



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 12:13 AM UTC

PDB ID : 9KP4 / pdb_00009kp4
Title : Crystal structure of human CASTOR1 in apo form
Authors : Liu, C.; Ding, J.; Zhang, T.
Deposited on : 2024-11-22
Resolution : 3.08 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

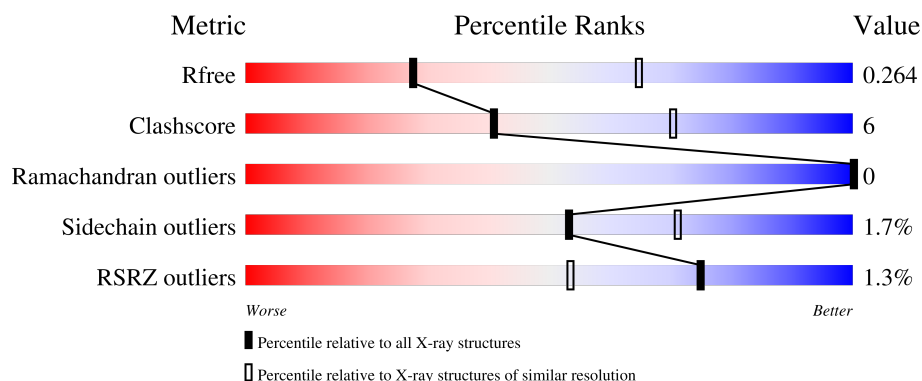
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.08 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	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	704	<div> <div>0%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>7%</div> </div> </div>
1	B	704	<div> <div>0%</div> <div> <div></div> <div>77%</div> <div>12%</div> <div>11%</div> </div> </div>
1	C	704	<div> <div>2%</div> <div> <div></div> <div>61%</div> <div>15%</div> <div>23%</div> </div> </div>
1	D	704	<div> <div></div> <div> <div></div> <div>74%</div> <div>15%</div> <div>10%</div> </div> </div>
2	G	2	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	H	2	 100%
2	I	2	 100%
2	J	2	 50% 50%

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
4	ACY	D	403	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18780 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 Maltose/maltodextrin-binding periplasmic protein,Cytosolic arginine sensor for mTORC1 subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	656	Total	C	N	O	S	0	0	0
			4960	3201	804	941	14			
1	B	626	Total	C	N	O	S	0	0	0
			4758	3074	778	894	12			
1	C	540	Total	C	N	O	S	0	0	0
			4071	2643	663	753	12			
1	D	635	Total	C	N	O	S	0	0	0
			4875	3155	789	918	13			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-374	MET	-	initiating methionine	UNP P0AEX9
A	-292	ALA	ASP	conflict	UNP P0AEX9
A	-291	ALA	LYS	conflict	UNP P0AEX9
A	-202	ALA	GLU	conflict	UNP P0AEX9
A	-201	ALA	ASN	conflict	UNP P0AEX9
A	-135	ALA	LYS	conflict	UNP P0AEX9
A	-15	ALA	GLU	conflict	UNP P0AEX9
A	-12	ALA	LYS	conflict	UNP P0AEX9
A	-11	ALA	ASP	conflict	UNP P0AEX9
A	-7	ASN	-	linker	UNP P0AEX9
A	-6	ALA	-	linker	UNP P0AEX9
A	-5	VAL	-	linker	UNP P0AEX9
A	-4	ASP	-	linker	UNP P0AEX9
A	-3	SER	-	linker	UNP P0AEX9
A	-2	ALA	-	linker	UNP P0AEX9
A	-1	ALA	-	linker	UNP P0AEX9
A	0	ALA	-	linker	UNP P0AEX9
B	-374	MET	-	initiating methionine	UNP P0AEX9
B	-292	ALA	ASP	conflict	UNP P0AEX9
B	-291	ALA	LYS	conflict	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-202	ALA	GLU	conflict	UNP P0AEX9
B	-201	ALA	ASN	conflict	UNP P0AEX9
B	-135	ALA	LYS	conflict	UNP P0AEX9
B	-15	ALA	GLU	conflict	UNP P0AEX9
B	-12	ALA	LYS	conflict	UNP P0AEX9
B	-11	ALA	ASP	conflict	UNP P0AEX9
B	-7	ASN	-	linker	UNP P0AEX9
B	-6	ALA	-	linker	UNP P0AEX9
B	-5	VAL	-	linker	UNP P0AEX9
B	-4	ASP	-	linker	UNP P0AEX9
B	-3	SER	-	linker	UNP P0AEX9
B	-2	ALA	-	linker	UNP P0AEX9
B	-1	ALA	-	linker	UNP P0AEX9
B	0	ALA	-	linker	UNP P0AEX9
C	-374	MET	-	initiating methionine	UNP P0AEX9
C	-292	ALA	ASP	conflict	UNP P0AEX9
C	-291	ALA	LYS	conflict	UNP P0AEX9
C	-202	ALA	GLU	conflict	UNP P0AEX9
C	-201	ALA	ASN	conflict	UNP P0AEX9
C	-135	ALA	LYS	conflict	UNP P0AEX9
C	-15	ALA	GLU	conflict	UNP P0AEX9
C	-12	ALA	LYS	conflict	UNP P0AEX9
C	-11	ALA	ASP	conflict	UNP P0AEX9
C	-7	ASN	-	linker	UNP P0AEX9
C	-6	ALA	-	linker	UNP P0AEX9
C	-5	VAL	-	linker	UNP P0AEX9
C	-4	ASP	-	linker	UNP P0AEX9
C	-3	SER	-	linker	UNP P0AEX9
C	-2	ALA	-	linker	UNP P0AEX9
C	-1	ALA	-	linker	UNP P0AEX9
C	0	ALA	-	linker	UNP P0AEX9
D	-374	MET	-	initiating methionine	UNP P0AEX9
D	-292	ALA	ASP	conflict	UNP P0AEX9
D	-291	ALA	LYS	conflict	UNP P0AEX9
D	-202	ALA	GLU	conflict	UNP P0AEX9
D	-201	ALA	ASN	conflict	UNP P0AEX9
D	-135	ALA	LYS	conflict	UNP P0AEX9
D	-15	ALA	GLU	conflict	UNP P0AEX9
D	-12	ALA	LYS	conflict	UNP P0AEX9
D	-11	ALA	ASP	conflict	UNP P0AEX9
D	-7	ASN	-	linker	UNP P0AEX9
D	-6	ALA	-	linker	UNP P0AEX9

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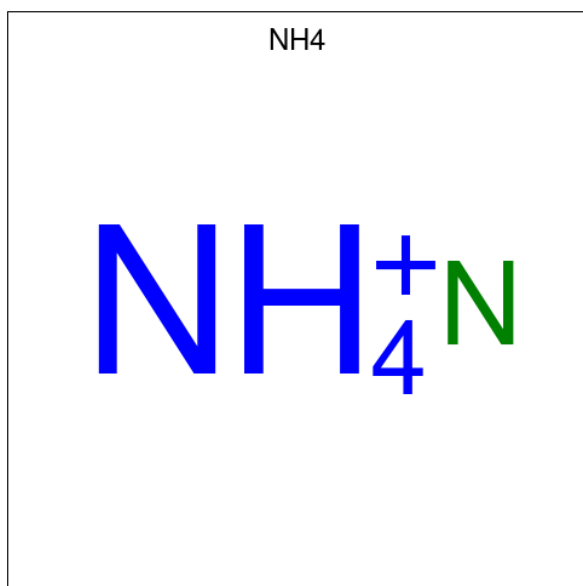
Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	VAL	-	linker	UNP P0AEX9
D	-4	ASP	-	linker	UNP P0AEX9
D	-3	SER	-	linker	UNP P0AEX9
D	-2	ALA	-	linker	UNP P0AEX9
D	-1	ALA	-	linker	UNP P0AEX9
D	0	ALA	-	linker	UNP P0AEX9

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



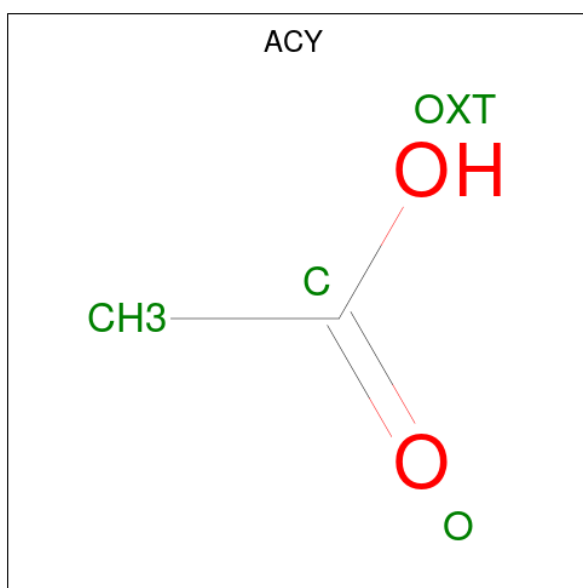
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	I	2	Total	C	O	0	0	0
			23	12	11			
2	G	2	Total	C	O	0	0	0
			23	12	11			
2	H	2	Total	C	O	0	0	0
			23	12	11			
2	J	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is AMMONIUM ION (CCD ID: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total N 1 1	0	0
3	A	1	Total N 1 1	0	0
3	C	1	Total N 1 1	0	0
3	D	1	Total N 1 1	0	0

- Molecule 4 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).

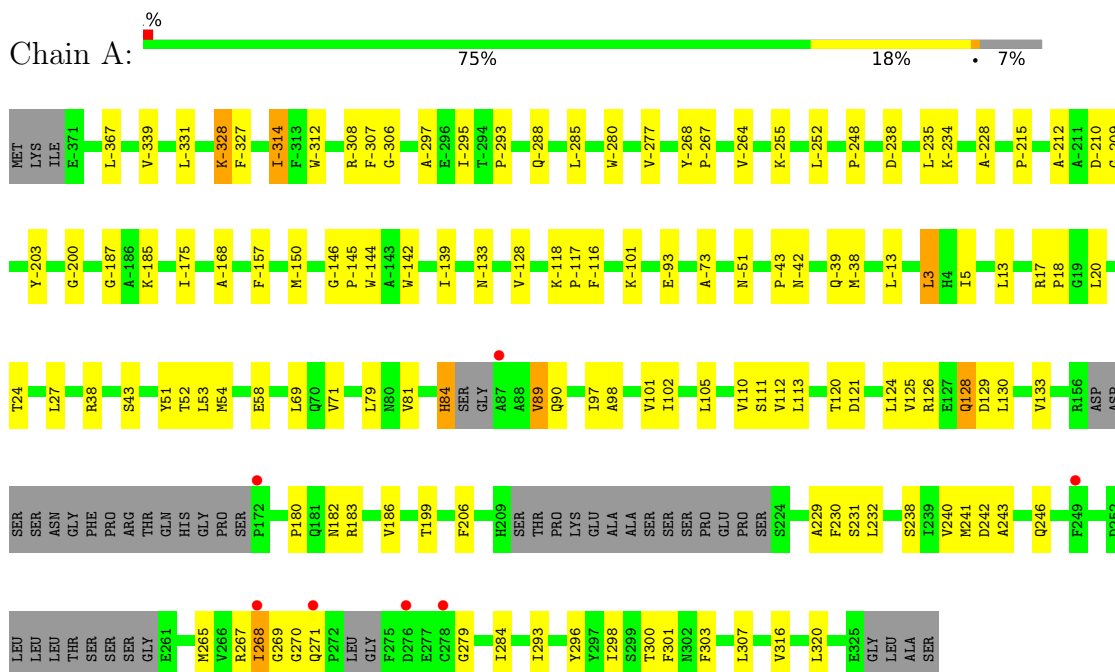


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0

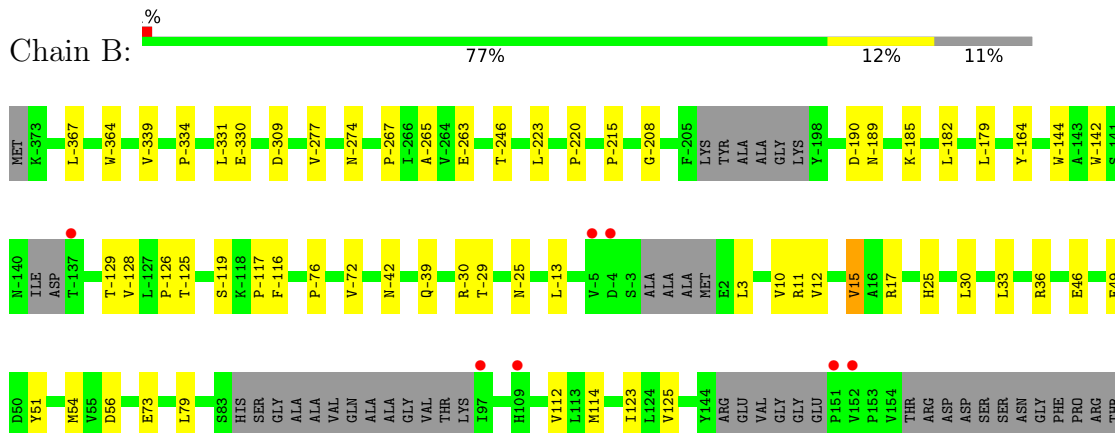
3 Residue-property plots

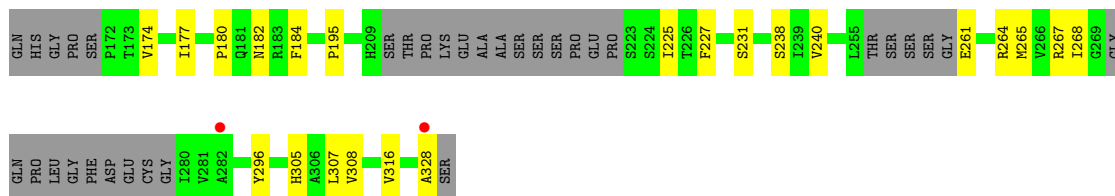
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Maltose/maltodextrin-binding periplasmic protein,Cytosolic arginine sensor for mTORC1 subunit 1

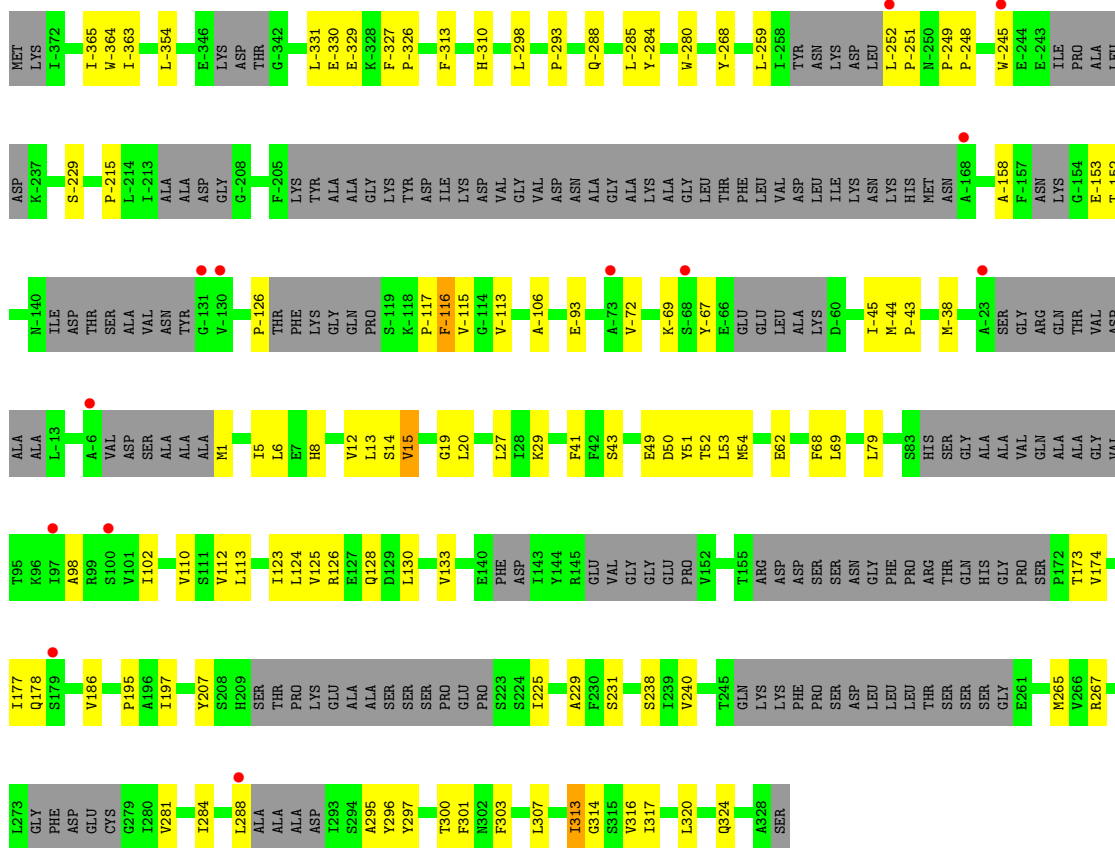


- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Cytosolic arginine sensor for mTORC1 subunit 1

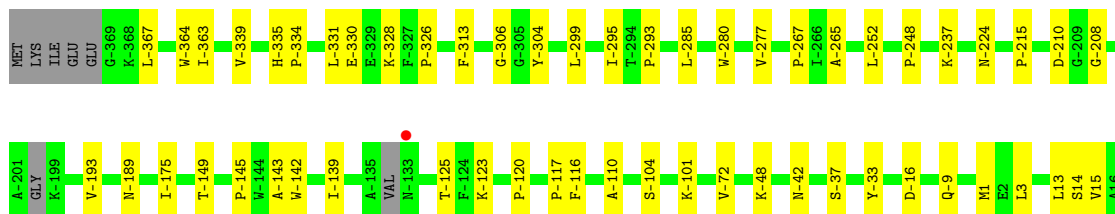


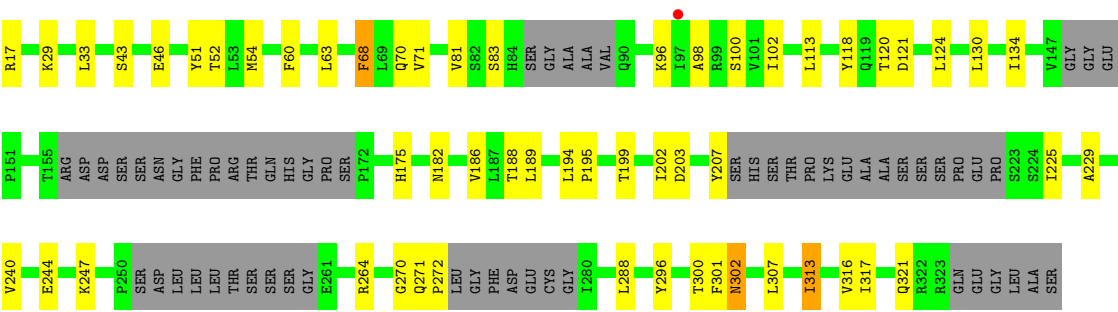


- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Cytosolic arginine sensor for mTORC1 subunit 1

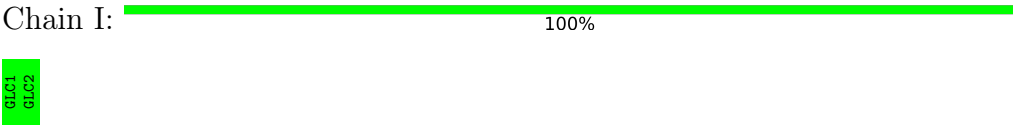


- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Cytosolic arginine sensor for mTORC1 subunit 1

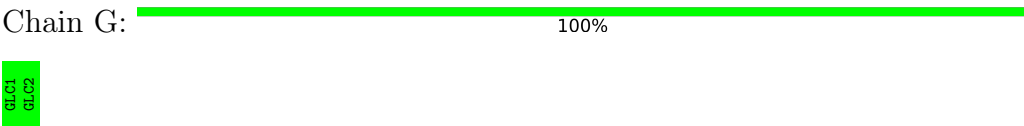




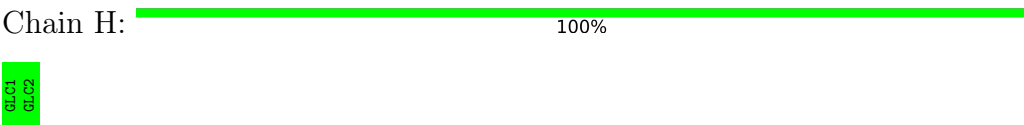
• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.77Å 168.78Å 98.76Å 90.00° 104.43° 90.00°	Depositor
Resolution (Å)	48.49 – 3.08 48.49 – 3.08	Depositor EDS
% Data completeness (in resolution range)	96.2 (48.49-3.08) 90.6 (48.49-3.08)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 3.07Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.225 , 0.264 0.225 , 0.264	Depositor DCC
R_{free} test set	2000 reflections (4.23%)	wwPDB-VP
Wilson B-factor (Å ²)	51.2	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18780	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.64 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2932e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACY, GLC, NH4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.15	0/5081	0.34	1/6943 (0.0%)
1	B	0.09	0/4871	0.27	0/6645
1	C	0.11	0/4162	0.28	0/5676
1	D	0.09	0/4992	0.28	0/6810
All	All	0.11	0/19106	0.30	1/26074 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	-209	GLY	N-CA-C	5.86	123.22	114.95

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4960	0	4778	74	0
1	B	4758	0	4592	48	0
1	C	4071	0	3913	60	0
1	D	4875	0	4771	62	0
2	G	23	0	21	0	0
2	H	23	0	21	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	23	0	21	0	0
2	J	23	0	21	0	0
3	A	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	4	0	3	1	0
4	C	4	0	3	0	0
4	D	12	0	9	2	0
All	All	18780	0	18153	239	0

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

All (239) 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:-142:TRP:HB2	1:B:-76:PRO:HG2	1.63	0.79
1:A:199:THR:HG21	1:B:195:PRO:HB3	1.64	0.79
1:A:-255:LYS:HB2	1:A:-133:ASN:HB3	1.65	0.79
1:B:296:TYR:HB3	1:B:307:LEU:HB2	1.68	0.76
1:C:296:TYR:HB3	1:C:307:LEU:HB2	1.68	0.74
1:D:-208:GLY:HA2	1:D:-189:ASN:HD21	1.52	0.74
1:D:-224:ASN:H	4:D:403:ACY:H2	1.53	0.74
1:D:182:ASN:ND2	1:D:225:ILE:O	2.20	0.74
1:C:195:PRO:HB3	1:D:199:THR:HG21	1.72	0.70
1:A:27:LEU:HD21	1:A:53:LEU:HD21	1.74	0.70
1:A:231:SER:HB2	1:A:238:SER:HB3	1.74	0.68
1:D:-295:ILE:HD12	1:D:-293:PRO:HD3	1.76	0.67
1:C:52:THR:HG21	1:C:301:PHE:H	1.60	0.66
1:A:269:GLY:O	1:A:303:PHE:CD2	2.48	0.66
1:D:52:THR:HG21	1:D:300:THR:HB	1.78	0.65
1:B:-208:GLY:HA2	1:B:-189:ASN:HD21	1.62	0.65
1:D:-277:VAL:HG21	1:D:-267:PRO:HD3	1.77	0.65
1:D:296:TYR:HB3	1:D:307:LEU:HB2	1.77	0.65
1:A:-252:LEU:HD21	1:A:-248:PRO:HD3	1.79	0.65
1:A:3:LEU:HD12	1:A:81:VAL:HG22	1.80	0.64
1:C:-72:VAL:HG21	1:C:-67:TYR:HD2	1.62	0.64
1:C:49:GLU:OE2	1:C:267:ARG:NH1	2.27	0.64
1:B:-220:PRO:HD3	1:B:-30:ARG:HG2	1.80	0.63
1:D:229:ALA:HB3	1:D:240:VAL:HG22	1.81	0.62
1:A:52:THR:HG21	1:A:301:PHE:H	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:-277:VAL:HG21	1:A:-267:PRO:HD3	1.83	0.61
1:B:112:VAL:HG12	1:B:125:VAL:HG12	1.83	0.60
1:B:17:ARG:NH2	1:B:46:GLU:OE2	2.34	0.60
1:B:-334:PRO:HD2	1:B:-331:LEU:HD13	1.83	0.60
1:C:-115:VAL:HB	1:C:-45:ILE:HA	1.81	0.60
1:D:13:LEU:HD22	1:D:71:VAL:HG22	1.83	0.60
1:A:269:GLY:O	1:A:303:PHE:CE2	2.54	0.60
1:B:11:ARG:NH1	1:B:73:GLU:O	2.35	0.59
1:A:13:LEU:HD22	1:A:71:VAL:HG22	1.84	0.59
1:D:-149:THR:OG1	4:D:403:ACY:O	2.21	0.59
1:B:-364:TRP:HB3	1:B:-331:LEU:HD11	1.85	0.59
1:A:-312:TRP:HB3	1:A:-307:PHE:HE1	1.67	0.58
1:A:296:TYR:HB3	1:A:307:LEU:HB2	1.85	0.58
1:A:-367:LEU:HB2	1:A:-339:VAL:HG22	1.84	0.58
1:B:174:VAL:HG13	1:B:328:ALA:H	1.69	0.58
1:B:-277:VAL:HG21	1:B:-267:PRO:HD3	1.85	0.58
1:C:265:MET:HE1	1:C:267:ARG:HD3	1.85	0.58
1:C:52:THR:HG21	1:C:300:THR:HB	1.85	0.58
1:C:313:ILE:HG23	1:C:314:GLY:H	1.69	0.58
1:C:79:LEU:HB2	1:C:123:ILE:HB	1.86	0.57
1:D:202:ILE:HG22	1:D:207:TYR:HE2	1.69	0.57
1:D:264:ARG:HB3	1:D:313:ILE:HD12	1.84	0.57
1:C:177:ILE:HD11	1:C:324:GLN:HG3	1.86	0.57
1:B:-367:LEU:HB2	1:B:-339:VAL:HG22	1.87	0.57
1:C:29:LYS:NZ	1:C:62:GLU:OE2	2.33	0.57
1:D:-306:GLY:HA3	1:D:-42:ASN:O	2.04	0.57
1:A:-331:LEU:HA	1:A:-328:LYS:HB2	1.87	0.57
1:C:5:ILE:HD13	1:C:130:LEU:HD11	1.87	0.56
1:C:12:VAL:HG22	1:C:54:MET:HG2	1.88	0.56
1:D:60:PHE:HA	1:D:63:LEU:HD12	1.86	0.56
1:C:15:VAL:HG13	1:C:51:TYR:HB2	1.87	0.55
1:D:-252:LEU:HD21	1:D:-248:PRO:HD3	1.88	0.55
1:A:111:SER:HB3	1:A:279:GLY:HA3	1.87	0.55
1:B:180:PRO:O	1:B:264:ARG:NH1	2.39	0.55
1:C:-259:LEU:HD12	1:C:-126:PRO:HD3	1.89	0.54
1:C:43:SER:HB3	1:C:54:MET:HB2	1.90	0.54
1:A:-268:TYR:OH	1:A:-93:GLU:OE2	2.26	0.54
1:D:244:GLU:HA	1:D:247:LYS:HD3	1.90	0.54
1:A:52:THR:HG21	1:A:300:THR:HB	1.89	0.54
1:B:265:MET:HE3	1:B:267:ARG:HB2	1.88	0.54
1:D:15:VAL:HG13	1:D:51:TYR:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:-252:LEU:HB3	1:C:-251:PRO:HD3	1.89	0.53
1:D:-193:VAL:O	1:D:-9:GLN:NE2	2.40	0.53
1:B:49:GLU:OE2	1:B:267:ARG:NH2	2.26	0.53
1:A:-215:PRO:HG3	1:A:-117:PRO:HB3	1.90	0.52
1:B:3:LEU:HD11	1:B:79:LEU:HD23	1.91	0.52
1:C:-158:ALA:O	1:C:-153:GLU:N	2.42	0.52
1:A:268:ILE:HD11	1:A:320:LEU:HD13	1.92	0.52
1:C:112:VAL:HG12	1:C:125:VAL:HG12	1.90	0.52
1:D:-120:PRO:HB3	1:D:-48:LYS:HD3	1.91	0.52
1:A:5:ILE:HD13	1:A:130:LEU:HD11	1.92	0.52
1:C:1:MET:SD	1:C:1:MET:N	2.74	0.52
1:B:-223:LEU:HD23	1:B:-179:LEU:HD21	1.92	0.52
1:A:-306:GLY:HA3	1:A:-42:ASN:O	2.10	0.51
1:A:293:ILE:HD13	1:A:316:VAL:HG22	1.92	0.51
1:C:126:ARG:HB3	1:C:128:GLN:HG2	1.91	0.51
1:A:-327:PHE:CG	1:A:-314:ILE:HD12	2.46	0.51
1:D:14:SER:HB3	1:D:70:GLN:HB2	1.91	0.51
1:C:-229:SER:HB2	1:C:-152:THR:HA	1.93	0.50
1:C:-245:TRP:CD1	1:C:-126:PRO:HB2	2.46	0.50
1:C:14:SER:OG	1:C:50:ASP:OD2	2.23	0.50
1:A:105:LEU:HB3	1:A:110:VAL:HB	1.94	0.50
1:D:-145:PRO:HA	1:D:-142:TRP:CE2	2.47	0.49
1:A:38:ARG:HG3	1:A:58:GLU:HG2	1.94	0.49
1:A:296:TYR:HE2	1:A:298:ILE:HD11	1.77	0.49
1:C:267:ARG:HG2	1:C:303:PHE:CD2	2.47	0.49
1:C:-116:PHE:HB3	1:C:-44:MET:HE2	1.93	0.49
1:B:308:VAL:HG21	1:B:316:VAL:HG21	1.94	0.49
1:D:113:LEU:HB2	1:D:124:LEU:HB2	1.95	0.49
1:D:203:ASP:HA	1:D:207:TYR:HD2	1.78	0.49
1:C:229:ALA:HB3	1:C:240:VAL:HG22	1.95	0.49
1:B:10:VAL:HA	1:B:56:ASP:HA	1.95	0.49
1:D:14:SER:HB2	1:D:301:PHE:CG	2.47	0.49
1:B:-309:ASP:HA	1:B:-42:ASN:HA	1.95	0.48
1:B:-265:ALA:HA	1:B:-72:VAL:HA	1.94	0.48
1:B:177:ILE:HA	1:B:268:ILE:HG12	1.95	0.48
1:D:-330:GLU:O	1:D:-304:TYR:OH	2.28	0.48
1:C:19:GLY:HA3	1:C:68:PHE:CG	2.49	0.48
1:C:-330:GLU:HG2	1:C:-329:GLU:HG3	1.95	0.48
1:C:110:VAL:HG11	1:C:133:VAL:HG22	1.96	0.48
1:C:313:ILE:O	1:C:317:ILE:HG12	2.13	0.48
1:D:15:VAL:HA	1:D:68:PHE:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:VAL:HG22	1:D:240:VAL:HG12	1.95	0.48
1:B:182:ASN:ND2	1:B:225:ILE:O	2.47	0.48
1:D:-125:THR:HG22	1:D:-120:PRO:HA	1.95	0.48
1:C:20:LEU:HD22	1:C:51:TYR:CZ	2.49	0.47
1:B:184:PHE:CE2	1:B:227:PHE:HB3	2.49	0.47
1:C:231:SER:HB3	1:C:238:SER:HB3	1.96	0.47
1:A:126:ARG:NH1	1:A:129:ASP:OD1	2.47	0.47
1:D:-285:LEU:HB2	1:D:-280:TRP:NE1	2.29	0.47
1:C:113:LEU:HB2	1:C:124:LEU:HB2	1.96	0.47
1:A:112:VAL:HG12	1:A:125:VAL:HG12	1.96	0.47
1:D:271:GLN:HA	1:D:302:ASN:HA	1.96	0.47
1:A:-312:TRP:NE1	1:A:-308:ARG:HG3	2.30	0.47
1:B:174:VAL:HG22	1:B:328:ALA:HB3	1.96	0.47
1:D:-364:TRP:CD2	1:D:-334:PRO:HG2	2.50	0.47
1:C:-364:TRP:HB3	1:C:-331:LEU:HD11	1.96	0.46
1:C:-293:PRO:HG2	1:C:-288:GLN:HG2	1.97	0.46
1:D:98:ALA:HA	1:D:102:ILE:HB	1.97	0.46
1:A:20:LEU:HD22	1:A:51:TYR:CZ	2.50	0.46
1:A:230:PHE:HE1	1:A:232:LEU:HB2	1.81	0.46
1:C:-215:PRO:HG3	1:C:-117:PRO:HA	1.97	0.46
1:D:17:ARG:NH2	1:D:46:GLU:OE2	2.38	0.46
1:D:-331:LEU:HA	1:D:-328:LYS:HB2	1.98	0.46
1:B:-263:GLU:HB3	1:B:-144:TRP:HZ3	1.81	0.46
1:C:27:LEU:HD21	1:C:53:LEU:HD11	1.97	0.46
1:D:270:GLY:O	1:D:272:PRO:HD3	2.16	0.46
1:A:241:MET:HE3	1:A:246:GLN:HG3	1.97	0.45
1:C:-285:LEU:HD12	1:C:-280:TRP:CZ2	2.51	0.45
1:A:24:THR:HG21	1:B:25:HIS:CD2	2.52	0.45
1:C:6:LEU:HB3	1:C:8:HIS:HD2	1.81	0.45
1:C:8:HIS:HD1	1:C:41:PHE:HB2	1.80	0.45
1:D:-104:SER:O	1:D:-101:LYS:NZ	2.48	0.45
1:D:-367:LEU:HB2	1:D:-339:VAL:HG22	1.97	0.45
1:C:295:ALA:HB3	1:C:297:TYR:CZ	2.51	0.45
1:D:-265:ALA:HA	1:D:-72:VAL:HA	1.97	0.45
1:C:13:LEU:HD13	1:C:69:LEU:HD11	1.99	0.45
1:D:317:ILE:O	1:D:321:GLN:HG2	2.17	0.45
1:B:231:SER:OG	1:B:238:SER:HB3	2.17	0.45
1:D:-363:ILE:HA	1:D:-313:PHE:HB2	1.98	0.45
1:D:3:LEU:HD12	1:D:81:VAL:HG22	1.99	0.45
1:C:-310:HIS:CE1	1:C:-113:VAL:H	2.35	0.45
1:B:-330:GLU:OE1	1:B:-330:GLU:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:-164:TYR:HA	4:B:401:ACY:H1	1.98	0.44
1:D:-237:LYS:HB2	1:D:-237:LYS:HE3	1.73	0.44
1:A:-128:VAL:HA	1:A:-51:ASN:HD21	1.81	0.44
1:A:24:THR:HG21	1:B:25:HIS:HD2	1.83	0.44
1:A:-150:MET:HE3	1:A:-150:MET:HB2	1.83	0.44
1:A:268:ILE:HB	1:A:284:ILE:HD11	1.98	0.44
1:B:114:MET:HG2	1:B:123:ILE:HD13	1.98	0.44
1:A:-203:TYR:CZ	1:A:-200:GLY:HA2	2.53	0.44
1:A:43:SER:HB3	1:A:54:MET:HB2	1.99	0.44
1:D:-326:PRO:HA	1:D:-299:LEU:HD13	1.99	0.44
1:D:43:SER:HB3	1:D:54:MET:HB2	1.97	0.44
1:A:182:ASN:HB3	1:A:242:ASP:OD1	2.17	0.44
1:B:267:ARG:HD2	1:B:305:HIS:NE2	2.33	0.44
1:C:-365:ILE:HG21	1:C:-354:LEU:HD21	2.00	0.44
1:D:-335:HIS:O	1:D:-335:HIS:ND1	2.50	0.44
1:A:120:THR:OG1	1:A:121:ASP:N	2.49	0.44
1:B:3:LEU:HD21	1:B:79:LEU:HD23	2.00	0.44
1:A:113:LEU:HB2	1:A:124:LEU:HB2	1.99	0.44
1:D:288:LEU:HD21	1:D:316:VAL:HG13	2.00	0.43
1:A:97:ILE:O	1:A:101:VAL:HB	2.18	0.43
1:A:180:PRO:HG3	1:A:265:MET:HE2	1.99	0.43
1:A:-157:PHE:HE2	1:A:-139:ILE:HD13	1.83	0.43
1:D:-210:ASP:CG	1:D:-123:LYS:HD3	2.43	0.43
1:D:-16:ASP:OD1	1:D:-16:ASP:N	2.51	0.43
1:D:313:ILE:O	1:D:313:ILE:HG12	2.18	0.43
1:A:-39:GLN:OE1	1:A:-39:GLN:N	2.48	0.43
1:A:-285:LEU:HD12	1:A:-280:TRP:CZ2	2.54	0.43
1:A:128:GLN:H	1:A:128:GLN:HG3	1.61	0.43
1:C:-327:PHE:HB3	1:C:-326:PRO:HD3	2.01	0.43
1:D:-313:PHE:CE1	1:D:-110:ALA:HB2	2.54	0.43
1:A:-264:VAL:HB	1:A:-73:ALA:HB3	2.01	0.43
1:B:15:VAL:HG13	1:B:51:TYR:HB2	2.01	0.43
1:C:98:ALA:HA	1:C:102:ILE:HB	2.00	0.43
1:B:-190:ASP:O	1:B:-185:LYS:NZ	2.52	0.43
1:A:79:LEU:HD11	1:A:133:VAL:HG11	2.01	0.42
1:A:98:ALA:HA	1:A:102:ILE:HB	2.01	0.42
1:A:-238:ASP:OD2	1:A:-234:LYS:HE2	2.19	0.42
1:C:284:ILE:HG23	1:C:320:LEU:HD11	2.01	0.42
1:D:-37:SER:O	1:D:-33:TYR:HD1	2.03	0.42
1:D:1:MET:HE2	1:D:83:SER:HB3	2.02	0.42
1:A:-175:ILE:HG21	1:A:-168:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:130:LEU:O	1:D:134:ILE:HG13	2.20	0.42
1:A:17:ARG:N	1:A:18:PRO:HD2	2.34	0.42
1:A:84:HIS:CE1	1:A:89:VAL:HG22	2.53	0.42
1:C:-268:TYR:OH	1:C:-93:GLU:OE2	2.20	0.42
1:C:207:TYR:CE1	1:D:29:LYS:HB2	2.55	0.42
1:A:-210:ASP:O	1:A:-187:GLY:HA3	2.18	0.42
1:A:183:ARG:O	1:A:243:ALA:N	2.45	0.42
1:A:186:VAL:HG22	1:A:240:VAL:HG12	2.01	0.42
1:C:-284:TYR:CE1	1:C:-69:LYS:HG2	2.55	0.42
1:A:-185:LYS:HG2	1:A:-13:LEU:HD12	2.01	0.42
1:B:-215:PRO:HG3	1:B:-117:PRO:HA	2.01	0.42
1:B:33:LEU:HB3	1:B:36:ARG:HG2	2.02	0.42
1:A:-295:ILE:O	1:A:-295:ILE:HG13	2.20	0.42
1:A:-145:PRO:HA	1:A:-142:TRP:CE2	2.55	0.42
1:A:-43:PRO:O	1:A:-38:MET:HG3	2.20	0.42
1:D:-215:PRO:HG3	1:D:-117:PRO:HB3	2.02	0.42
1:D:120:THR:OG1	1:D:121:ASP:N	2.53	0.41
1:A:-238:ASP:O	1:A:-234:LYS:HG2	2.20	0.41
1:C:-363:ILE:HA	1:C:-313:PHE:HB2	2.02	0.41
1:D:-143:ALA:O	1:D:-139:ILE:HG13	2.20	0.41
1:D:96:LYS:HE2	1:D:100:SER:OG	2.20	0.41
1:A:-235:LEU:HD13	1:A:-228:ALA:HA	2.03	0.41
1:A:-146:GLY:HA3	1:A:-144:TRP:CH2	2.55	0.41
1:C:-249:PRO:HA	1:C:-248:PRO:HD3	1.96	0.41
1:A:-212:ALA:O	1:A:-118:LYS:HD2	2.19	0.41
1:B:-29:THR:O	1:B:-25:ASN:HB2	2.21	0.41
1:C:-43:PRO:O	1:C:-38:MET:HG3	2.21	0.41
1:B:-367:LEU:HD23	1:B:-367:LEU:HA	1.94	0.41
1:C:186:VAL:HG22	1:C:240:VAL:HG12	2.03	0.41
1:A:-238:ASP:HA	1:A:-228:ALA:HB2	2.02	0.41
1:A:24:THR:HG22	1:A:206:PHE:CD1	2.55	0.41
1:C:178:GLN:O	1:C:267:ARG:N	2.52	0.41
1:A:270:GLY:O	1:A:271:GLN:C	2.64	0.41
1:D:194:LEU:HB3	1:D:195:PRO:HD3	2.02	0.41
1:A:-293:PRO:HG2	1:A:-288:GLN:HE21	1.86	0.41
1:A:13:LEU:HD13	1:A:69:LEU:HD11	2.03	0.41
1:A:229:ALA:HB3	1:A:240:VAL:HG22	2.04	0.40
1:B:-182:LEU:HD22	1:B:-13:LEU:HD21	2.03	0.40
1:B:264:ARG:N	1:B:308:VAL:O	2.37	0.40
1:D:118:TYR:CD1	1:D:188:THR:HB	2.56	0.40
1:B:-246:THR:HG22	1:B:-125:THR:OG1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:VAL:HG22	1:B:54:MET:HG2	2.02	0.40
1:C:8:HIS:ND1	1:C:41:PHE:HB2	2.36	0.40
1:B:-129:THR:OG1	1:B:-128:VAL:N	2.54	0.40
1:A:-297:ALA:HB2	1:A:-101:LYS:HE3	2.04	0.40
1:B:-274:ASN:O	1:B:-274:ASN:ND2	2.46	0.40
1:B:-126:PRO:O	1:B:-119:SER:OG	2.36	0.40
1:C:-298:LEU:O	1:C:-106:ALA:HB2	2.20	0.40
1:C:288:LEU:HD21	1:C:316:VAL:HG13	2.02	0.40
1:D:52:THR:HG21	1:D:301:PHE:H	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	644/704 (92%)	620 (96%)	24 (4%)	0	100	100
1	B	606/704 (86%)	589 (97%)	17 (3%)	0	100	100
1	C	500/704 (71%)	480 (96%)	20 (4%)	0	100	100
1	D	617/704 (88%)	597 (97%)	20 (3%)	0	100	100
All	All	2367/2816 (84%)	2286 (97%)	81 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	503/576 (87%)	493 (98%)	10 (2%)	48	69
1	B	483/576 (84%)	477 (99%)	6 (1%)	63	75
1	C	407/576 (71%)	399 (98%)	8 (2%)	48	69
1	D	504/576 (88%)	496 (98%)	8 (2%)	55	72
All	All	1897/2304 (82%)	1865 (98%)	32 (2%)	53	71

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

Mol	Chain	Res	Type
1	A	-328	LYS
1	A	-314	ILE
1	A	-116	PHE
1	A	3	LEU
1	A	84	HIS
1	A	89	VAL
1	A	90	GLN
1	A	128	GLN
1	A	267	ARG
1	A	268	ILE
1	B	-116	PHE
1	B	-39	GLN
1	B	15	VAL
1	B	30	LEU
1	B	240	VAL
1	B	261	GLU
1	C	-116	PHE
1	C	15	VAL
1	C	173	THR
1	C	174	VAL
1	C	197	ILE
1	C	225	ILE
1	C	281	VAL
1	C	313	ILE
1	D	-175	ILE
1	D	-116	PHE
1	D	33	LEU
1	D	68	PHE
1	D	175	HIS
1	D	189	LEU
1	D	302	ASN
1	D	313	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-288	GLN
1	A	-92	ASN
1	A	108	HIS
1	A	302	ASN
1	B	-288	GLN
1	B	-222	GLN
1	B	-92	ASN
1	B	108	HIS
1	B	209	HIS
1	B	246	GLN
1	B	283	GLN
1	C	-250	ASN
1	D	-189	ASN
1	D	175	HIS

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 ⓘ

8 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	GLC	G	1	2	12,12,12	0.49	0	17,17,17	0.67	0
2	GLC	G	2	2	11,11,12	0.57	0	15,15,17	0.65	0
2	GLC	H	1	2	12,12,12	0.49	0	17,17,17	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	H	2	2	11,11,12	0.61	0	15,15,17	0.71	0
2	GLC	I	1	2	12,12,12	0.52	0	17,17,17	0.50	0
2	GLC	I	2	2	11,11,12	0.58	0	15,15,17	0.76	0
2	GLC	J	1	2	12,12,12	0.54	0	17,17,17	0.52	0
2	GLC	J	2	2	11,11,12	0.57	0	15,15,17	0.73	1 (6%)

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	GLC	G	1	2	-	0/2/22/22	0/1/1/1
2	GLC	G	2	2	-	0/2/19/22	0/1/1/1
2	GLC	H	1	2	-	2/2/22/22	0/1/1/1
2	GLC	H	2	2	-	0/2/19/22	0/1/1/1
2	GLC	I	1	2	-	0/2/22/22	0/1/1/1
2	GLC	I	2	2	-	0/2/19/22	0/1/1/1
2	GLC	J	1	2	-	0/2/22/22	0/1/1/1
2	GLC	J	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	2	GLC	C1-O5-C5	2.05	114.94	112.19

There are no chirality outliers.

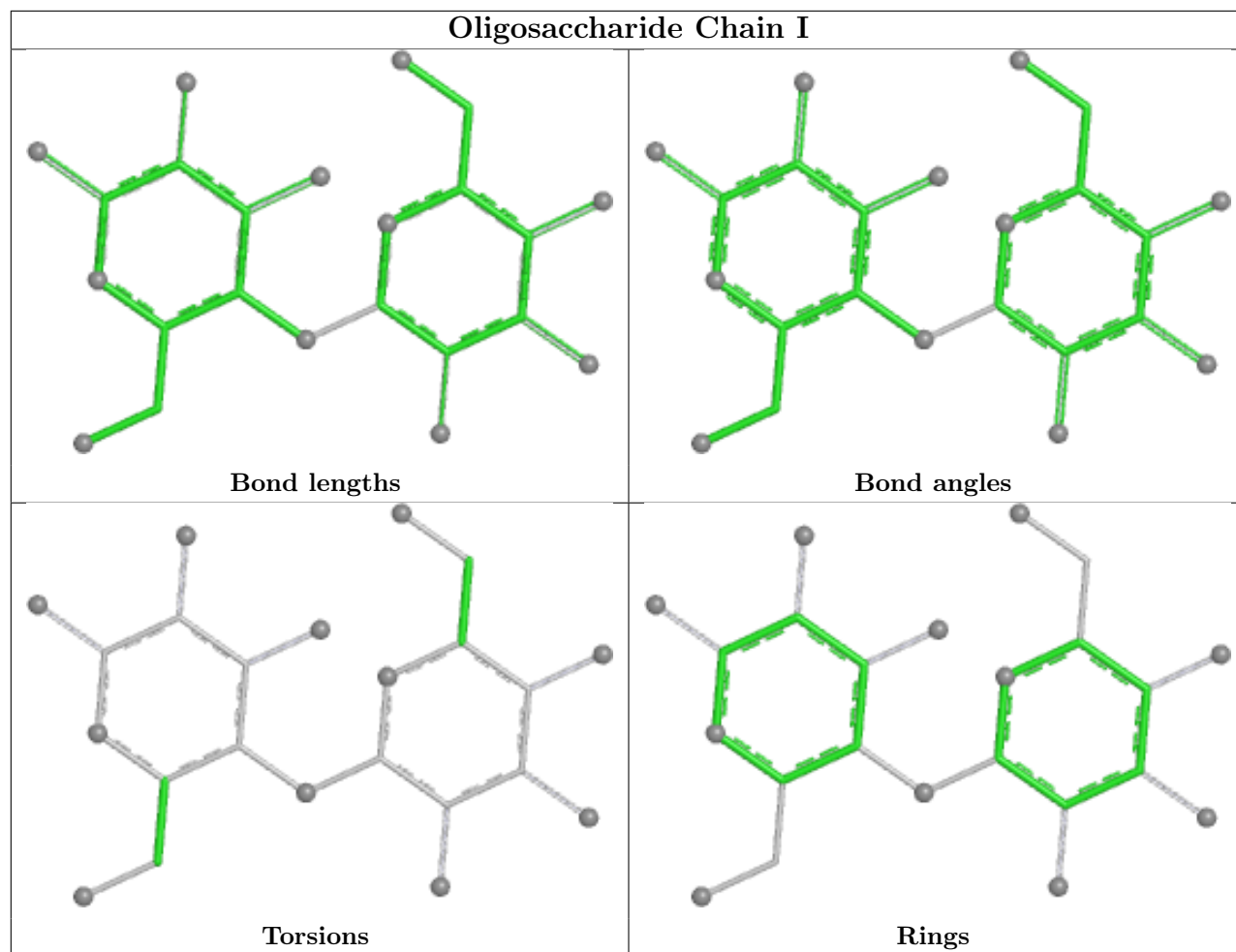
All (2) torsion outliers are listed below:

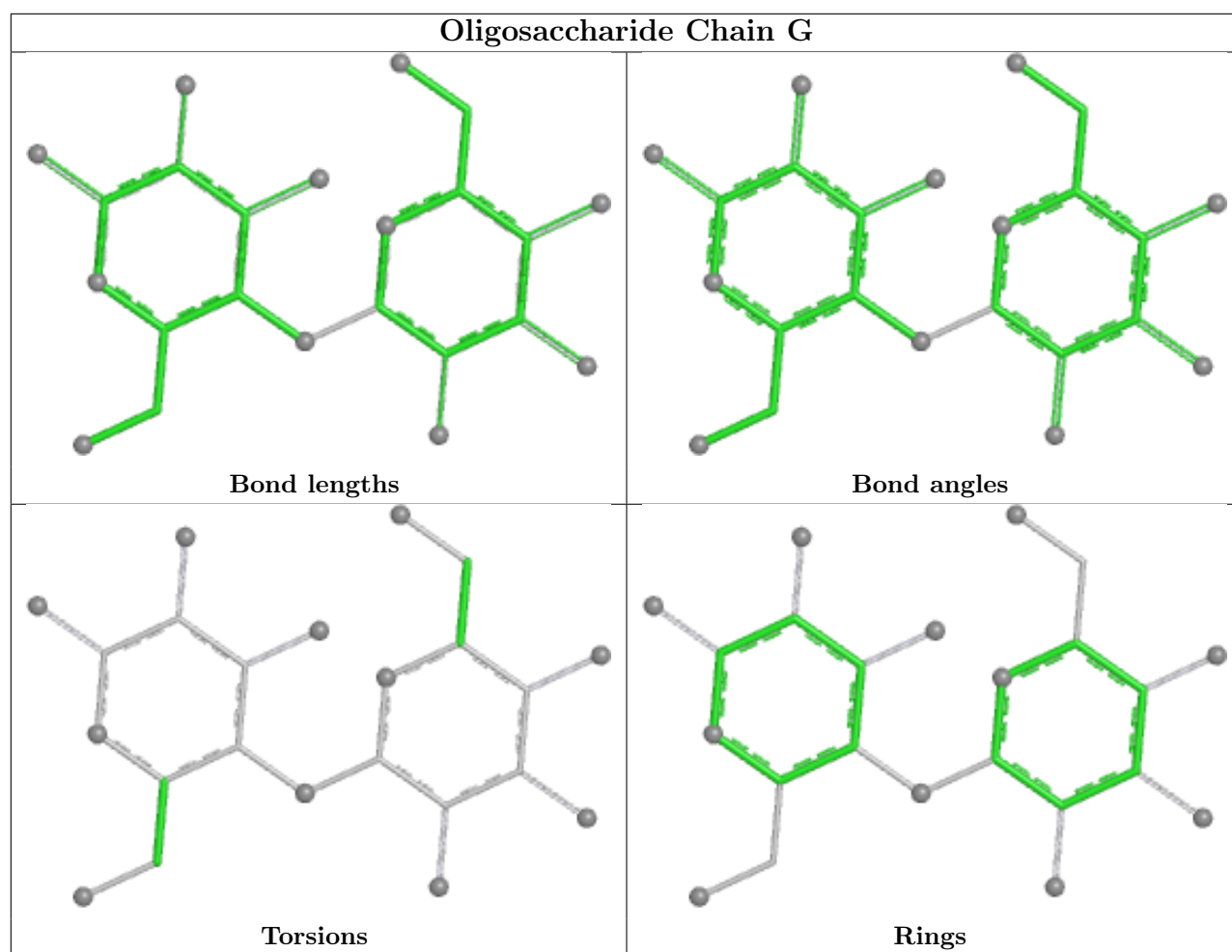
Mol	Chain	Res	Type	Atoms
2	H	1	GLC	C4-C5-C6-O6
2	H	1	GLC	O5-C5-C6-O6

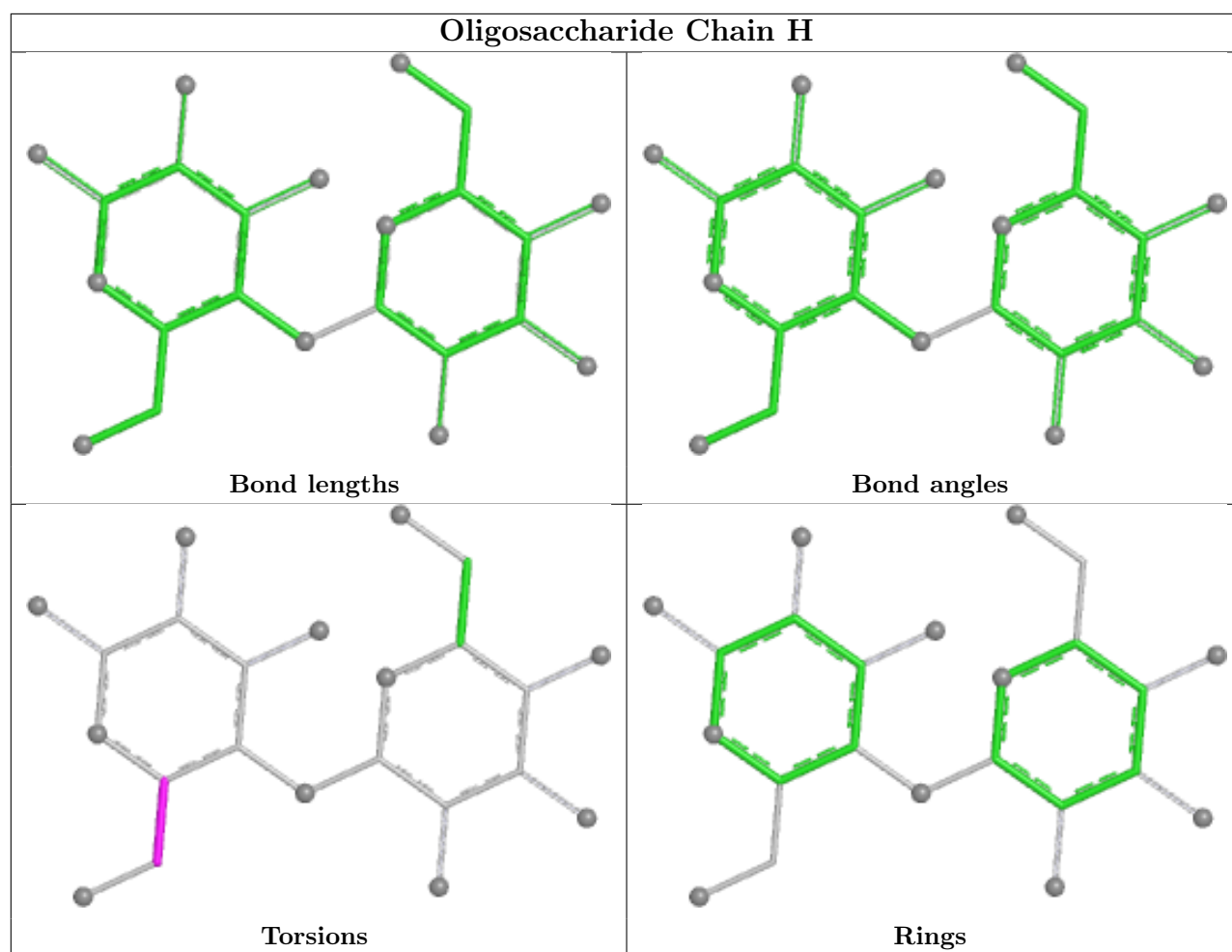
There are no ring outliers.

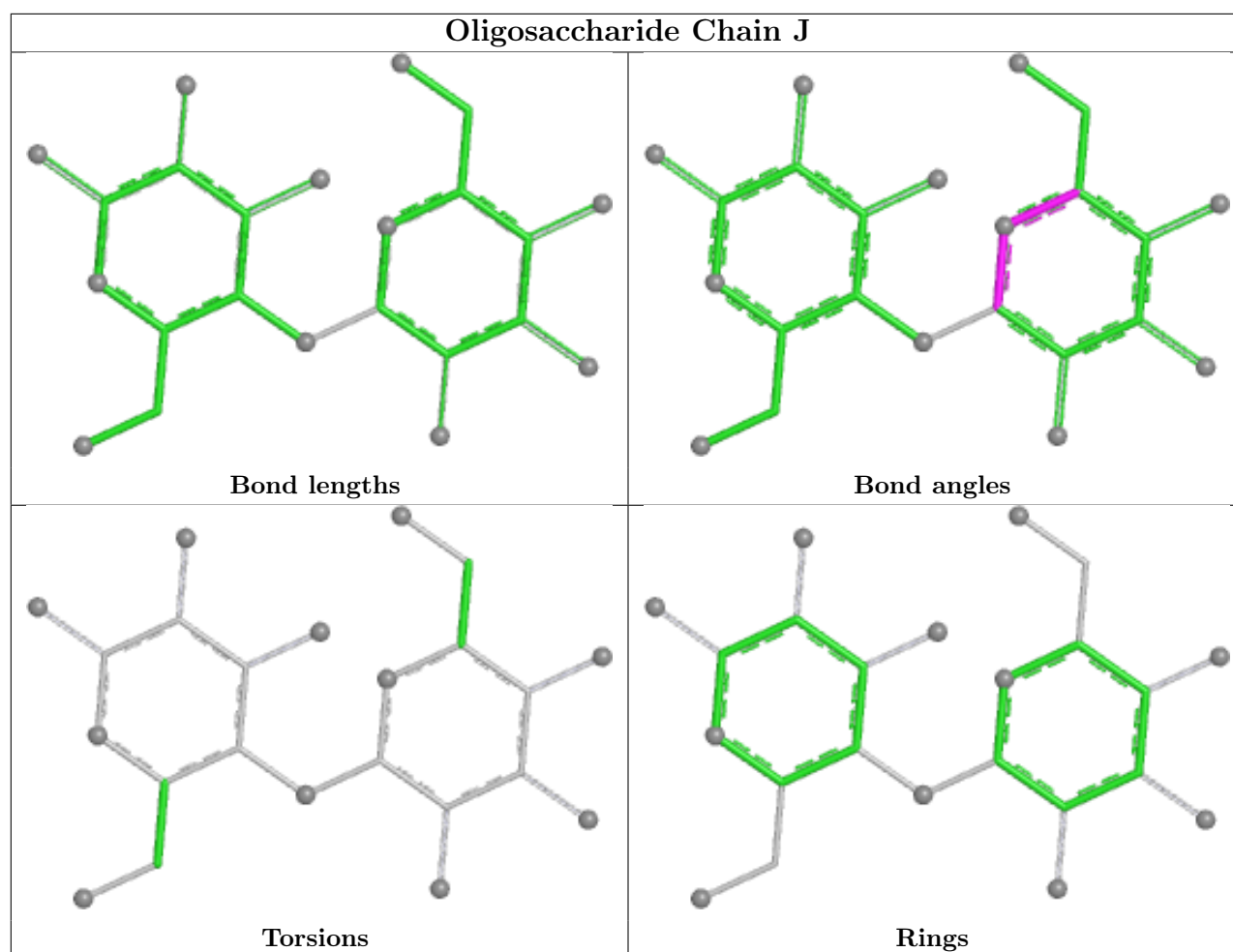
No monomer is involved in short contacts.

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









5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are modelled with single atom - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ACY	D	404	-	3,3,3	1.51	0	3,3,3	1.70	1 (33%)
4	ACY	B	401	-	3,3,3	1.48	0	3,3,3	1.73	1 (33%)
4	ACY	C	402	-	3,3,3	1.48	0	3,3,3	1.69	1 (33%)
4	ACY	D	403	-	3,3,3	1.47	0	3,3,3	1.71	1 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ACY	D	402	-	3,3,3	1.52	0	3,3,3	1.70	1 (33%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	B	401	ACY	O-C-CH3	-2.36	112.83	122.53
4	D	403	ACY	O-C-CH3	-2.34	112.95	122.53
4	D	404	ACY	O-C-CH3	-2.32	113.00	122.53
4	D	402	ACY	O-C-CH3	-2.32	113.01	122.53
4	C	402	ACY	O-C-CH3	-2.31	113.06	122.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	401	ACY	1	0
4	D	403	ACY	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	656/704 (93%)	-0.08	7 (1%) 78 57	24, 48, 88, 114	0
1	B	626/704 (88%)	0.21	9 (1%) 73 51	44, 64, 93, 112	0
1	C	540/704 (76%)	0.43	13 (2%) 59 37	42, 75, 100, 117	0
1	D	635/704 (90%)	-0.09	2 (0%) 90 80	23, 49, 79, 101	0
All	All	2457/2816 (87%)	0.10	31 (1%) 75 53	23, 59, 92, 117	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	278	CYS	4.5
1	C	-252	LEU	3.4
1	B	-137	THR	3.1
1	D	-133	ASN	3.0
1	D	97	ILE	3.0
1	B	-5	VAL	3.0
1	A	87	ALA	2.8
1	A	172	PRO	2.8
1	C	-245	TRP	2.8
1	C	-6	ALA	2.6
1	A	271	GLN	2.6
1	C	288	LEU	2.6
1	C	-68	SER	2.6
1	C	-131	GLY	2.5
1	A	268	ILE	2.5
1	B	-4	ASP	2.4
1	B	328	ALA	2.3
1	C	-130	VAL	2.3
1	C	100	SER	2.3
1	B	109	HIS	2.3
1	A	249	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	282	ALA	2.2
1	C	-168	ALA	2.2
1	C	179	SER	2.2
1	C	97	ILE	2.2
1	B	152	VAL	2.1
1	B	97	ILE	2.1
1	B	151	PRO	2.1
1	C	-73	ALA	2.1
1	A	276	ASP	2.0
1	C	-23	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

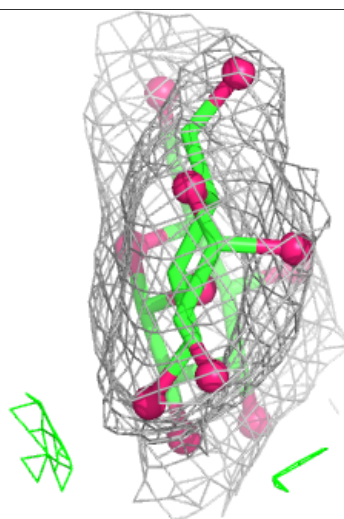
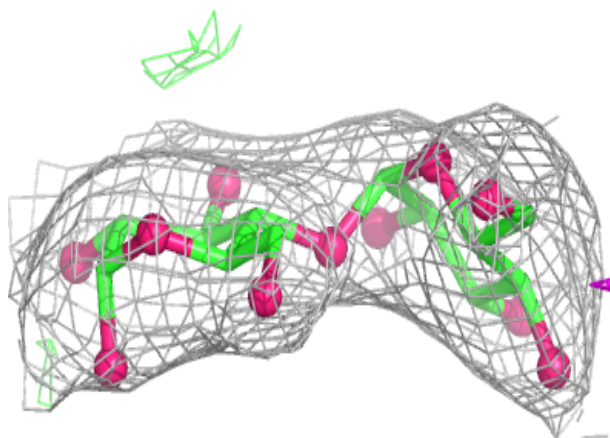
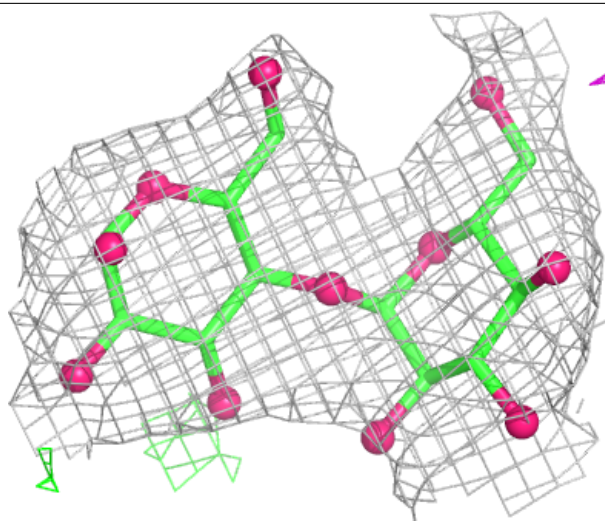
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	I	1	12/12	-	-	50,55,58,59	0
2	GLC	I	2	11/12	-	-	60,66,67,70	0
2	GLC	G	2	11/12	0.94	0.09	45,50,52,56	0
2	GLC	G	1	12/12	0.96	0.07	47,55,60,61	0
2	GLC	H	1	12/12	0.97	0.07	22,26,31,33	0
2	GLC	H	2	11/12	0.97	0.07	26,29,32,33	0
2	GLC	J	1	12/12	-	-	22,25,31,33	0
2	GLC	J	2	11/12	-	-	25,29,31,35	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

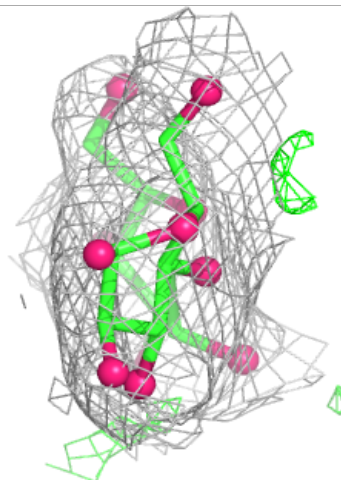
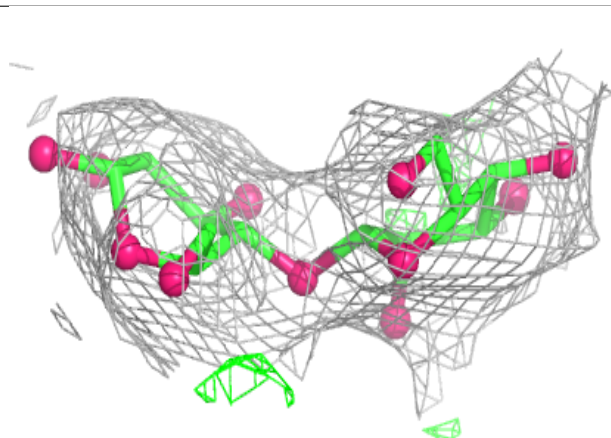
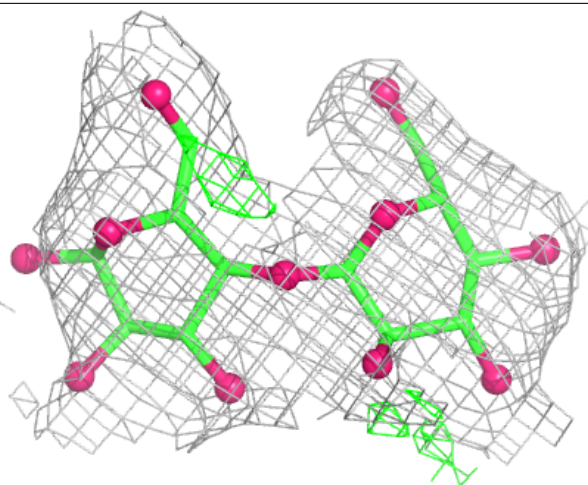
Electron density around Chain I:

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



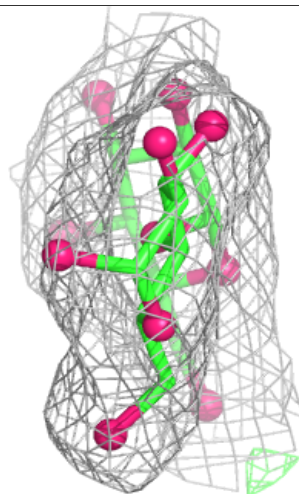
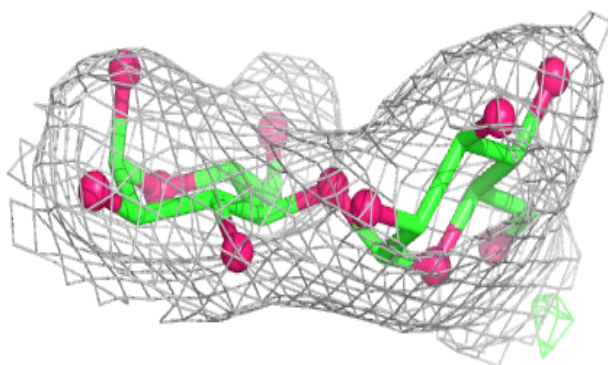
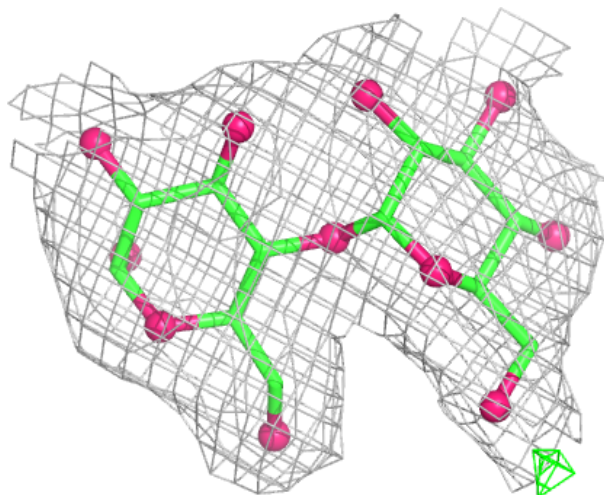
Electron density around Chain G:

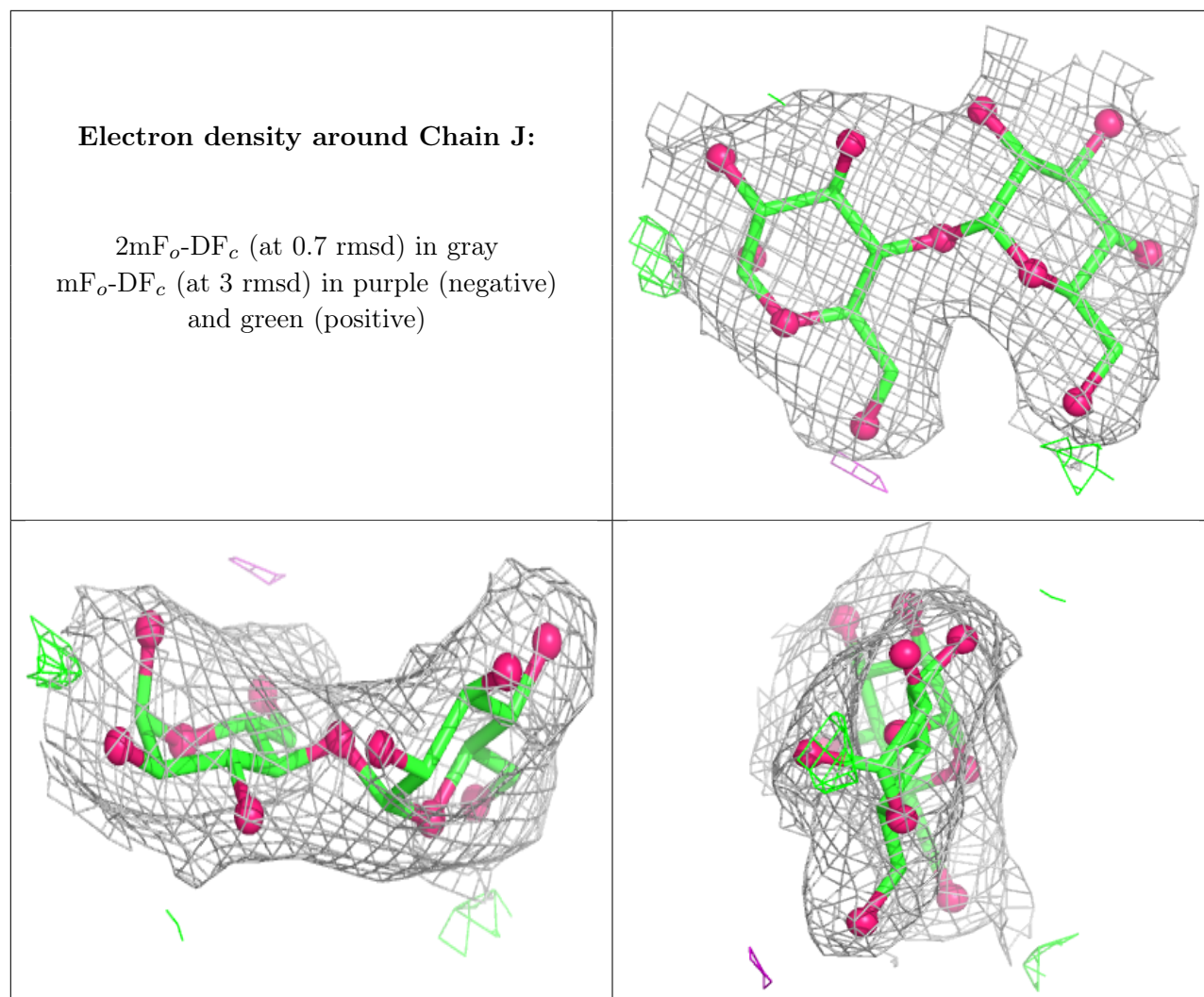
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

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





6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ACY	D	402	4/4	0.54	0.27	45,45,45,52	0
4	ACY	D	404	4/4	0.70	0.25	40,41,42,45	0
3	NH4	A	402	1/1	0.79	0.37	40,40,40,40	0
4	ACY	C	402	4/4	0.86	0.14	52,58,59,60	0
3	NH4	D	401	1/1	0.87	0.36	29,29,29,29	0
3	NH4	A	401	1/1	0.90	0.20	32,32,32,32	0
4	ACY	D	403	4/4	0.92	0.18	34,41,42,43	0
3	NH4	C	401	1/1	0.92	0.28	21,21,21,21	0
4	ACY	B	401	4/4	0.94	0.13	49,50,51,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.