



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:22 AM UTC

PDB ID : 8V06 / pdb_00008v06
Title : Crystal structure of mouse PLD3 co-crystallized with 5'Pi-ssDNA for 9 days
Authors : Yuan, M.; Wilson, I.A.
Deposited on : 2023-11-17
Resolution : 2.73 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:

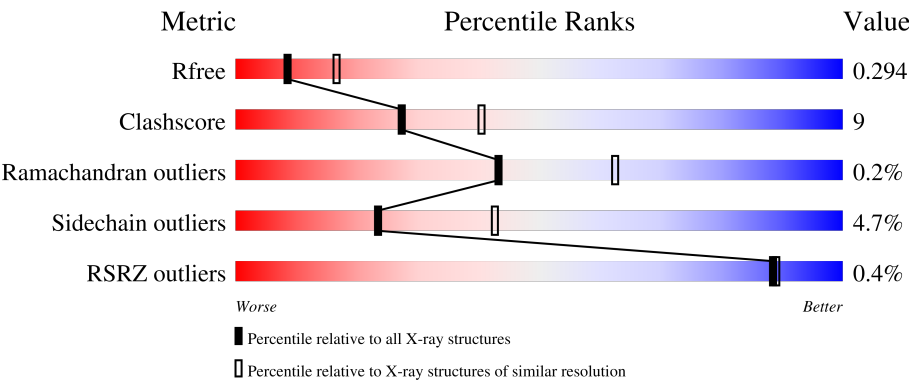
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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.



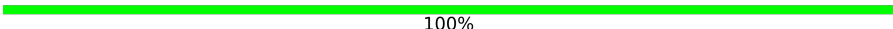
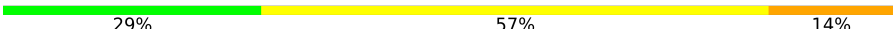
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	69%18%•12%
1	C	467	67%20%•12%
2	B	467	69%19%•11%
2	D	467	68%20%•12%
3	E	2	100%

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Mol	Chain	Length	Quality of chain
3	I	2	 50% 50%
4	F	3	 67% 33%
4	G	3	 100%
5	H	7	 29% 57% 14%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13397 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	A	412	Total	C	N	O	P	S	0	0	0
			3229	2040	562	609	1	17			
1	C	412	Total	C	N	O	P	S	0	0	0
			3227	2039	561	609	1	17			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
A	44	GLU	-	expression tag	UNP O35405
A	45	ASP	-	expression tag	UNP O35405
A	46	LEU	-	expression tag	UNP O35405

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Chain	Residue	Modelled	Actual	Comment	Reference
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
C	45	ASP	-	expression tag	UNP O35405
C	46	LEU	-	expression tag	UNP O35405
C	47	ALA	-	expression tag	UNP O35405

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Chain	Residue	Modelled	Actual	Comment	Reference
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

- Molecule 2 is a protein called 5'-3' exonuclease PLD3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	416	Total	C	N	O	S	0	0	0
			3252	2055	567	613	17			
2	D	413	Total	C	N	O	S	0	0	0
			3233	2045	564	607	17			

There are 82 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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

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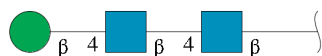
Chain	Residue	Modelled	Actual	Comment	Reference
D	38	GLN	-	expression tag	UNP O35405
D	39	LYS	-	expression tag	UNP O35405
D	40	LEU	-	expression tag	UNP O35405
D	41	ILE	-	expression tag	UNP O35405
D	42	SER	-	expression tag	UNP O35405
D	43	GLU	-	expression tag	UNP O35405
D	44	GLU	-	expression tag	UNP O35405
D	45	ASP	-	expression tag	UNP O35405
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 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



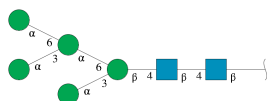
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 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.



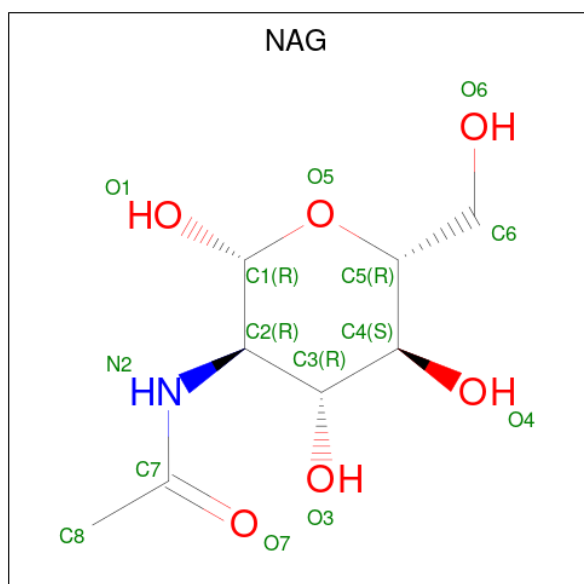
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 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.



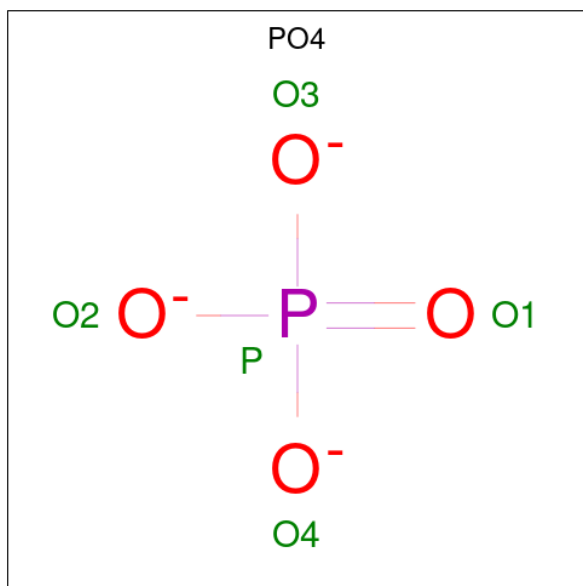
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	7	Total	C	N	O	0	0	0
			83	46	2	35			

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



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

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

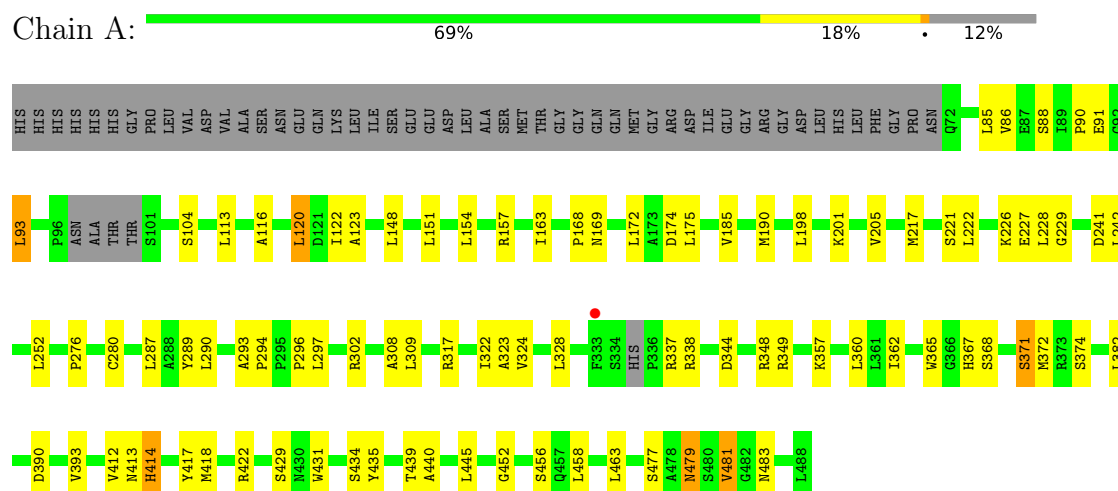
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	44	Total	O	0	0
			44	44		
8	B	50	Total	O	0	0
			50	50		
8	C	47	Total	O	0	0
			47	47		
8	D	46	Total	O	0	0
			46	46		

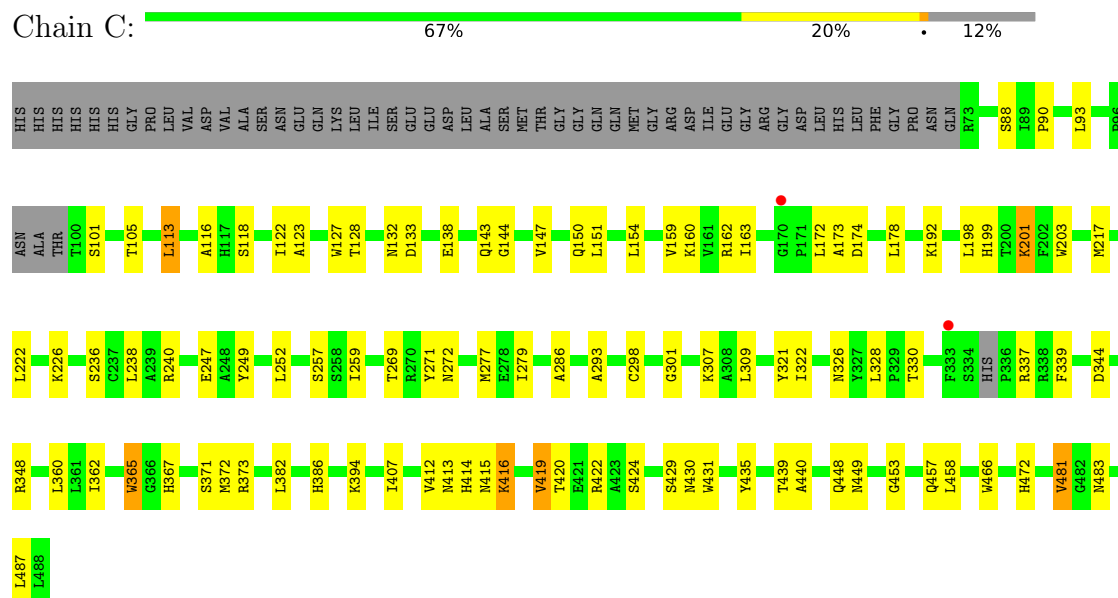
3 Residue-property plots

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

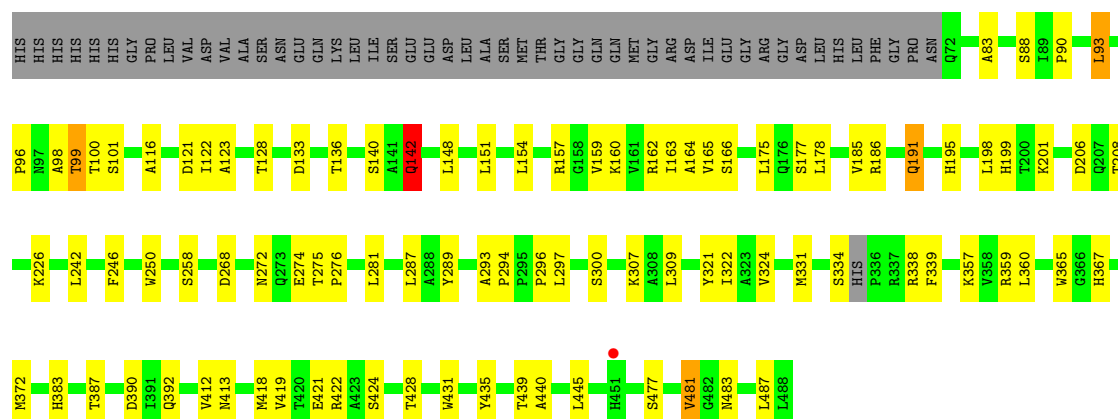


• Molecule 1: 5'-3' exonuclease PLD3



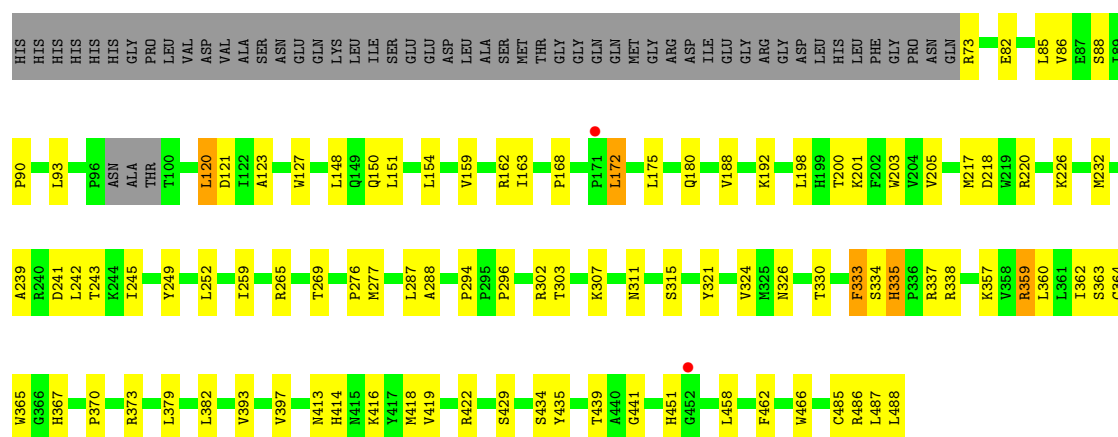
• Molecule 2: 5'-3' exonuclease PLD3

Chain B: 

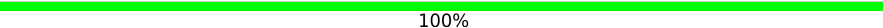


- Molecule 2: 5'-3' exonuclease PLD3

Chain D: 



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

Chain E: 



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

Chain I: 



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

Chain F:  67% 33%

MAN1
MAN2
BMA3

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

Chain G:  100%

MAN1
MAN2
BMA3

- Molecule 5: 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:  29% 57% 14%

MAN1
MAN2
BMA3
MAN4
MAN5
MAN6
MAN7

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.16Å 54.19Å 202.77Å 96.61° 89.16° 90.10°	Depositor
Resolution (Å)	49.92 – 2.73 49.92 – 2.73	Depositor EDS
% Data completeness (in resolution range)	93.8 (49.92-2.73) 88.0 (49.92-2.73)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.73Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.255 , 0.295 0.257 , 0.294	Depositor DCC
R_{free} test set	2643 reflections (4.34%)	wwPDB-VP
Wilson B-factor (Å ²)	37.2	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 22.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.159 for h,-k,-l 0.139 for -h,k,-k-l 0.110 for -h,-k,k+l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	13397	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.64% 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: BMA, NEP, NAG, MAN, PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.12	0/3297	0.31	0/4491
1	C	0.22	0/3295	0.41	1/4489 (0.0%)
2	B	0.19	0/3337	0.39	1/4550 (0.0%)
2	D	0.24	0/3319	0.43	2/4526 (0.0%)
All	All	0.20	0/13248	0.39	4/18056 (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
2	D	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	142	GLN	CA-CB-CG	5.99	126.07	114.10
2	D	359	ARG	CB-CG-CD	-5.69	98.21	111.30
1	C	449	ASN	N-CA-CB	5.57	116.59	110.35
2	D	333	PHE	CB-CA-C	-5.38	109.39	115.79

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	486	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3229	0	3129	53	0
1	C	3227	0	3129	70	0
2	B	3252	0	3156	55	0
2	D	3233	0	3137	61	0
3	E	28	0	25	0	0
3	I	28	0	25	1	0
4	F	39	0	34	0	0
4	G	39	0	32	0	0
5	H	83	0	70	1	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
6	D	14	0	13	0	0
7	B	5	0	0	1	0
7	D	5	0	0	0	0
8	A	44	0	0	0	0
8	B	50	0	0	4	0
8	C	47	0	0	8	0
8	D	46	0	0	5	0
All	All	13397	0	12776	236	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 (236) 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)
2:B:122:ILE:O	8:B:601:HOH:O	1.92	0.86
2:B:331:MET:HG3	2:B:338:ARG:HD2	1.58	0.85
1:C:269:THR:HG22	1:C:271:TYR:H	1.46	0.77
2:B:123:ALA:O	2:B:201:LYS:HA	1.85	0.76
1:C:88:SER:O	1:C:226:LYS:HA	1.85	0.76
2:D:88:SER:O	2:D:226:LYS:HA	1.86	0.75
1:C:151:LEU:HB3	1:C:178:LEU:HD21	1.69	0.75
1:A:168:PRO:HG3	1:A:172:LEU:HD11	1.66	0.75
1:A:322:ILE:HG12	1:A:418:MET:HG3	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:ASP:OD1	8:C:501:HOH:O	2.07	0.72
1:A:88:SER:O	1:A:226:LYS:HA	1.89	0.72
2:B:435:TYR:HA	2:B:439:THR:HB	1.72	0.71
1:C:174:ASP:OD1	8:C:501:HOH:O	2.07	0.71
1:A:172:LEU:HD13	1:A:175:LEU:HD12	1.72	0.69
1:C:365:TRP:CE2	1:C:367:HIS:HB2	2.27	0.69
2:B:88:SER:O	2:B:226:LYS:HA	1.94	0.68
1:C:113:LEU:HD21	1:C:151:LEU:HG	1.75	0.68
2:D:123:ALA:O	2:D:201:LYS:HA	1.94	0.68
2:D:435:TYR:HA	2:D:439:THR:HB	1.76	0.67
2:D:277:MET:O	2:D:287:LEU:HA	1.95	0.67
2:D:150:GLN:NE2	8:D:601:HOH:O	2.25	0.67
2:D:357:LYS:H	2:D:357:LYS:HD2	1.60	0.67
2:D:359:ARG:HB3	2:D:466:TRP:CZ3	2.30	0.66
2:B:372:MET:HE3	2:B:487:LEU:HD11	1.78	0.64
2:B:164:ALA:N	8:B:601:HOH:O	2.12	0.64
2:B:322:ILE:HG12	2:B:418:MET:HG3	1.80	0.64
1:C:419:VAL:HB	1:C:458:LEU:HD23	1.81	0.62
1:C:88:SER:OG	1:C:105:THR:OG1	2.12	0.62
2:D:294:PRO:HB2	2:D:296:PRO:HD2	1.81	0.62
1:A:344:ASP:OD2	1:A:348:ARG:NH2	2.30	0.61
2:B:186:ARG:NH1	2:B:250:TRP:O	2.34	0.61
1:A:452:GLY:HA2	1:A:456:SER:HB3	1.84	0.60
1:C:88:SER:HG	1:C:105:THR:HG1	1.42	0.59
1:A:328:LEU:HD13	1:A:372:MET:HG3	1.84	0.59
2:B:294:PRO:HB2	2:B:296:PRO:HD2	1.83	0.59
1:C:203:TRP:HZ2	1:C:217:MET:HE1	1.68	0.59
1:A:294:PRO:HB2	1:A:296:PRO:HD2	1.84	0.59
1:A:317:ARG:HG3	1:A:422:ARG:HH12	1.67	0.59
1:C:435:TYR:HA	1:C:439:THR:HB	1.85	0.59
2:B:98:ALA:O	2:B:99:THR:C	2.45	0.58
2:D:226:LYS:NZ	8:D:606:HOH:O	2.36	0.58
2:D:357:LYS:HD2	2:D:357:LYS:N	2.18	0.58
1:C:307:LYS:NZ	8:C:511:HOH:O	2.36	0.58
2:D:200:THR:HG22	2:D:441:GLY:HA2	1.84	0.58
2:D:321:TYR:O	2:D:418:MET:HA	2.04	0.58
1:A:435:TYR:HA	1:A:439:THR:HB	1.86	0.58
1:C:328:LEU:HD12	1:C:372:MET:HG3	1.86	0.57
2:B:357:LYS:HZ2	2:B:359:ARG:HE	1.52	0.57
2:B:383:HIS:NE2	2:B:390:ASP:OD1	2.38	0.57
1:C:386:HIS:CD2	2:D:370:PRO:HB2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:PRO:HD2	1:A:93:LEU:HD22	1.85	0.57
1:C:154:LEU:HD12	1:C:159:VAL:HG11	1.87	0.56
1:C:132:ASN:ND2	8:C:515:HOH:O	2.38	0.56
1:C:143:GLN:HB3	1:C:222:LEU:HD23	1.86	0.56
1:C:226:LYS:HB3	1:C:413:ASN:HA	1.86	0.56
2:D:148:LEU:HA	2:D:151:LEU:HD12	1.88	0.56
2:B:191:GLN:OE1	2:B:195:HIS:HA	2.06	0.56
1:C:128:THR:HG22	1:C:133:ASP:HB3	1.88	0.56
2:D:365:TRP:CE2	2:D:367:HIS:HB2	2.41	0.56
2:D:203:TRP:HZ2	2:D:217:MET:HE1	1.71	0.55
2:D:188:VAL:HB	2:D:198:LEU:HD12	1.86	0.55
1:A:365:TRP:CE2	1:A:367:HIS:HB2	2.42	0.55
1:C:123:ALA:O	1:C:201:LYS:HA	2.05	0.55
1:A:190:MET:HE2	1:A:440:ALA:HB2	1.89	0.55
1:A:217:MET:HE3	1:A:217:MET:HA	1.88	0.55
1:C:322:ILE:HB	1:C:360:LEU:HD12	1.88	0.55
1:C:90:PRO:HD2	1:C:93:LEU:HD12	1.88	0.55
1:A:123:ALA:O	1:A:201:LYS:HA	2.06	0.54
2:B:294:PRO:HD2	2:B:297:LEU:HD12	1.89	0.54
2:B:121:ASP:HB3	2:B:246:PHE:CE2	2.42	0.54
2:D:303:THR:HG23	2:D:307:LYS:HD3	1.88	0.54
2:B:206:ASP:O	5:H:5:MAN:O6	2.25	0.53
1:C:422:ARG:NH1	1:C:448:GLN:O	2.40	0.53
2:B:122:ILE:HB	2:B:163:ILE:HD13	1.91	0.52
1:A:322:ILE:HB	1:A:360:LEU:HD12	1.92	0.52
1:A:228:LEU:HD22	1:A:417:TYR:CD1	2.44	0.52
1:C:309:LEU:HD11	1:C:431:TRP:CE2	2.45	0.52
2:D:379:LEU:HA	2:D:382:LEU:HD23	1.92	0.52
2:D:422:ARG:NH2	8:D:607:HOH:O	2.37	0.52
2:B:116:ALA:O	2:B:157:ARG:NH2	2.33	0.52
2:D:414:HIS:O	2:D:416:LYS:HE3	2.10	0.52
1:A:348:ARG:HH11	1:A:382:LEU:HD11	1.75	0.51
2:B:421:GLU:OE2	2:B:422:ARG:NH1	2.44	0.51
2:D:120:LEU:HD12	2:D:205:VAL:HG22	1.92	0.51
2:D:485:CYS:SG	2:D:488:LEU:HD12	2.50	0.51
1:A:122:ILE:HB	1:A:163:ILE:HD13	1.91	0.51
2:D:172:LEU:HD13	2:D:175:LEU:HD12	1.93	0.51
2:B:275:THR:O	2:B:275:THR:OG1	2.26	0.51
2:B:128:THR:HG22	2:B:133:ASP:HB3	1.93	0.51
2:B:365:TRP:CE2	2:B:367:HIS:HB2	2.45	0.51
1:C:150:GLN:O	1:C:154:LEU:HD23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:429:SER:HB3	1:C:435:TYR:HB3	1.92	0.51
1:A:477:SER:OG	1:A:479:ASN:OD1	2.29	0.51
2:B:383:HIS:HD2	2:B:390:ASP:HA	1.74	0.50
1:C:226:LYS:NZ	8:C:503:HOH:O	2.44	0.50
2:B:268:ASP:OD2	2:B:300:SER:OG	2.28	0.50
2:D:429:SER:HB3	2:D:435:TYR:HB3	1.92	0.50
1:C:199:HIS:O	1:C:201:LYS:NZ	2.45	0.50
2:B:324:VAL:HG11	2:B:431:TRP:CD1	2.47	0.50
2:D:277:MET:HB2	2:D:288:ALA:O	2.11	0.50
2:D:321:TYR:CD2	2:D:462:PHE:HB3	2.46	0.50
2:D:321:TYR:CE1	2:D:359:ARG:CZ	2.95	0.49
2:D:359:ARG:HD3	2:D:462:PHE:HE1	1.77	0.49
2:D:120:LEU:N	8:D:612:HOH:O	2.46	0.49
2:B:226:LYS:HB3	2:B:413:ASN:HA	1.93	0.49
1:A:337:ARG:O	1:A:338:ARG:HD3	2.13	0.49
1:A:349:ARG:HG3	2:B:339:PHE:HB3	1.94	0.49
1:C:394:LYS:HG3	1:C:466:TRP:CZ2	2.48	0.49
2:D:218:ASP:OD2	2:D:220:ARG:NH2	2.45	0.49
2:D:241:ASP:OD2	2:D:302:ARG:NH2	2.43	0.49
2:D:360:LEU:HB3	2:D:393:VAL:HG22	1.95	0.49
1:C:373:ARG:NH1	1:C:487:LEU:O	2.45	0.49
1:A:481:VAL:HG12	1:A:483:ASN:H	1.78	0.49
1:C:293:ALA:O	1:C:440:ALA:HA	2.13	0.49
2:D:360:LEU:HG	2:D:362:ILE:HD11	1.95	0.48
1:C:192:LYS:NZ	8:C:504:HOH:O	2.44	0.48
1:C:415:ASN:C	1:C:416:LYS:HG2	2.37	0.48
1:A:308:ALA:HB1	1:A:445:LEU:HD21	1.94	0.48
1:C:412:VAL:HG12	1:C:413:ASN:N	2.29	0.48
2:D:334:SER:O	2:D:335:HIS:HB2	2.13	0.48
1:C:277:MET:HG2	1:C:279:ILE:HG23	1.96	0.48
2:B:96:PRO:HD2	2:B:99:THR:HG21	1.96	0.47
2:B:322:ILE:HB	2:B:360:LEU:HD12	1.95	0.47
1:C:286:ALA:HB2	1:C:448:GLN:HG3	1.96	0.47
2:D:252:LEU:HD21	2:D:259:ILE:HD13	1.96	0.47
1:A:148:LEU:HA	1:A:151:LEU:HD12	1.96	0.47
2:D:168:PRO:HG3	2:D:172:LEU:HD21	1.95	0.47
1:C:360:LEU:HG	1:C:362:ILE:CD1	2.43	0.47
1:A:357:LYS:HD3	1:A:390:ASP:HB3	1.95	0.47
1:C:481:VAL:HG12	1:C:483:ASN:H	1.79	0.47
1:A:201:LYS:NZ	1:A:414:NEP:O2P	2.40	0.47
2:D:239:ALA:O	2:D:243:THR:OG1	2.24	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:321:TYR:HB2	2:D:419:VAL:HG13	1.96	0.47
1:A:116:ALA:O	1:A:157:ARG:NH2	2.42	0.47
1:C:162:ARG:NH2	1:C:247:GLU:OE2	2.30	0.47
1:C:249:TYR:OH	1:C:440:ALA:HB1	2.15	0.47
1:C:321:TYR:HB2	1:C:419:VAL:HG13	1.96	0.47
1:A:289:TYR:CZ	1:A:445:LEU:HD13	2.50	0.46
1:C:144:GLY:O	1:C:147:VAL:HG22	2.15	0.46
2:B:359:ARG:NH2	8:B:613:HOH:O	2.47	0.46
1:A:163:ILE:HB	1:A:185:VAL:HG22	1.98	0.46
1:A:226:LYS:HB3	1:A:413:ASN:HA	1.98	0.46
1:A:324:VAL:HG11	1:A:431:TRP:CD1	2.51	0.46
2:D:276:PRO:HB2	2:D:287:LEU:HB3	1.96	0.46
1:C:344:ASP:CG	1:C:348:ARG:HE	2.23	0.46
2:D:373:ARG:NH1	2:D:487:LEU:O	2.48	0.46
1:A:241:ASP:OD1	1:A:302:ARG:NH2	2.49	0.46
2:B:99:THR:O	2:B:100:THR:C	2.58	0.45
2:B:309:LEU:HD11	2:B:431:TRP:CE2	2.51	0.45
1:A:113:LEU:HD22	1:A:154:LEU:HD11	1.97	0.45
2:B:383:HIS:CD2	2:B:390:ASP:HA	2.51	0.45
1:C:113:LEU:HD12	1:C:113:LEU:HA	1.80	0.45
2:D:232:MET:HE2	2:D:232:MET:HB2	1.80	0.45
2:D:360:LEU:HD12	2:D:360:LEU:HA	1.84	0.45
2:B:199:HIS:NE2	7:B:502:PO4:O4	2.41	0.45
1:C:252:LEU:HD21	1:C:259:ILE:HG13	1.98	0.45
1:C:430:ASN:HB2	1:C:435:TYR:CE2	2.52	0.45
1:C:422:ARG:HH12	1:C:448:GLN:C	2.25	0.45
2:D:330:THR:HB	2:D:338:ARG:O	2.16	0.45
2:D:73:ARG:N	8:D:613:HOH:O	2.50	0.45
1:A:309:LEU:HD11	1:A:431:TRP:CE2	2.52	0.44
1:A:323:ALA:HB3	1:A:417:TYR:CE1	2.52	0.44
1:C:127:TRP:CH2	1:C:217:MET:HE2	2.53	0.44
1:C:344:ASP:OD2	1:C:348:ARG:NE	2.47	0.44
2:D:82:GLU:OE2	3:I:1:NAG:O6	2.25	0.44
2:B:160:LYS:HE2	2:B:162:ARG:HD3	1.99	0.44
2:D:121:ASP:HA	2:D:162:ARG:O	2.18	0.44
1:A:228:LEU:HG	1:A:229:GLY:N	2.32	0.44
2:B:274:GLU:OE2	2:B:307:LYS:NZ	2.45	0.44
2:B:142:GLN:C	2:B:142:GLN:CD	2.86	0.44
1:C:360:LEU:HG	1:C:362:ILE:HD11	2.00	0.44
2:B:121:ASP:HB3	2:B:246:PHE:CD2	2.53	0.43
2:B:154:LEU:HD13	2:B:159:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:175:LEU:HD13	2:B:185:VAL:HG11	2.00	0.43
2:B:321:TYR:HB2	2:B:419:VAL:HG13	1.99	0.43
2:D:458:LEU:HD23	2:D:458:LEU:HA	1.85	0.43
2:D:90:PRO:HD2	2:D:93:LEU:HD22	1.99	0.43
2:B:293:ALA:O	2:B:440:ALA:HA	2.19	0.43
1:C:199:HIS:HE1	1:C:416:LYS:NZ	2.16	0.43
1:C:453:GLY:O	1:C:457:GLN:HG3	2.18	0.43
2:D:127:TRP:CE2	2:D:217:MET:HG3	2.53	0.43
1:A:293:ALA:O	1:A:440:ALA:HA	2.18	0.43
1:A:360:LEU:HG	1:A:362:ILE:HD11	2.00	0.43
2:D:359:ARG:HD3	2:D:462:PHE:CE1	2.53	0.43
1:A:120:LEU:HD12	1:A:205:VAL:HG22	1.99	0.43
1:A:242:LEU:HD13	1:A:290:LEU:HD13	2.00	0.43
1:A:328:LEU:HD12	1:A:328:LEU:HA	1.79	0.43
2:B:164:ALA:HA	2:B:186:ARG:O	2.17	0.43
1:A:458:LEU:HD23	1:A:458:LEU:HA	1.87	0.43
1:C:138:GLU:HG3	1:C:407:ILE:HG12	2.00	0.43
1:A:252:LEU:HD23	1:A:252:LEU:HA	1.84	0.43
2:B:331:MET:HG3	2:B:338:ARG:CD	2.39	0.43
1:C:122:ILE:HB	1:C:163:ILE:HD13	2.00	0.43
1:C:127:TRP:HB2	1:C:172:LEU:HD13	2.01	0.43
1:A:252:LEU:HD12	1:A:297:LEU:HD21	2.00	0.42
1:C:422:ARG:HA	1:C:422:ARG:HD2	1.87	0.42
2:B:151:LEU:HB3	2:B:178:LEU:HD21	2.02	0.42
1:C:113:LEU:HG	1:C:154:LEU:HD21	2.00	0.42
2:D:200:THR:HG22	2:D:441:GLY:CA	2.48	0.42
2:D:333:PHE:HB3	2:D:334:SER:H	1.61	0.42
2:B:289:TYR:CZ	2:B:445:LEU:HD13	2.54	0.42
1:C:236:SER:O	1:C:240:ARG:HG3	2.19	0.42
1:A:276:PRO:HB2	1:A:287:LEU:HB3	2.01	0.42
2:B:281:LEU:HD12	2:B:281:LEU:HA	1.87	0.42
1:C:113:LEU:HD23	1:C:150:GLN:HB2	2.02	0.42
1:C:269:THR:O	1:C:301:GLY:HA3	2.20	0.42
2:D:321:TYR:HD2	2:D:462:PHE:HB3	1.83	0.42
1:C:330:THR:HG22	1:C:339:PHE:HD1	1.85	0.42
2:D:200:THR:HG21	2:D:249:TYR:OH	2.20	0.42
1:A:221:SER:OG	1:A:227:GLU:OE2	2.31	0.42
1:C:173:ALA:N	8:C:501:HOH:O	2.53	0.42
2:D:363:SER:OG	2:D:413:ASN:HB3	2.20	0.42
1:C:160:LYS:HE2	1:C:162:ARG:HD2	2.01	0.41
1:C:326:ASN:HB2	1:C:430:ASN:CG	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:481:VAL:HG12	2:B:483:ASN:H	1.84	0.41
2:D:311:ASN:OD1	2:D:315:SER:OG	2.38	0.41
2:D:364:CYS:O	2:D:397:VAL:HG13	2.19	0.41
1:A:371:SER:HB2	2:B:387:THR:HG22	2.02	0.41
2:B:90:PRO:HD2	2:B:93:LEU:HD12	2.03	0.41
2:B:359:ARG:NH2	8:B:607:HOH:O	2.39	0.41
1:C:116:ALA:HB3	1:C:154:LEU:HD11	2.02	0.41
1:A:429:SER:HB3	1:A:435:TYR:HB3	2.03	0.41
1:A:174:ASP:OD1	1:A:174:ASP:N	2.52	0.41
2:B:165:VAL:HG11	2:B:175:LEU:HD11	2.02	0.41
2:B:83:ALA:HB2	2:B:281:LEU:HD11	2.03	0.41
2:B:276:PRO:HB2	2:B:287:LEU:HB3	2.02	0.41
1:A:294:PRO:HD3	1:A:440:ALA:HA	2.02	0.40
1:A:360:LEU:HB3	1:A:393:VAL:HG22	2.03	0.40
1:C:412:VAL:CG1	1:C:413:ASN:N	2.84	0.40
1:C:472:HIS:CE1	1:C:481:VAL:HG22	2.55	0.40
2:D:180:GLN:O	2:D:180:GLN:HG2	2.21	0.40
2:D:242:LEU:HD23	2:D:245:ILE:HD12	2.03	0.40
2:D:324:VAL:HG22	2:D:326:ASN:H	1.87	0.40
1:C:348:ARG:NH1	1:C:382:LEU:HD11	2.36	0.40
1:A:85:LEU:HD23	1:A:85:LEU:HA	1.89	0.40
1:C:422:ARG:NH2	8:C:516:HOH:O	2.45	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	405/467 (87%)	389 (96%)	16 (4%)	0	100	100
1	C	405/467 (87%)	390 (96%)	15 (4%)	0	100	100
2	B	412/467 (88%)	396 (96%)	15 (4%)	1 (0%)	43	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	409/467 (88%)	393 (96%)	14 (3%)	2 (0%)	24	40
All	All	1631/1868 (87%)	1568 (96%)	60 (4%)	3 (0%)	43	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	335	HIS
2	B	99	THR
2	D	337	ARG

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	352/397 (89%)	335 (95%)	17 (5%)	23	42
1	C	352/397 (89%)	335 (95%)	17 (5%)	23	42
2	B	356/398 (89%)	335 (94%)	21 (6%)	18	32
2	D	354/398 (89%)	342 (97%)	12 (3%)	32	55
All	All	1414/1590 (89%)	1347 (95%)	67 (5%)	23	43

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	VAL
1	A	91	GLU
1	A	93	LEU
1	A	104	SER
1	A	120	LEU
1	A	169	ASN
1	A	198	LEU
1	A	222	LEU
1	A	280	CYS
1	A	368	SER
1	A	371	SER

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Mol	Chain	Res	Type
1	A	374	SER
1	A	412	VAL
1	A	434	SER
1	A	463	LEU
1	A	479	ASN
1	A	481	VAL
2	B	93	LEU
2	B	101	SER
2	B	136	THR
2	B	140	SER
2	B	142	GLN
2	B	148	LEU
2	B	166	SER
2	B	177	SER
2	B	191	GLN
2	B	198	LEU
2	B	208	THR
2	B	242	LEU
2	B	258	SER
2	B	272	ASN
2	B	334	SER
2	B	392	GLN
2	B	412	VAL
2	B	424	SER
2	B	428	THR
2	B	477	SER
2	B	481	VAL
1	C	101	SER
1	C	113	LEU
1	C	118	SER
1	C	198	LEU
1	C	201	LYS
1	C	238	LEU
1	C	257	SER
1	C	272	ASN
1	C	298	CYS
1	C	337	ARG
1	C	365	TRP
1	C	371	SER
1	C	416	LYS
1	C	419	VAL
1	C	420	THR

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Mol	Chain	Res	Type
1	C	424	SER
1	C	481	VAL
2	D	85	LEU
2	D	86	VAL
2	D	120	LEU
2	D	154	LEU
2	D	159	VAL
2	D	163	ILE
2	D	172	LEU
2	D	192	LYS
2	D	265	ARG
2	D	269	THR
2	D	434	SER
2	D	451	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	HIS
1	A	184	GLN
1	A	386	HIS
1	A	457	GLN
2	B	414	HIS
1	C	135	HIS
1	C	199	HIS
1	C	386	HIS
1	C	430	ASN
1	C	457	GLN
2	D	216	ASN
2	D	386	HIS
2	D	413	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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$
1	NEP	A	414	1	11,14,15	1.23	1 (9%)	8,20,22	1.27	0
1	NEP	C	414	1	11,14,15	3.45	3 (27%)	8,20,22	2.94	1 (12%)

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
1	NEP	A	414	1	-	3/5/12/14	0/1/1/1
1	NEP	C	414	1	-	2/5/12/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	414	NEP	P-O3P	10.05	1.61	1.46
1	C	414	NEP	P-O1P	-4.04	1.46	1.56
1	A	414	NEP	CD2-CG	2.55	1.40	1.36
1	C	414	NEP	CD2-CG	2.46	1.40	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	414	NEP	O2P-P-O3P	-7.71	93.98	112.95

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	414	NEP	O-C-CA-CB
1	A	414	NEP	N-CA-CB-CG
1	A	414	NEP	C-CA-CB-CG
1	C	414	NEP	N-CA-CB-CG
1	C	414	NEP	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	414	NEP	1	0

5.5 Carbohydrates [i](#)

17 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$
3	NAG	E	1	1,3	14,14,15	0.29	0	17,19,21	0.51	0
3	NAG	E	2	3	14,14,15	0.30	0	17,19,21	0.40	0
4	NAG	F	1	2,4	14,14,15	0.45	0	17,19,21	0.88	0
4	NAG	F	2	4	14,14,15	0.42	0	17,19,21	1.08	1 (5%)
4	BMA	F	3	4	11,11,12	0.81	0	15,15,17	0.72	0
4	NAG	G	1	2,4	14,14,15	0.30	0	17,19,21	0.63	0
4	NAG	G	2	4	14,14,15	0.21	0	17,19,21	0.45	0
4	BMA	G	3	4	11,11,12	0.60	0	15,15,17	0.66	0
5	NAG	H	1	1,5	14,14,15	0.35	0	17,19,21	0.71	0
5	NAG	H	2	5	14,14,15	0.29	0	17,19,21	0.50	0
5	BMA	H	3	5	11,11,12	0.77	0	15,15,17	1.12	2 (13%)
5	MAN	H	4	5	11,11,12	0.71	0	15,15,17	0.93	1 (6%)
5	MAN	H	5	5	11,11,12	0.63	0	15,15,17	0.89	2 (13%)
5	MAN	H	6	5	11,11,12	0.67	0	15,15,17	0.89	1 (6%)
5	MAN	H	7	5	11,11,12	0.68	0	15,15,17	0.98	2 (13%)
3	NAG	I	1	2,3	14,14,15	0.29	0	17,19,21	0.54	0
3	NAG	I	2	3	14,14,15	0.20	0	17,19,21	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
3	NAG	E	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
4	NAG	F	1	2,4	-	4/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	NAG	G	1	2,4	-	4/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
5	NAG	H	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	H	2	5	-	2/6/23/26	0/1/1/1
5	BMA	H	3	5	-	0/2/19/22	0/1/1/1
5	MAN	H	4	5	-	1/2/19/22	0/1/1/1
5	MAN	H	5	5	-	0/2/19/22	0/1/1/1
5	MAN	H	6	5	-	1/2/19/22	0/1/1/1
5	MAN	H	7	5	-	2/2/19/22	0/1/1/1
3	NAG	I	1	2,3	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	2	NAG	C3-C4-C5	3.34	116.28	110.23
5	H	7	MAN	C1-O5-C5	2.42	115.44	112.19
5	H	3	BMA	C1-O5-C5	2.22	115.16	112.19
5	H	3	BMA	C1-C2-C3	2.22	112.88	109.64
5	H	5	MAN	O2-C2-C3	-2.16	105.68	110.15
5	H	7	MAN	O2-C2-C3	-2.11	105.79	110.15
5	H	6	MAN	O2-C2-C3	-2.10	105.80	110.15
5	H	4	MAN	O2-C2-C3	-2.10	105.80	110.15
5	H	5	MAN	C1-O5-C5	2.01	114.88	112.19

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	7	MAN	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
5	H	7	MAN	C4-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6

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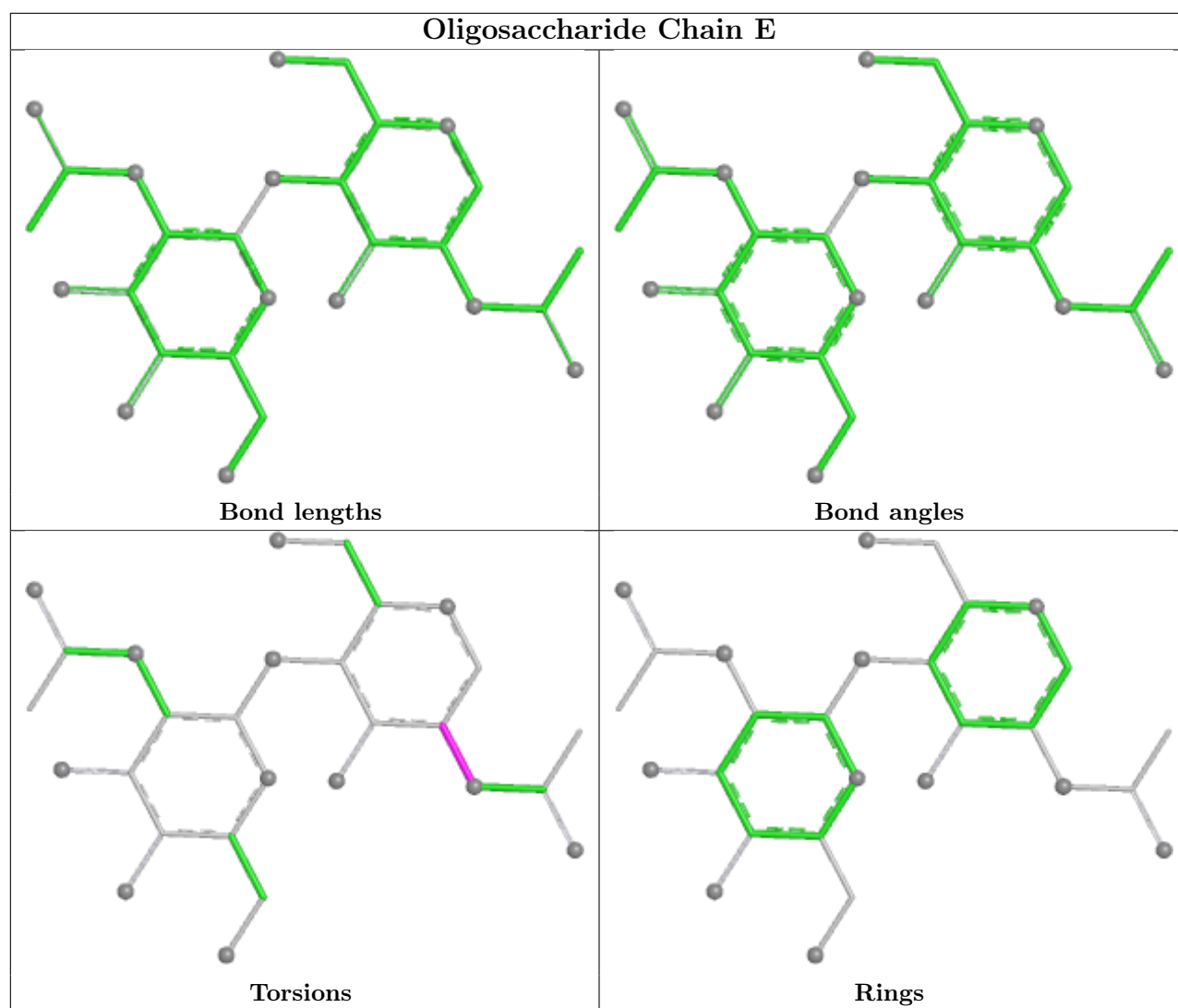
Mol	Chain	Res	Type	Atoms
3	I	2	NAG	O5-C5-C6-O6
5	H	2	NAG	O5-C5-C6-O6
5	H	2	NAG	C4-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	I	1	NAG	C8-C7-N2-C2
3	I	1	NAG	O7-C7-N2-C2
3	I	2	NAG	C4-C5-C6-O6
5	H	4	MAN	O5-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
5	H	6	MAN	O5-C5-C6-O6
4	G	1	NAG	C4-C5-C6-O6
4	G	1	NAG	O5-C5-C6-O6
4	F	1	NAG	C3-C2-N2-C7
4	G	1	NAG	C3-C2-N2-C7
5	H	1	NAG	C3-C2-N2-C7
4	F	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C1-C2-N2-C7
4	F	1	NAG	C1-C2-N2-C7
4	G	1	NAG	C1-C2-N2-C7
5	H	1	NAG	C1-C2-N2-C7

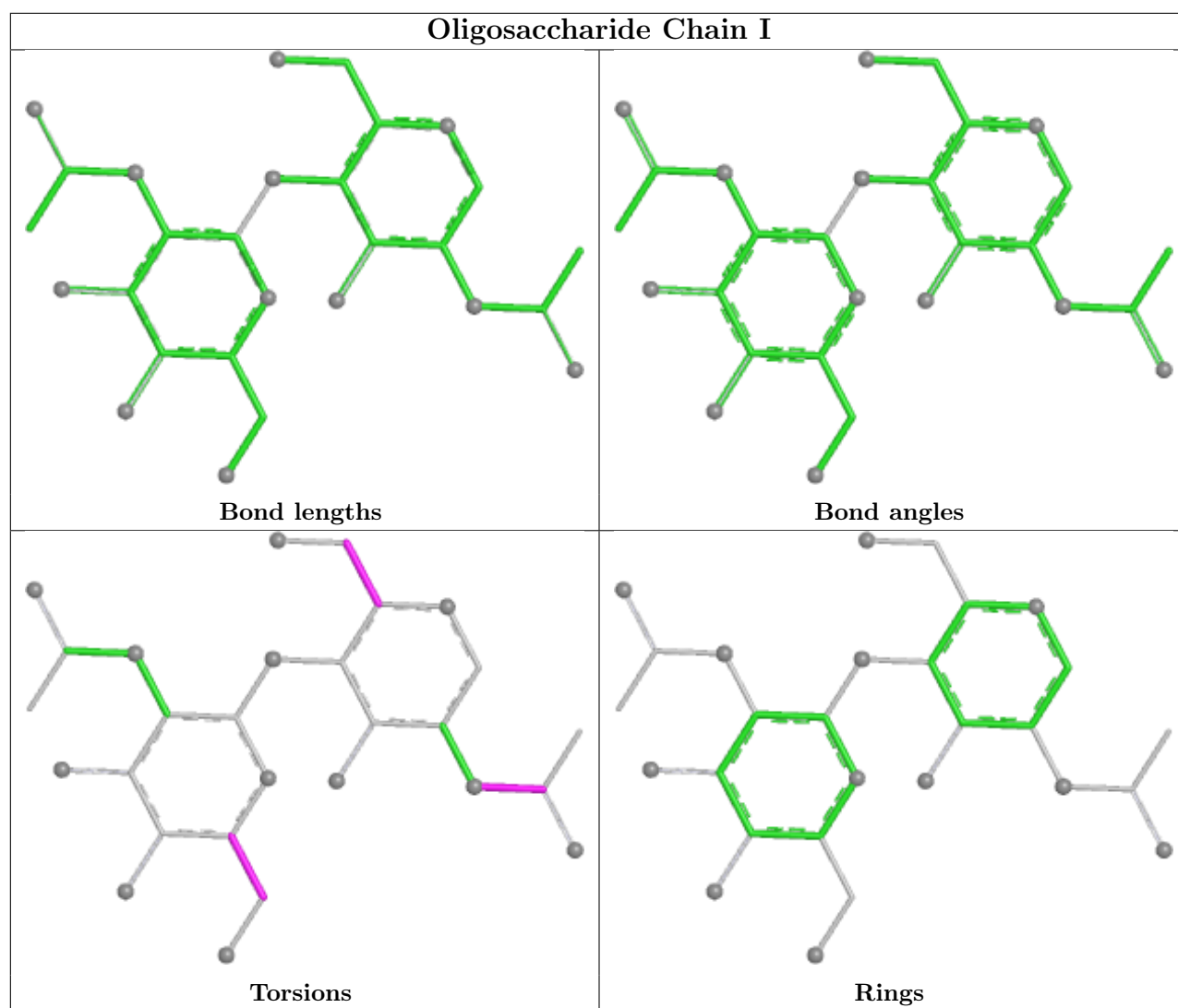
There are no ring outliers.

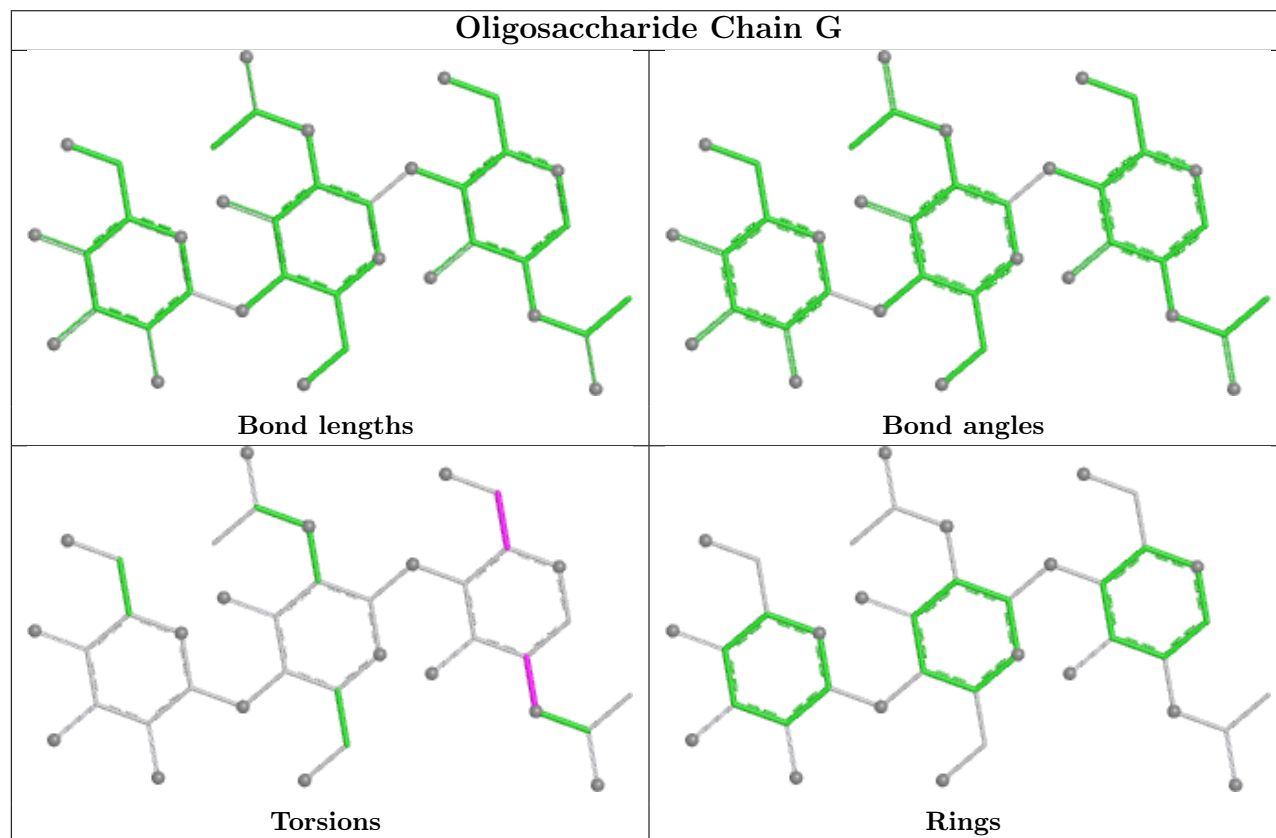
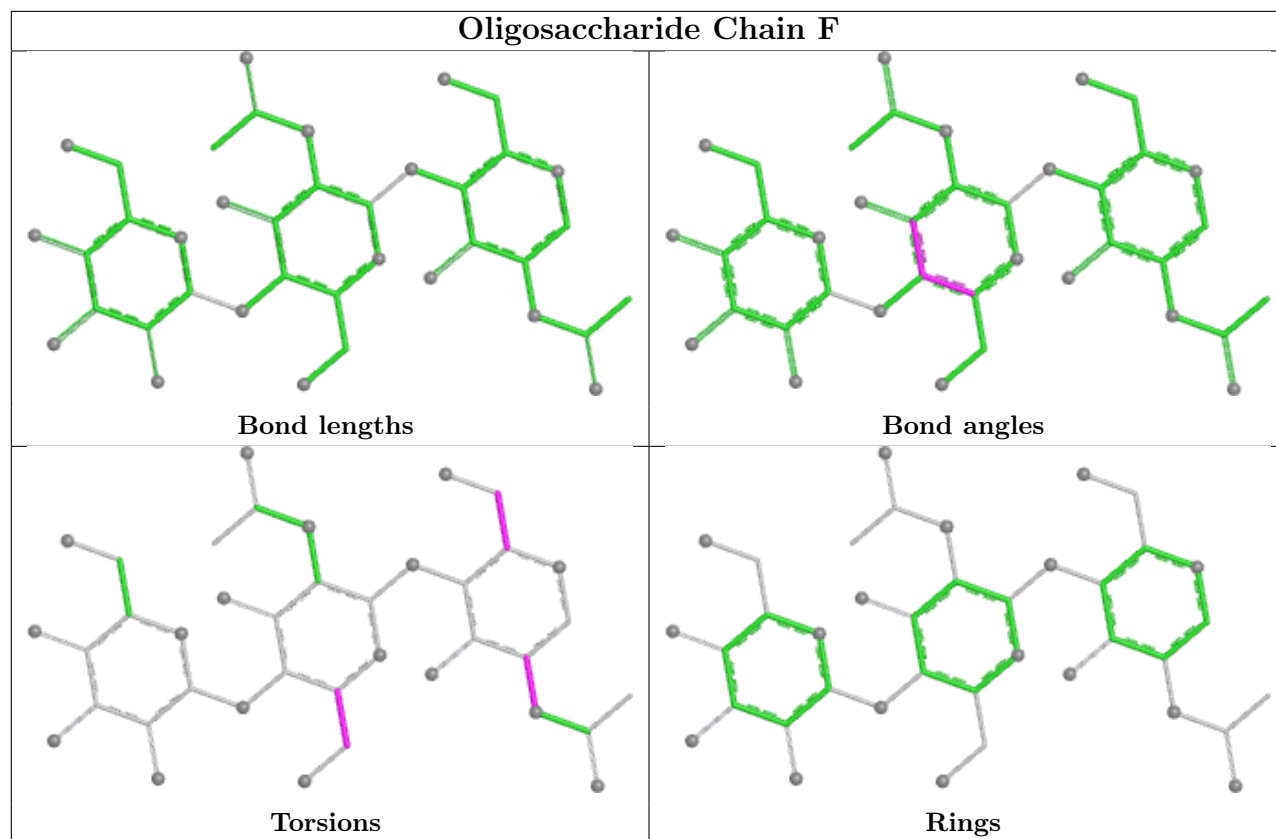
2 monomers are involved in 2 short contacts:

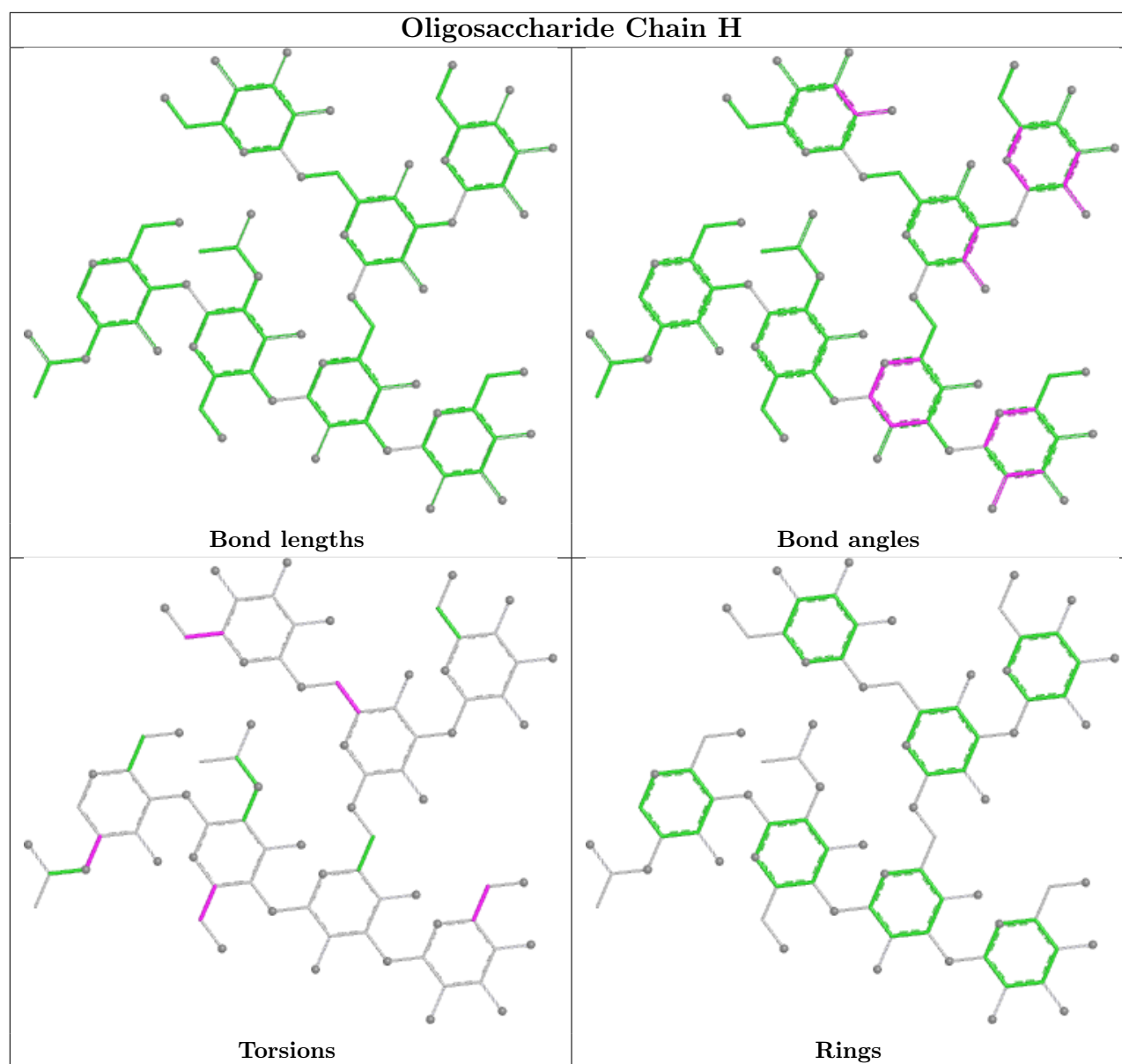
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	1	NAG	1	0
5	H	5	MAN	1	0

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](#)

5 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	NAG	D	501	2	14,14,15	0.31	0	17,19,21	0.50	0
6	NAG	B	501	2	14,14,15	0.27	0	17,19,21	0.48	0
7	PO4	B	502	-	4,4,4	0.95	0	6,6,6	0.47	0
7	PO4	D	502	-	4,4,4	0.97	0	6,6,6	0.47	0
6	NAG	A	501	1	14,14,15	0.31	0	17,19,21	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
6	NAG	B	501	2	-	0/6/23/26	0/1/1/1
6	NAG	A	501	1	-	2/6/23/26	0/1/1/1
6	NAG	D	501	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	501	NAG	O5-C5-C6-O6
6	A	501	NAG	C4-C5-C6-O6
6	D	501	NAG	C8-C7-N2-C2
6	D	501	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	502	PO4	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	411/467 (88%)	-0.98	1 (0%) 91 92	17, 30, 53, 125	0
1	C	411/467 (88%)	-0.46	2 (0%) 87 87	33, 51, 76, 159	0
2	B	416/467 (89%)	-0.94	1 (0%) 91 92	19, 31, 60, 127	0
2	D	413/467 (88%)	-0.34	2 (0%) 87 87	30, 56, 88, 160	0
All	All	1651/1868 (88%)	-0.68	6 (0%) 88 89	17, 45, 75, 160	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	170	GLY	4.7
2	D	452	GLY	3.2
1	C	333	PHE	3.1
1	A	333	PHE	2.6
2	D	171	PRO	2.5
2	B	451	HIS	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	NEP	C	414	14/15	0.98	0.07	33,51,66,74	0
1	NEP	A	414	14/15	0.99	0.05	11,32,50,53	0

6.3 Carbohydrates ⓘ

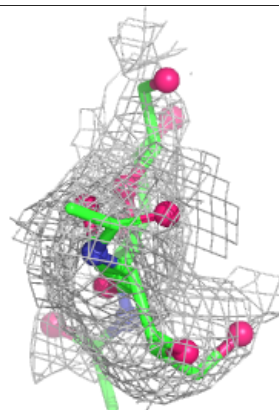
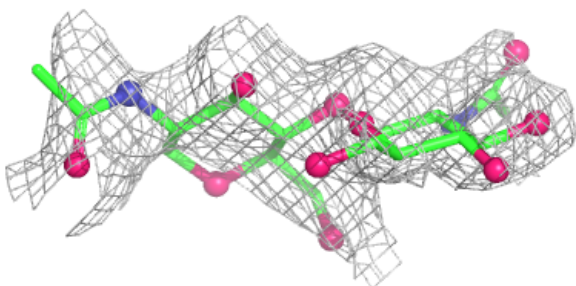
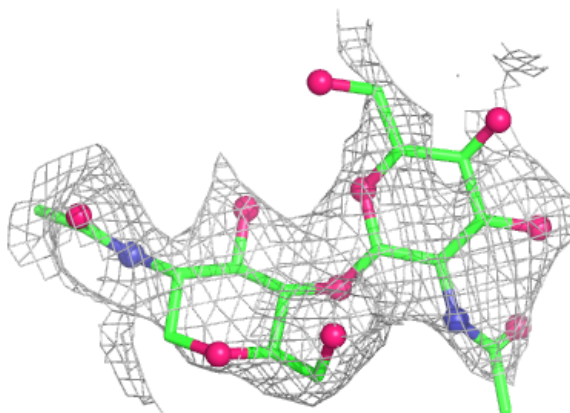
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	E	2	14/15	0.94	0.10	47,59,72,81	0
4	NAG	F	2	14/15	0.95	0.11	48,74,108,124	0
4	BMA	F	3	11/12	0.95	0.13	63,85,109,120	0
3	NAG	I	2	14/15	0.96	0.10	37,74,97,106	0
4	NAG	G	2	14/15	0.96	0.09	40,60,82,88	0
5	NAG	H	1	14/15	0.96	0.07	35,58,70,71	0
5	MAN	H	4	11/12	0.96	0.09	41,61,73,74	0
5	MAN	H	6	11/12	0.96	0.09	49,76,89,90	0
4	NAG	F	1	14/15	0.97	0.08	30,56,73,81	0
4	BMA	G	3	11/12	0.97	0.07	48,60,71,74	0
3	NAG	I	1	14/15	0.97	0.07	54,69,86,86	0
3	NAG	E	1	14/15	0.97	0.08	40,52,59,62	0
5	MAN	H	5	11/12	0.97	0.08	46,56,68,86	0
4	NAG	G	1	14/15	0.97	0.07	38,50,60,63	0
5	NAG	H	2	14/15	0.98	0.06	44,55,65,72	0
5	MAN	H	7	11/12	0.98	0.07	32,55,69,72	0
5	BMA	H	3	11/12	0.99	0.04	41,45,50,58	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.

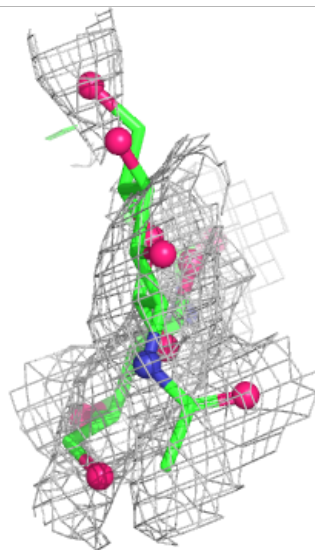
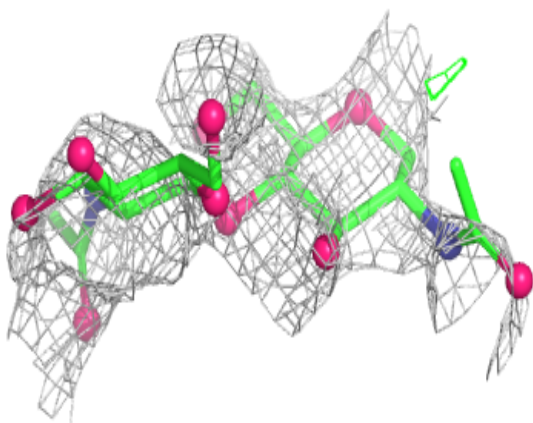
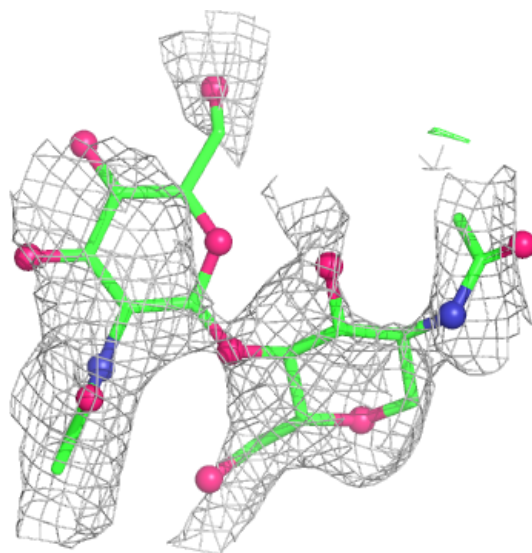
Electron density around Chain E:

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



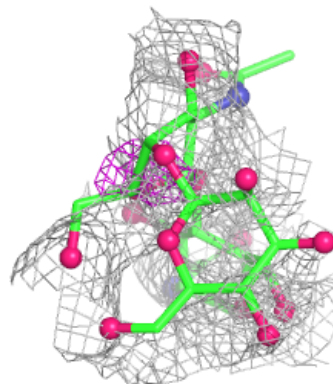
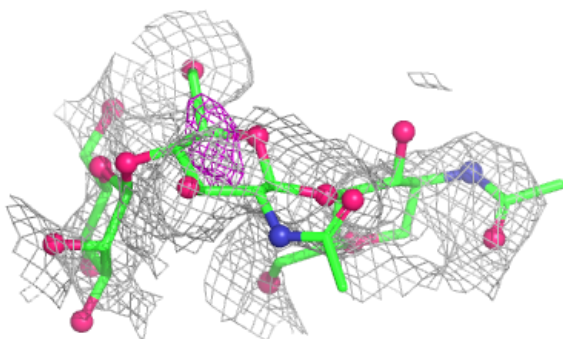
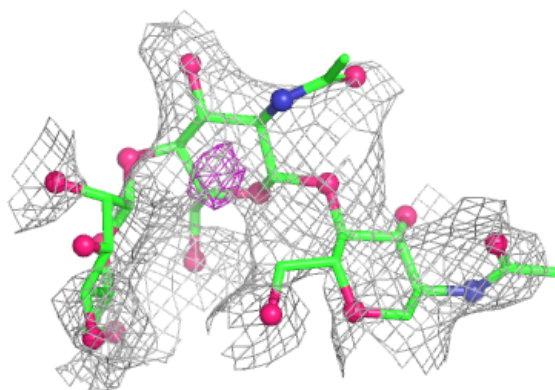
Electron density around Chain I:

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



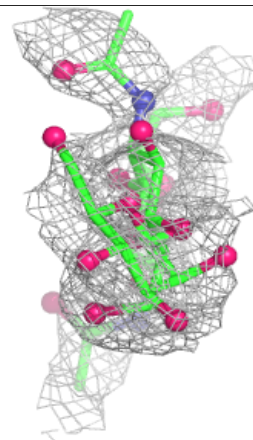
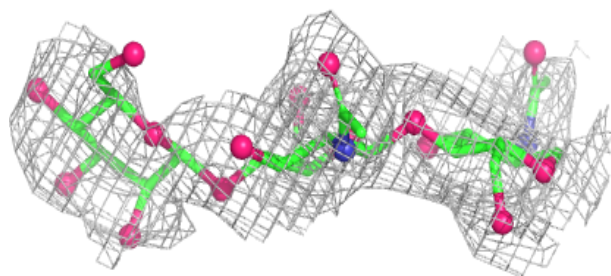
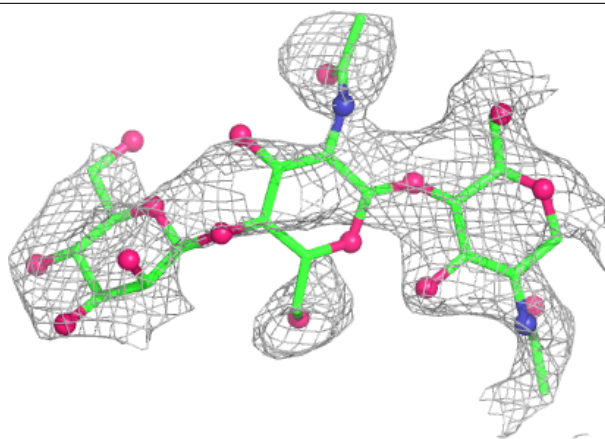
Electron density around Chain F:

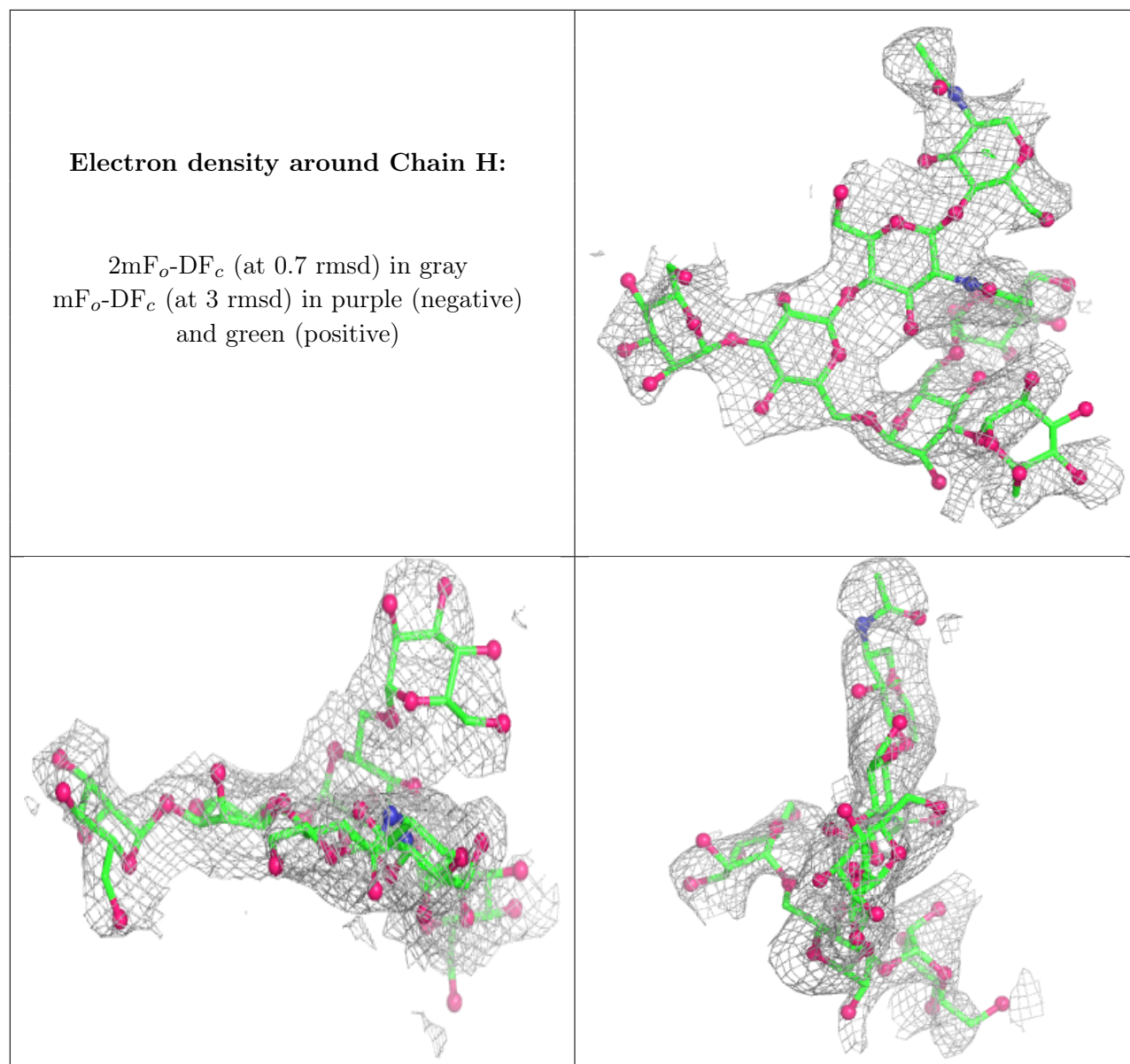
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain 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 [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
6	NAG	B	501	14/15	0.95	0.09	45,63,77,85	0
6	NAG	D	501	14/15	0.96	0.11	49,76,84,84	0
6	NAG	A	501	14/15	0.97	0.07	34,52,64,65	0
7	PO4	B	502	5/5	0.99	0.04	25,26,38,45	0
7	PO4	D	502	5/5	0.99	0.04	46,46,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.