,12	1.00	1 (9%)	15,15,17	1.52	1 (6%)
2	MAN	H	7	2	11,11,12	1.24	0	15,15,17	1.37	2 (13%)
4	NAG	I	1	1,4	14,14,15	0.20	0	17,19,21	0.60	0
4	NAG	I	2	4	14,14,15	0.23	0	17,19,21	0.73	0
4	BMA	I	3	4	11,11,12	0.99	0	15,15,17	0.81	0
4	MAN	I	4	4	11,11,12	0.92	0	15,15,17	0.99	2 (13%)
3	NAG	J	1	1,3	14,14,15	0.41	0	17,19,21	0.58	0
3	NAG	J	2	3	14,14,15	0.68	1 (7%)	17,19,21	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	K	1	1,3	14,14,15	0.48	0	17,19,21	0.95	1 (5%)
3	NAG	K	2	3	14,14,15	0.28	0	17,19,21	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4	2	-	0/2/19/22	0/1/1/1
2	MAN	E	5	2	-	2/2/19/22	0/1/1/1
2	MAN	E	6	2	-	0/2/19/22	0/1/1/1
2	MAN	E	7	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	-	0/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	BMA	H	3	2	-	0/2/19/22	0/1/1/1
2	MAN	H	4	2	-	0/2/19/22	0/1/1/1
2	MAN	H	5	2	-	2/2/19/22	0/1/1/1
2	MAN	H	6	2	-	2/2/19/22	0/1/1/1
2	MAN	H	7	2	-	2/2/19/22	0/1/1/1
4	NAG	I	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	MAN	I	4	4	-	2/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
3	NAG	K	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	K	2	3	-	2/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	4	MAN	C2-C3	3.93	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	5	MAN	C2-C3	-3.74	1.46	1.52
2	H	3	BMA	C2-C3	3.22	1.57	1.52
2	E	2	NAG	O5-C1	-3.06	1.38	1.43
2	H	5	MAN	O5-C5	2.96	1.49	1.43
2	E	5	MAN	C2-C3	2.57	1.56	1.52
2	H	6	MAN	O5-C5	2.51	1.48	1.43
2	E	5	MAN	O5-C5	2.38	1.48	1.43
3	J	2	NAG	C1-C2	2.22	1.55	1.52
2	E	7	MAN	C1-C2	2.20	1.57	1.52
2	E	4	MAN	O5-C5	2.17	1.47	1.43
2	H	1	NAG	O5-C1	-2.14	1.40	1.43
2	E	3	BMA	C2-C3	2.00	1.55	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	6	MAN	C1-O5-C5	4.84	118.67	112.19
2	H	5	MAN	O2-C2-C3	-4.07	101.73	110.15
2	H	4	MAN	C1-O5-C5	3.98	117.52	112.19
2	H	7	MAN	C1-O5-C5	3.62	117.04	112.19
2	E	7	MAN	C1-O5-C5	3.43	116.78	112.19
2	H	3	BMA	C1-O5-C5	3.25	116.54	112.19
2	E	5	MAN	C1-O5-C5	3.10	116.35	112.19
3	K	1	NAG	C1-O5-C5	2.65	115.74	112.19
2	E	4	MAN	C1-O5-C5	2.56	115.62	112.19
2	H	2	NAG	C1-O5-C5	2.50	115.53	112.19
2	E	3	BMA	C1-O5-C5	2.43	115.44	112.19
2	H	5	MAN	C1-C2-C3	2.34	113.05	109.64
4	I	4	MAN	C1-O5-C5	2.23	115.18	112.19
4	I	4	MAN	O2-C2-C3	-2.23	105.54	110.15
2	H	4	MAN	O2-C2-C3	-2.23	105.54	110.15
2	E	6	MAN	C1-O5-C5	2.22	115.16	112.19
2	E	7	MAN	O2-C2-C3	-2.07	105.86	110.15
2	E	2	NAG	C1-O5-C5	2.07	114.96	112.19
2	H	7	MAN	O2-C2-C3	-2.06	105.88	110.15
2	E	2	NAG	O4-C4-C5	-2.06	104.25	109.32
2	H	5	MAN	C1-O5-C5	2.05	114.93	112.19

There are no chirality outliers.

All (22) torsion outliers are listed below:

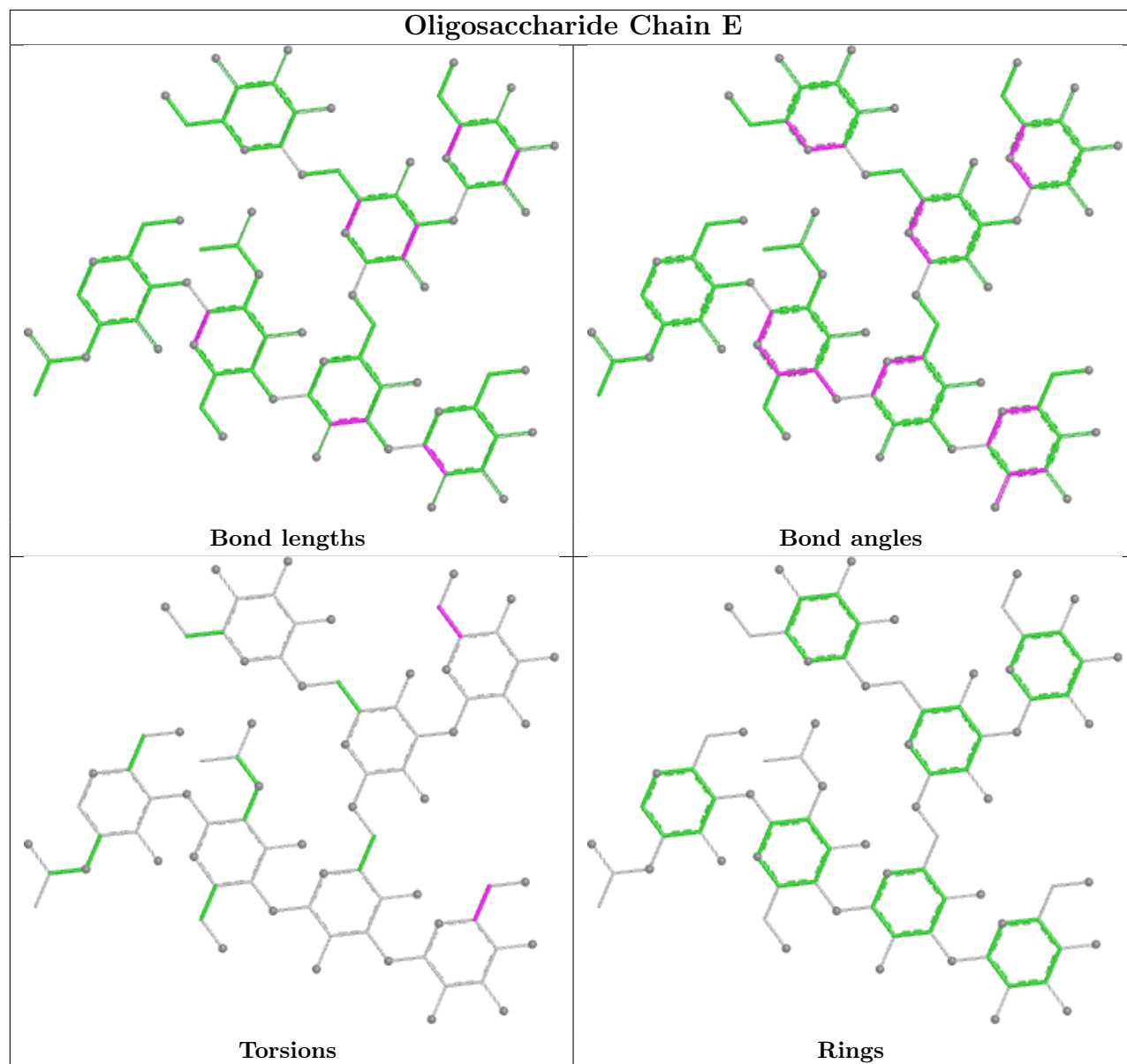
Mol	Chain	Res	Type	Atoms
2	E	7	MAN	O5-C5-C6-O6
2	H	6	MAN	O5-C5-C6-O6
2	H	7	MAN	C4-C5-C6-O6
2	H	6	MAN	C4-C5-C6-O6
2	H	7	MAN	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
2	E	7	MAN	C4-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	K	2	NAG	C4-C5-C6-O6
3	K	2	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
2	H	5	MAN	O5-C5-C6-O6
4	I	4	MAN	C4-C5-C6-O6
3	K	1	NAG	C1-C2-N2-C7
3	J	2	NAG	C4-C5-C6-O6
4	I	4	MAN	O5-C5-C6-O6
3	K	1	NAG	C3-C2-N2-C7
3	J	2	NAG	O5-C5-C6-O6
2	H	5	MAN	C4-C5-C6-O6
2	E	5	MAN	O5-C5-C6-O6
2	E	5	MAN	C4-C5-C6-O6

There are no ring outliers.

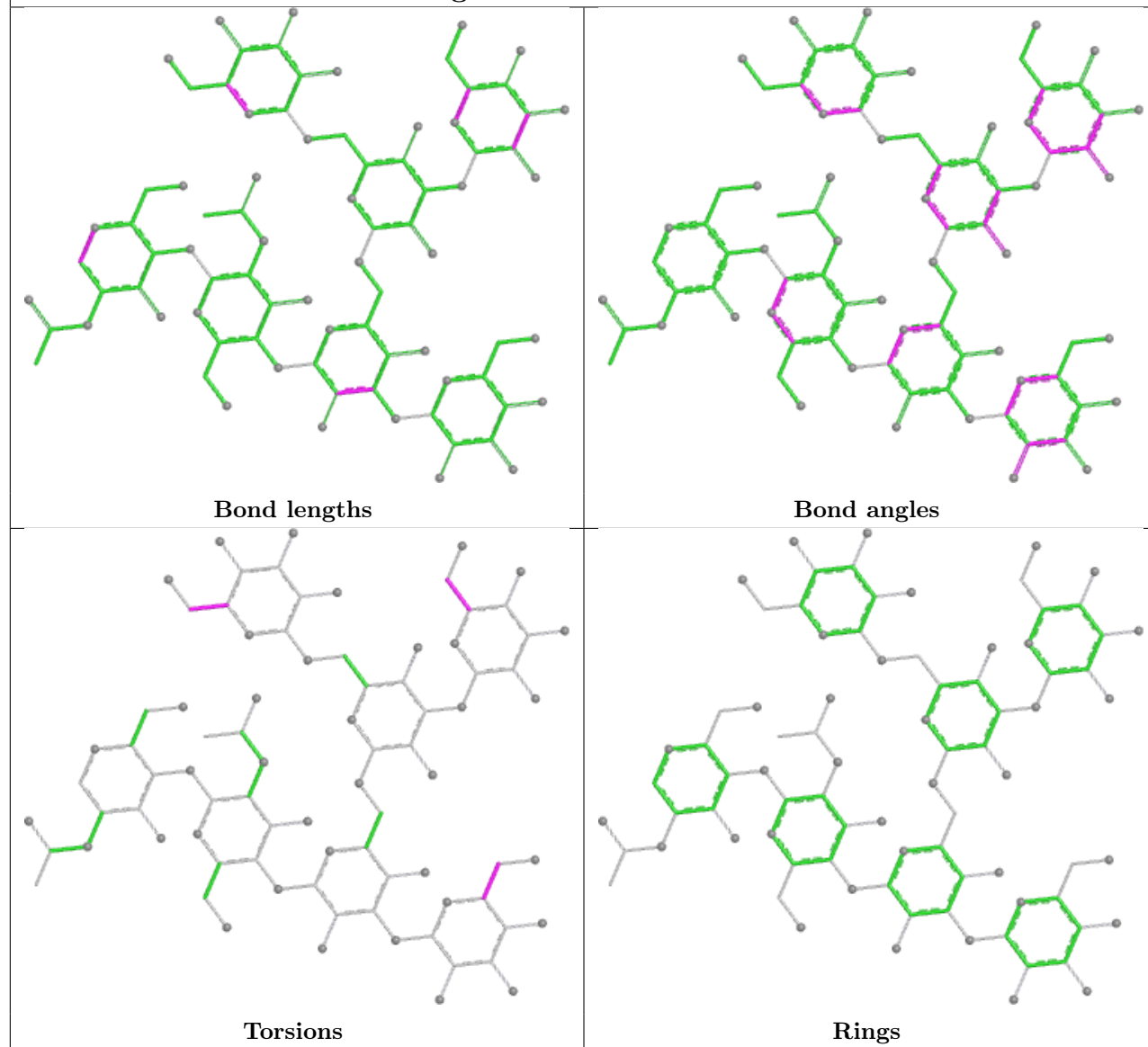
3 monomers are involved in 2 short contacts:

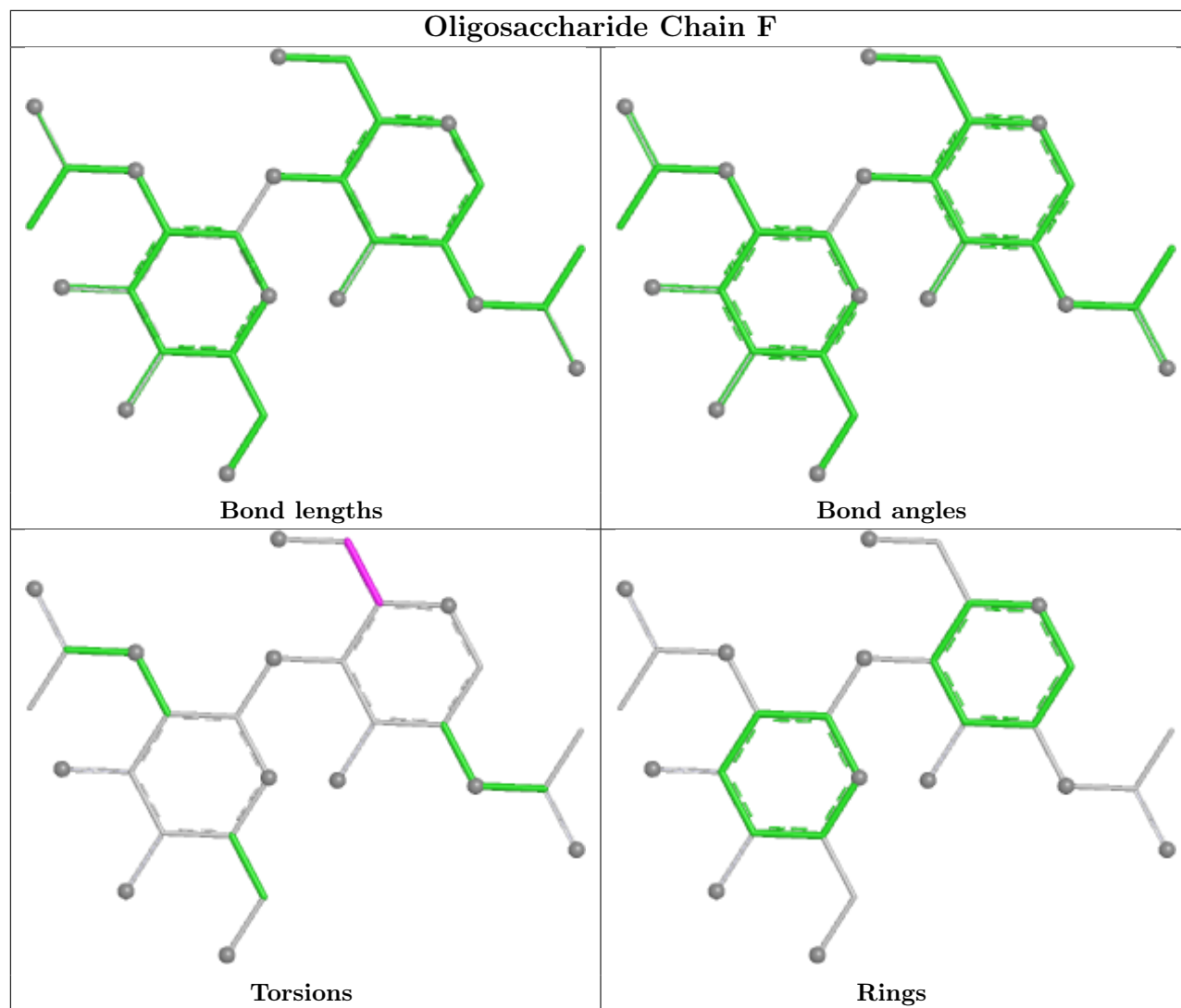
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	1	NAG	1	0
2	H	5	MAN	1	0
2	H	2	NAG	1	0

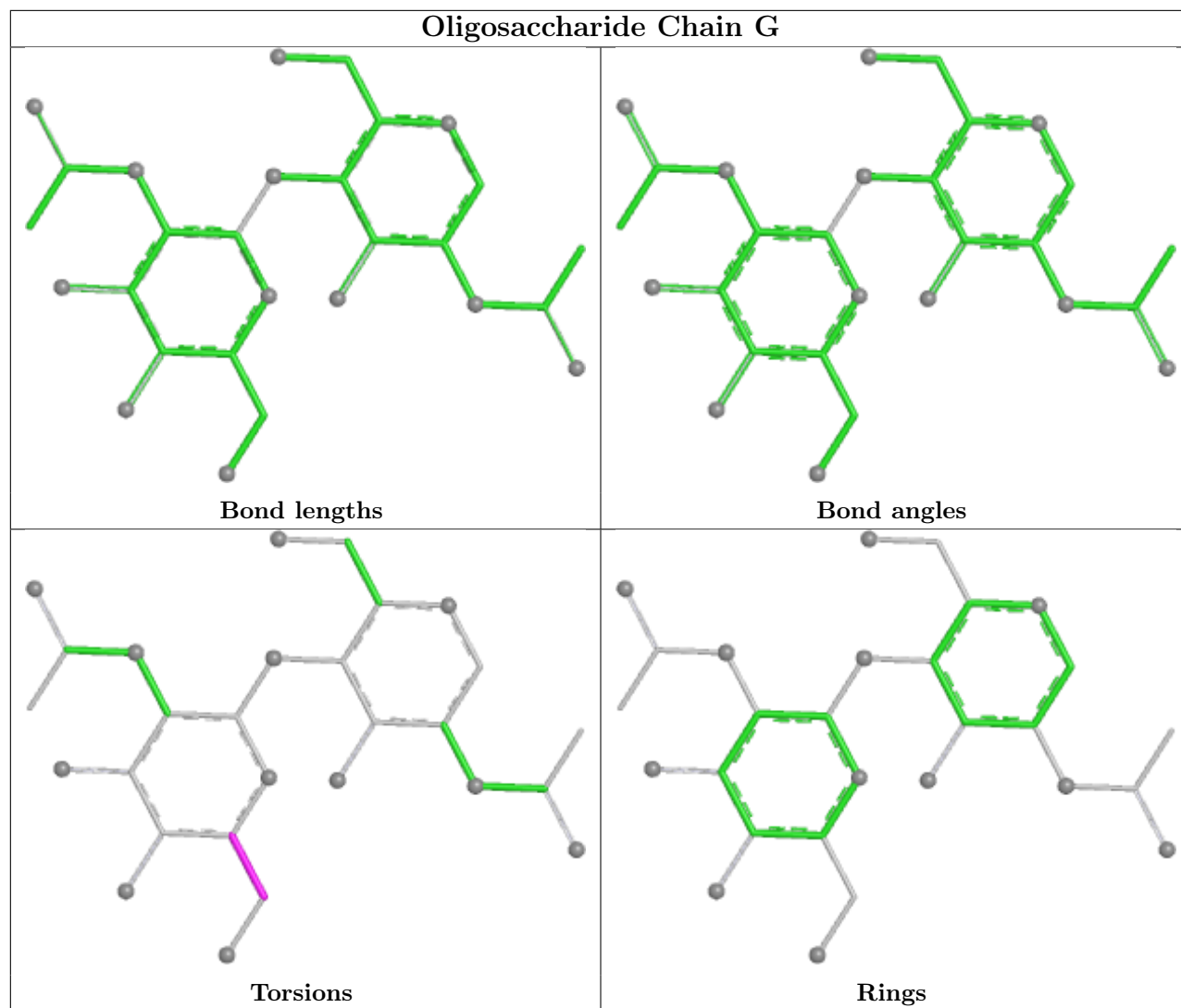
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

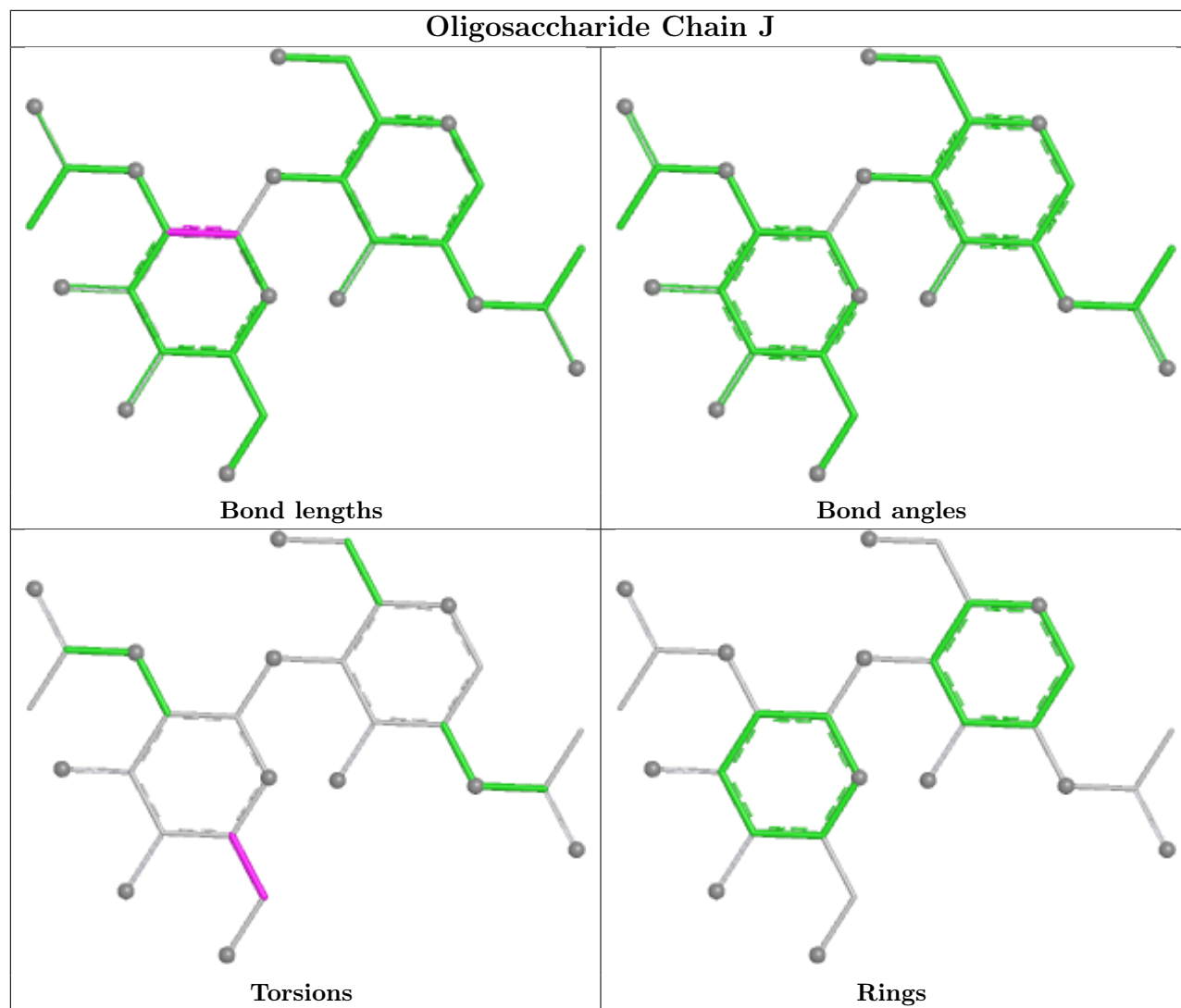


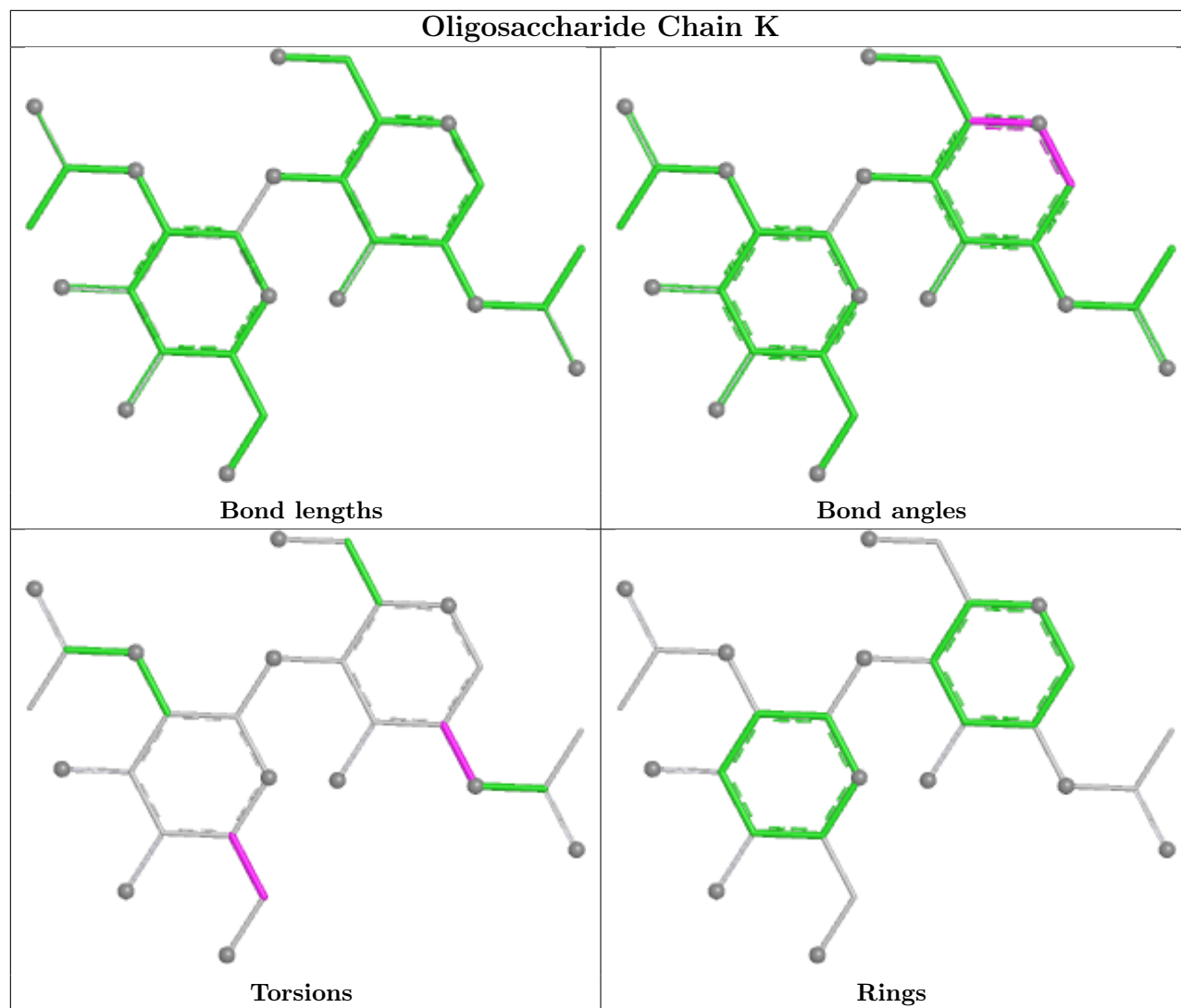
Oligosaccharide Chain H

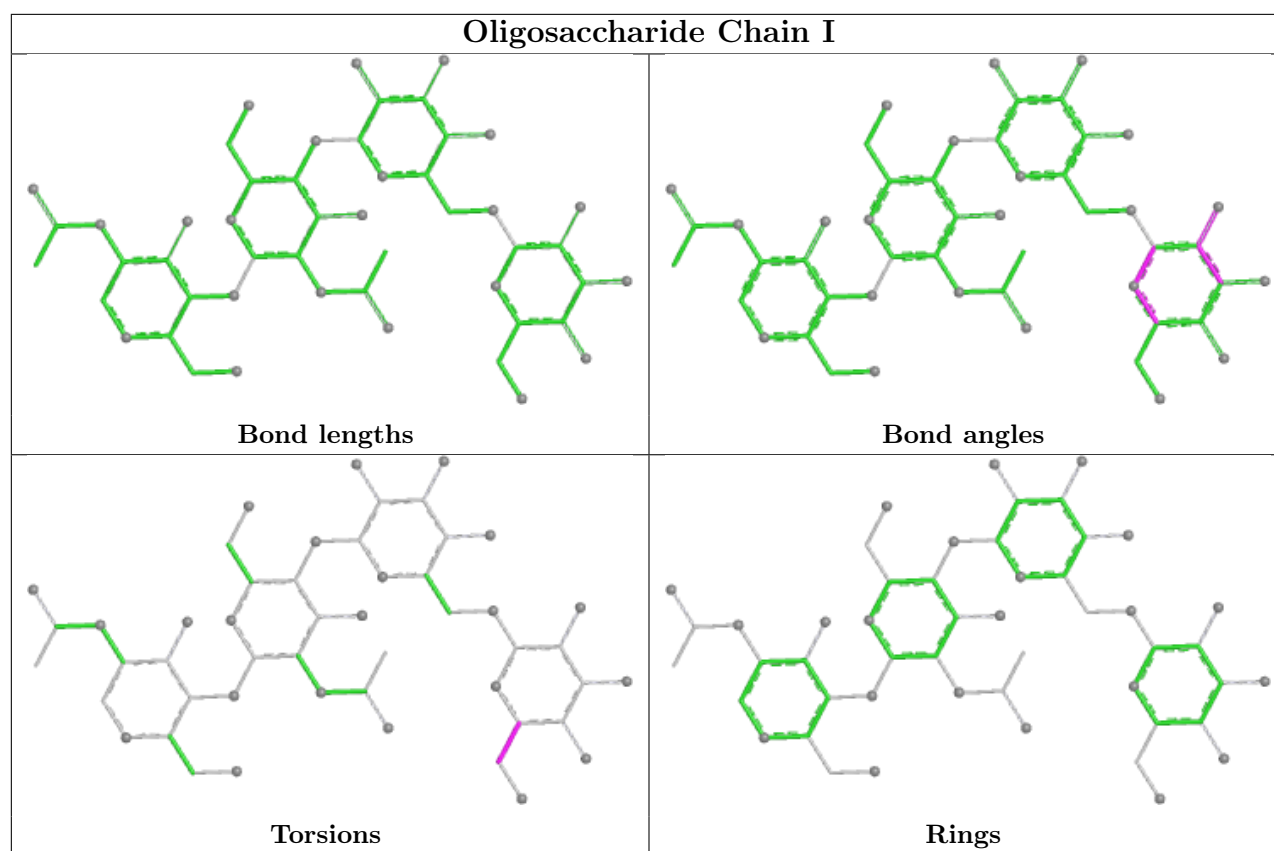












5.6 Ligand geometry [i](#)

13 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	$\# Z > 2$
6	GOL	D	502	-	5,5,5	0.93	0	5,5,5	1.15	1 (20%)
6	GOL	D	501	-	5,5,5	0.99	0	5,5,5	0.87	0
6	GOL	A	502	-	5,5,5	1.39	1 (20%)	5,5,5	1.08	0
6	GOL	C	501	-	5,5,5	1.57	1 (20%)	5,5,5	1.21	0
8	PO4	B	505	-	4,4,4	1.49	1 (25%)	6,6,6	0.56	0
7	ACE	B	503	-	1,2,2	1.11	0	0,1,1	-	-
8	PO4	A	503	-	4,4,4	1.11	0	6,6,6	1.23	1 (16%)
6	GOL	B	504	-	5,5,5	0.94	0	5,5,5	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PO4	D	503	-	4,4,4	1.38	0	6,6,6	0.91	0
5	CIT	B	501	-	12,12,12	1.02	0	17,17,17	1.72	6 (35%)
8	PO4	C	502	-	4,4,4	1.21	0	6,6,6	0.66	0
6	GOL	B	502	-	5,5,5	1.49	1 (20%)	5,5,5	1.08	1 (20%)
9	NAG	A	501	1	14,14,15	1.19	2 (14%)	17,19,21	0.74	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	D	502	-	-	4/4/4/4	-
6	GOL	D	501	-	-	2/4/4/4	-
6	GOL	A	502	-	-	4/4/4/4	-
6	GOL	C	501	-	-	2/4/4/4	-
6	GOL	B	504	-	-	2/4/4/4	-
5	CIT	B	501	-	-	7/16/16/16	-
6	GOL	B	502	-	-	2/4/4/4	-
9	NAG	A	501	1	-	4/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	501	NAG	C1-C2	3.18	1.56	1.52
6	B	502	GOL	O2-C2	-2.88	1.35	1.43
9	A	501	NAG	O5-C1	2.88	1.48	1.43
6	C	501	GOL	C3-C2	-2.35	1.42	1.51
8	B	505	PO4	P-O2	-2.35	1.47	1.54
6	A	502	GOL	O2-C2	-2.18	1.37	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	501	CIT	C3-C4-C5	-3.46	104.45	113.92
5	B	501	CIT	O6-C6-C3	2.61	118.15	113.14
5	B	501	CIT	C2-C3-C6	2.47	115.50	110.03
5	B	501	CIT	O2-C1-C2	2.46	122.13	114.35
5	B	501	CIT	C4-C3-C6	-2.41	104.70	110.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	503	PO4	O3-P-O1	-2.21	103.12	110.95
5	B	501	CIT	O2-C1-O1	-2.14	117.84	123.33
6	B	502	GOL	O1-C1-C2	-2.05	101.16	110.38
6	D	502	GOL	C3-C2-C1	-2.00	104.45	111.80

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	CIT	O7-C3-C4-C5
5	B	501	CIT	C6-C3-C4-C5
5	B	501	CIT	C2-C3-C6-O5
5	B	501	CIT	C2-C3-C6-O6
5	B	501	CIT	O7-C3-C6-O5
5	B	501	CIT	O7-C3-C6-O6
6	B	502	GOL	O1-C1-C2-C3
6	B	504	GOL	C1-C2-C3-O3
6	A	502	GOL	O1-C1-C2-O2
6	A	502	GOL	O1-C1-C2-C3
6	A	502	GOL	C1-C2-C3-O3
6	D	502	GOL	C1-C2-C3-O3
9	A	501	NAG	C1-C2-N2-C7
9	A	501	NAG	O5-C5-C6-O6
5	B	501	CIT	C2-C3-C4-C5
9	A	501	NAG	C4-C5-C6-O6
6	C	501	GOL	C1-C2-C3-O3
6	D	501	GOL	C1-C2-C3-O3
6	D	502	GOL	O1-C1-C2-C3
6	B	502	GOL	O1-C1-C2-O2
6	B	504	GOL	O2-C2-C3-O3
6	D	501	GOL	O2-C2-C3-O3
6	A	502	GOL	O2-C2-C3-O3
6	D	502	GOL	O2-C2-C3-O3
6	C	501	GOL	O2-C2-C3-O3
6	D	502	GOL	O1-C1-C2-O2
9	A	501	NAG	C3-C2-N2-C7

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	502	GOL	1	0
6	A	502	GOL	1	0
6	C	501	GOL	1	0
8	B	505	PO4	1	0
6	B	504	GOL	3	0
8	D	503	PO4	3	0
5	B	501	CIT	4	0
6	B	502	GOL	1	0
9	A	501	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 [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	408/467 (87%)	-1.09	0 100 100	17, 34, 54, 91	2 (0%)
1	B	408/467 (87%)	-1.19	0 100 100	22, 31, 50, 72	0
1	C	408/467 (87%)	-1.18	0 100 100	23, 31, 51, 77	0
1	D	407/467 (87%)	-1.05	0 100 100	18, 36, 57, 72	2 (0%)
All	All	1631/1868 (87%)	-1.13	0 100 100	17, 33, 54, 91	4 (0%)

There are no RSRZ outliers to report.

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	MAN	E	6	11/12	0.97	0.06	62,64,68,68	0
2	MAN	H	6	11/12	0.97	0.05	64,66,67,70	0
3	NAG	J	2	14/15	0.97	0.06	52,69,76,82	0
3	NAG	K	2	14/15	0.97	0.06	65,73,78,79	0
2	MAN	H	7	11/12	0.98	0.05	41,44,48,51	0
3	NAG	F	2	14/15	0.98	0.05	35,48,56,69	0
3	NAG	G	2	14/15	0.98	0.05	46,59,65,65	0
3	NAG	J	1	14/15	0.98	0.04	50,62,64,65	0
2	BMA	H	3	11/12	0.98	0.04	42,45,47,47	0

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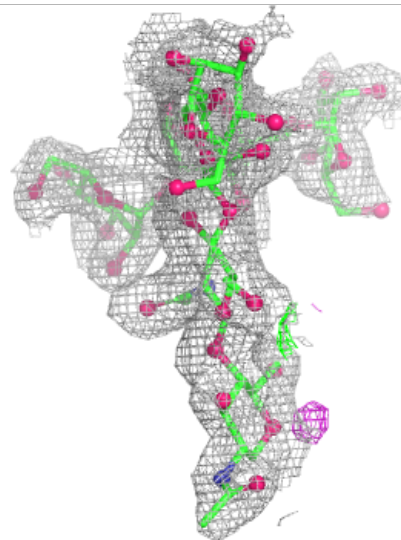
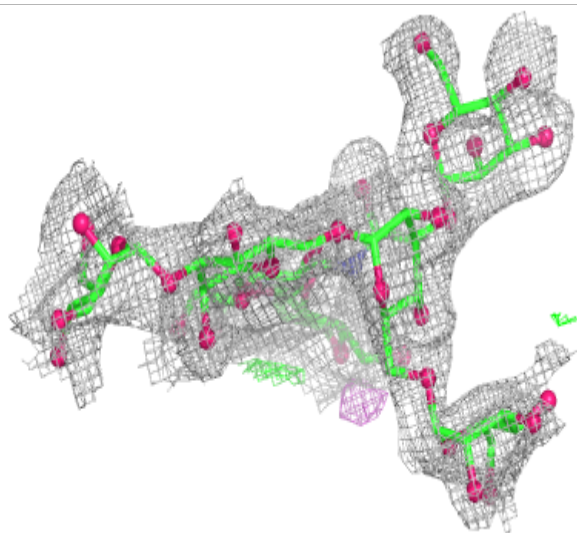
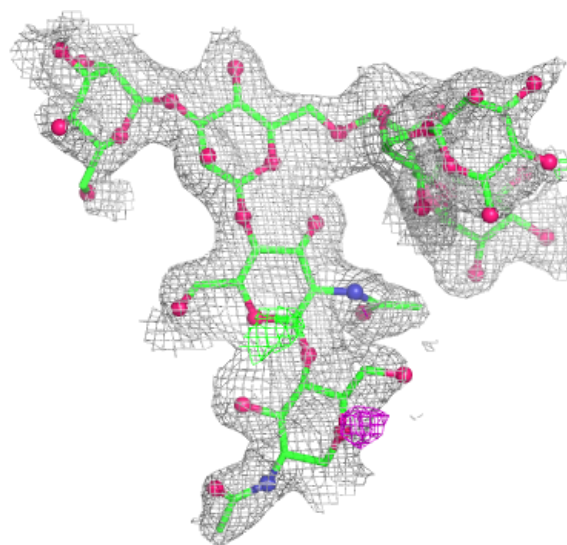
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MAN	E	7	11/12	0.98	0.05	60,66,69,72	0
4	NAG	I	2	14/15	0.98	0.04	40,51,58,65	0
2	MAN	H	5	11/12	0.99	0.03	44,51,55,55	0
2	MAN	E	4	11/12	0.99	0.03	36,44,51,54	0
2	MAN	E	5	11/12	0.99	0.04	37,41,43,56	0
3	NAG	F	1	14/15	0.99	0.04	42,44,51,54	0
2	NAG	E	1	14/15	0.99	0.04	33,41,45,47	0
3	NAG	G	1	14/15	0.99	0.03	42,50,54,58	0
2	NAG	E	2	14/15	0.99	0.04	40,46,50,62	0
2	NAG	H	1	14/15	0.99	0.03	30,37,40,41	0
2	NAG	H	2	14/15	0.99	0.04	37,41,44,46	0
3	NAG	K	1	14/15	0.99	0.03	44,51,59,70	0
2	BMA	E	3	11/12	0.99	0.03	41,46,50,53	0
4	NAG	I	1	14/15	0.99	0.03	38,42,45,47	0
2	MAN	H	4	11/12	0.99	0.04	43,49,57,59	0
4	BMA	I	3	11/12	0.99	0.04	56,60,64,65	0
4	MAN	I	4	11/12	0.99	0.04	58,61,65,66	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.

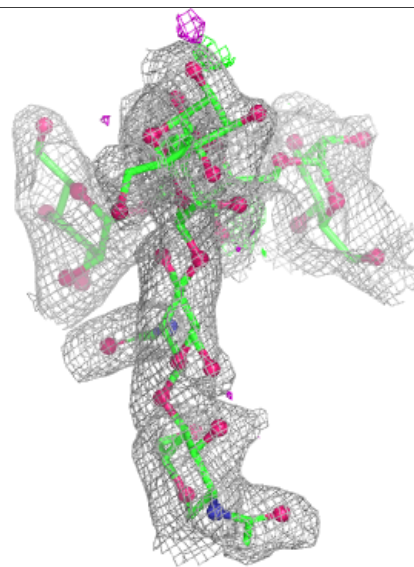
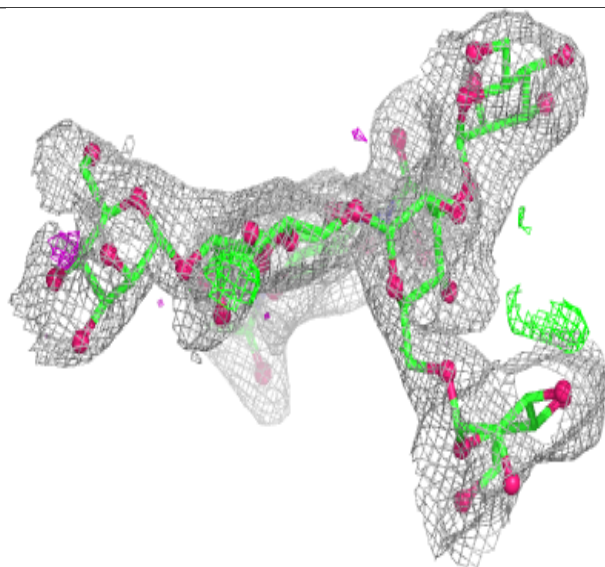
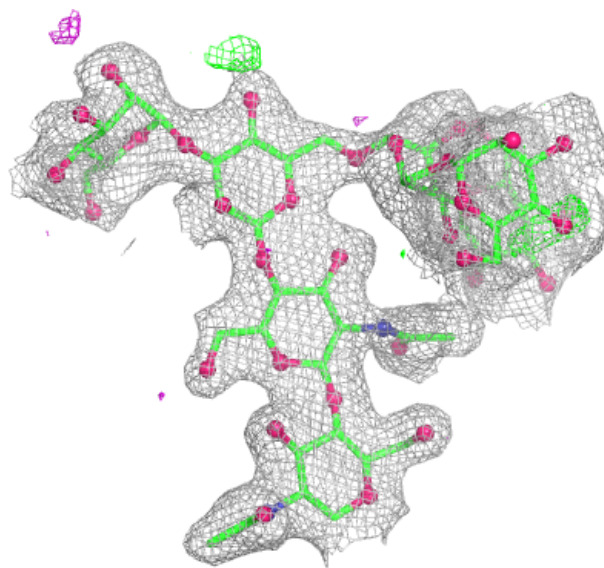
Electron density around Chain E:

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



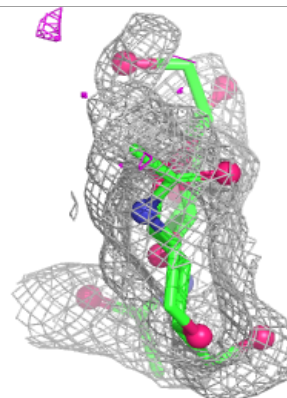
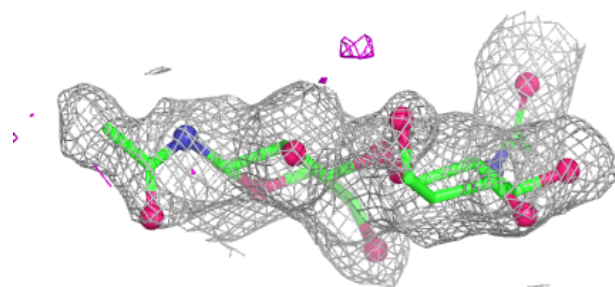
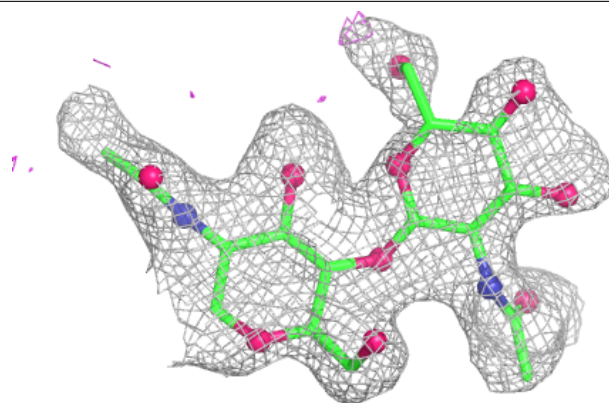
Electron density around Chain H:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

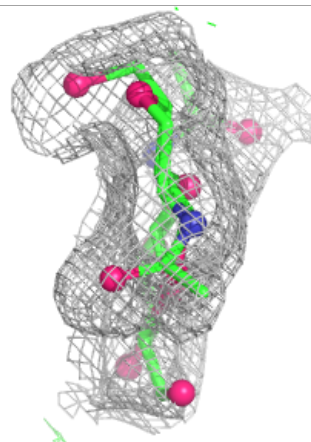
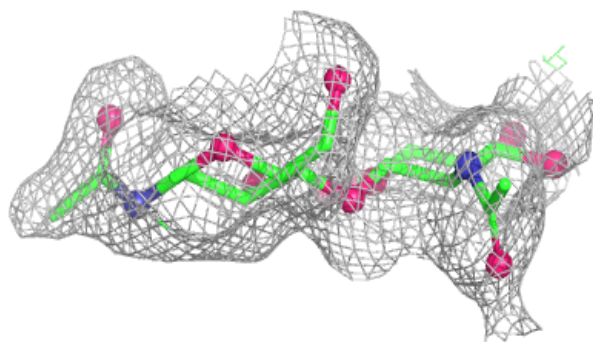
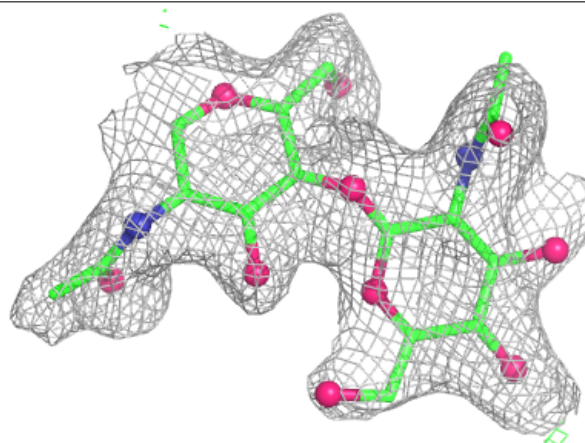


Electron density around Chain F:

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

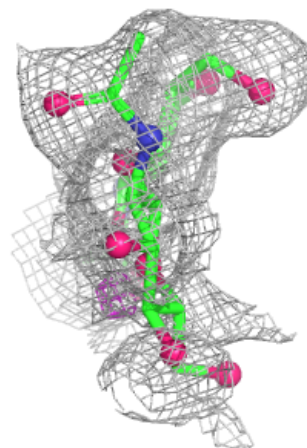
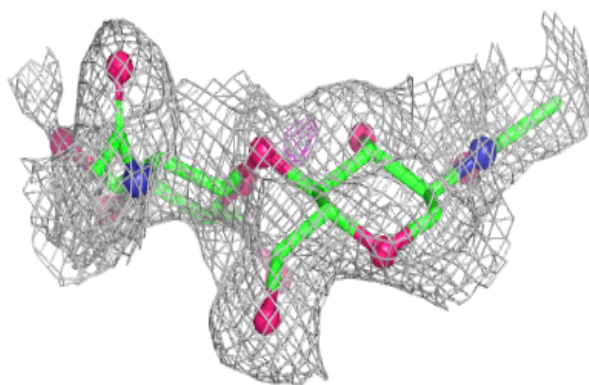
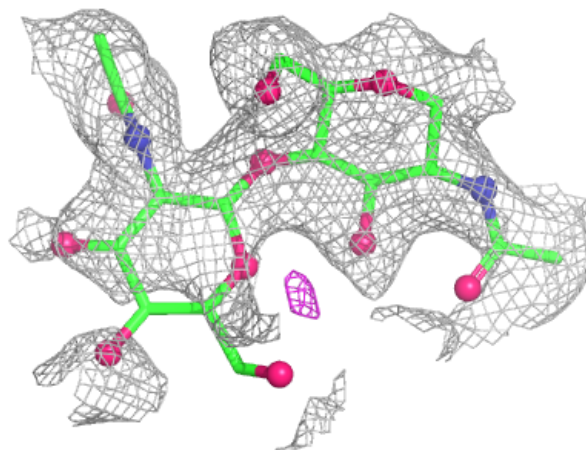
**Electron density around Chain G:**

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



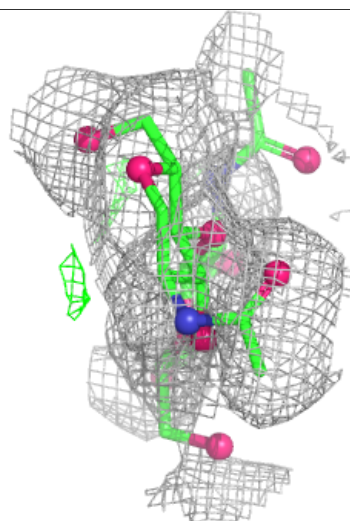
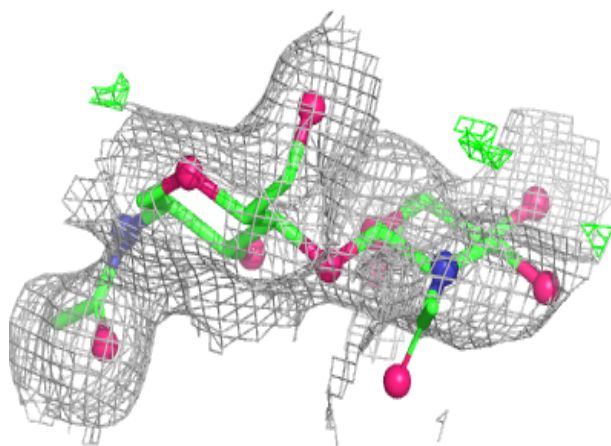
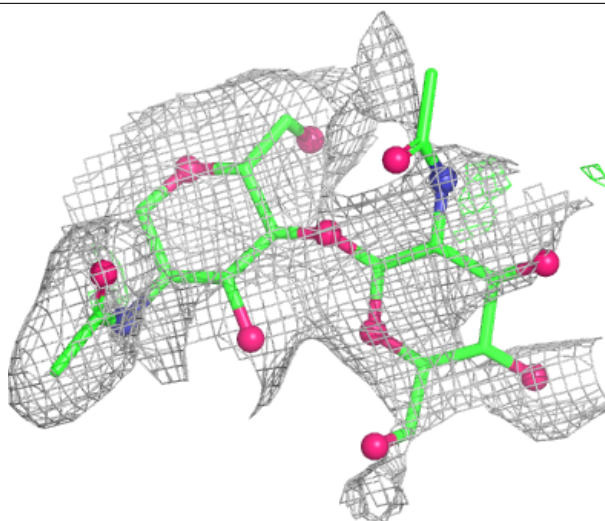
Electron density around Chain J:

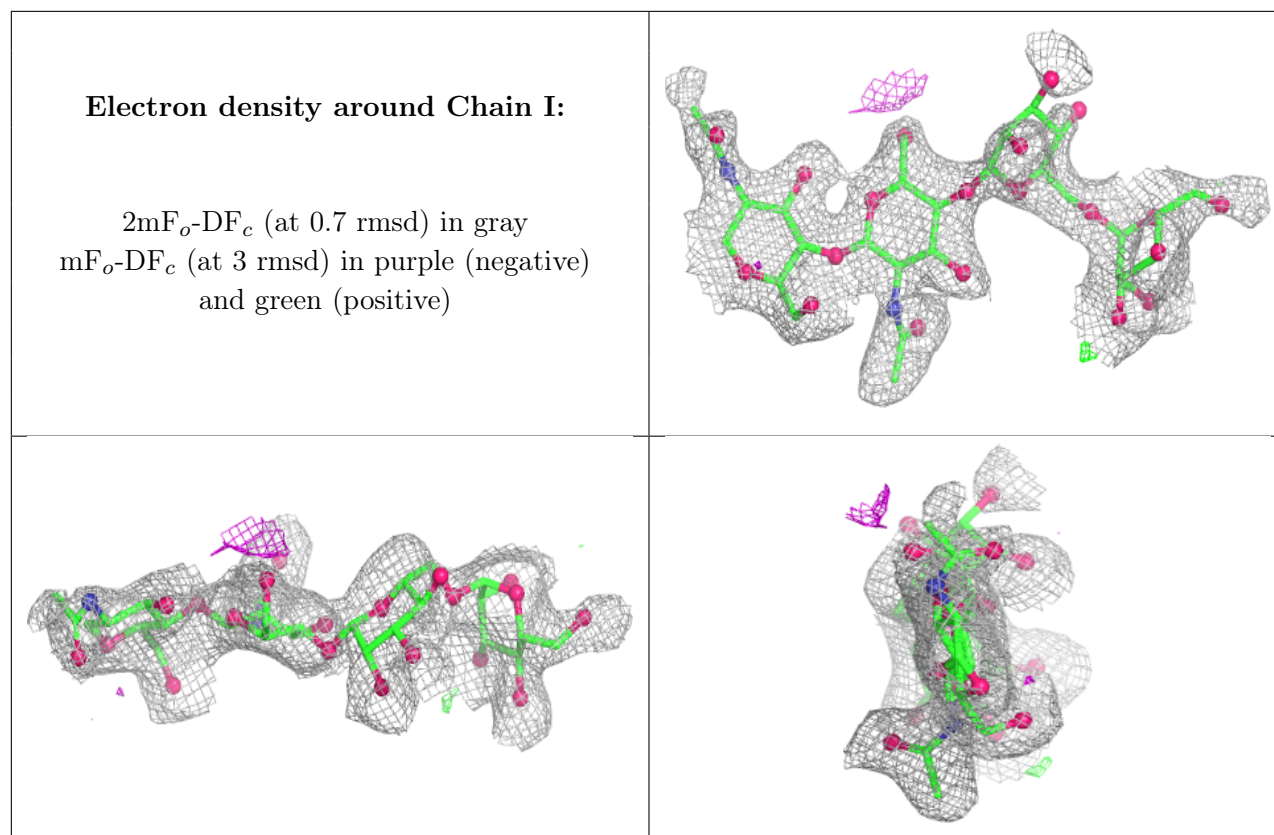
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	ACE	B	503	3/3	0.97	0.09	34,34,35,37	0
6	GOL	B	502	6/6	0.98	0.06	38,40,44,45	0
6	GOL	A	502	6/6	0.98	0.04	40,42,48,48	0
6	GOL	C	501	6/6	0.98	0.05	37,40,42,45	0
6	GOL	D	501	6/6	0.98	0.04	36,39,41,51	0
6	GOL	D	502	6/6	0.98	0.04	38,40,44,46	0
5	CIT	B	501	13/13	0.98	0.04	45,56,66,68	0
9	NAG	A	501	14/15	0.98	0.04	42,49,55,59	0
8	PO4	B	505	5/5	0.99	0.03	35,38,40,43	0
8	PO4	C	502	5/5	0.99	0.04	35,35,38,39	0
6	GOL	B	504	6/6	0.99	0.04	26,28,32,40	0
8	PO4	D	503	5/5	1.00	0.02	40,41,42,44	0
8	PO4	A	503	5/5	1.00	0.02	35,37,39,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.