



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 01:44 PM UTC

PDB ID : 1J0Z / pdb_00001j0z
Title : Beta-amylase from *Bacillus cereus* var. *mycoides* in complex with maltose
Authors : Oyama, T.; Miyake, H.; Kusunoki, M.; Nitta, Y.
Deposited on : 2002-11-25
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

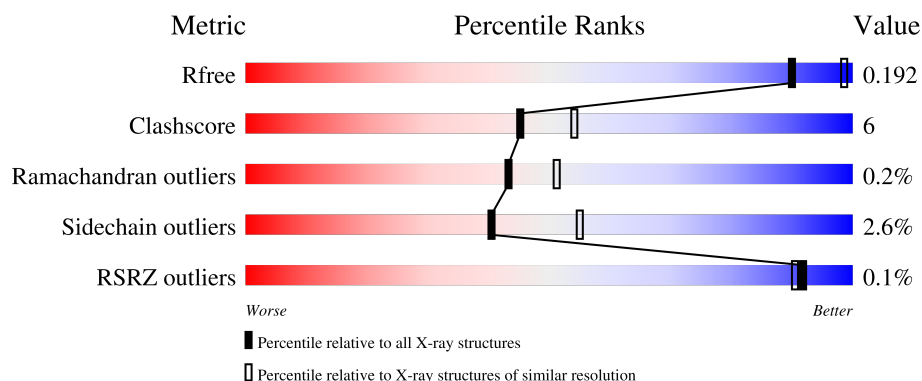
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.



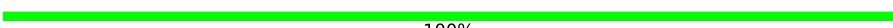
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	516	 82% 17% .
1	B	516	 79% 20% .
1	C	516	 85% 13% .
1	D	516	 83% 16% .
2	E	2	 50% 50%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	2	 50% 50%
2	G	2	 50% 50%
2	H	2	 50% 50%
2	J	2	 100%
2	L	2	 50% 50%
3	I	2	 100%
3	K	2	 100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GLC	I	1	X	-	-	-
3	GLC	K	1	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 17137 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 Beta-amylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	516	Total	C	N	O	S	0	0	0
			4119	2645	676	781	17			
1	B	516	Total	C	N	O	S	0	0	0
			4119	2645	676	781	17			
1	C	516	Total	C	N	O	S	0	0	0
			4119	2645	676	781	17			
1	D	516	Total	C	N	O	S	0	0	0
			4119	2645	676	781	17			

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			23	12	11			
2	F	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			
2	L	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	I	2	Total	C	O	0	0	0
			23	12	11			
3	K	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	145	Total	O	0	0
			145	145		
5	B	104	Total	O	0	0
			104	104		
5	C	130	Total	O	0	0
			130	130		
5	D	94	Total	O	0	0
			94	94		

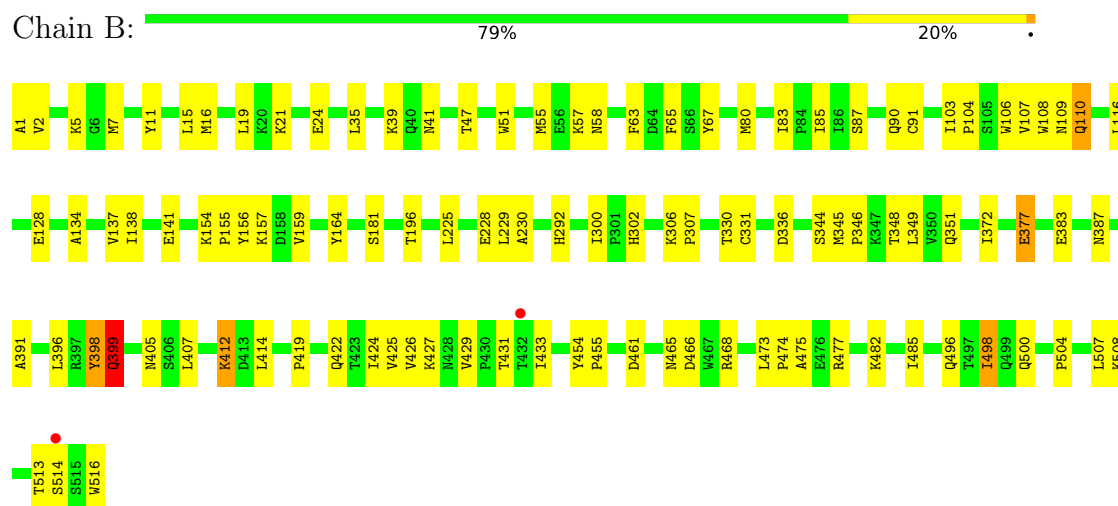
3 Residue-property plots

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.

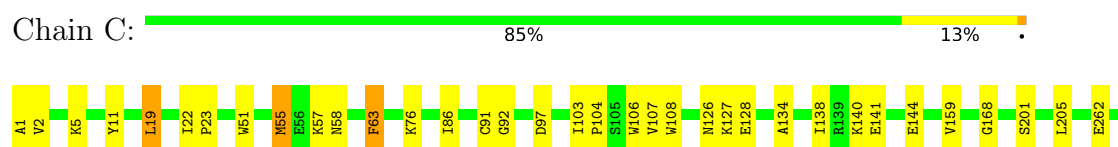
• Molecule 1: Beta-amylase



• Molecule 1: Beta-amylase



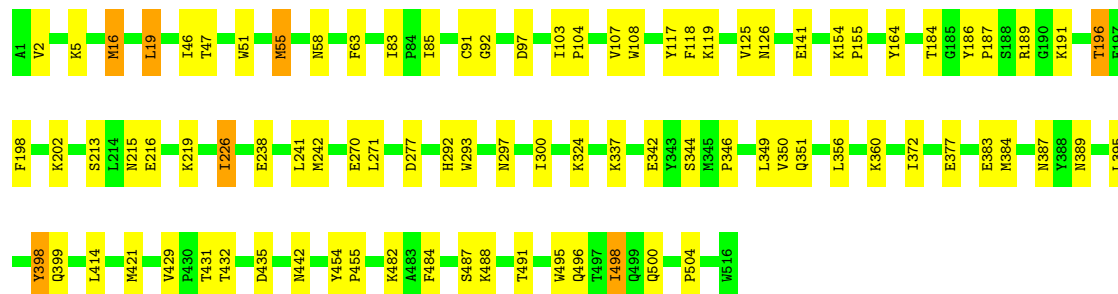
• Molecule 1: Beta-amylase





- Molecule 1: Beta-amylase

Chain D: 83% 16% •



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

Chain E: 50% 50%



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

Chain F: 50% 50%



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

Chain G: 50% 50%



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

Chain H: 50% 50%



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

Chain J: 100%

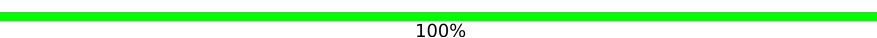


- Molecule 2: alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain L:  50% 50%

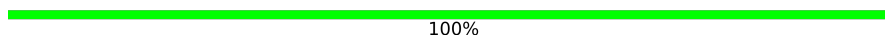


- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain I:  100%



- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain K:  100%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.90Å 112.90Å 146.20Å 90.00° 105.80° 90.00°	Depositor
Resolution (Å)	8.00 – 2.20 8.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	73.2 (8.00-2.20) 71.6 (8.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.10Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.186 , 0.238 0.195 , 0.192	Depositor DCC
R_{free} test set	5596 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.4	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	0.94	EDS
Total number of atoms	17137	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.41	0/4234	0.89	10/5751 (0.2%)
1	B	0.40	0/4234	0.88	10/5751 (0.2%)
1	C	0.41	0/4234	0.88	13/5751 (0.2%)
1	D	0.41	0/4234	0.87	12/5751 (0.2%)
All	All	0.41	0/16936	0.88	45/23004 (0.2%)

There are no bond length outliers.

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	58	ASN	N-CA-C	7.94	120.84	111.71
1	A	277	ASP	N-CA-C	7.89	120.58	111.11
1	A	57	LYS	N-CA-C	7.45	119.09	110.97
1	A	442	ASN	N-CA-C	7.34	119.28	111.28
1	C	277	ASP	N-CA-C	7.19	118.81	110.97
1	D	58	ASN	N-CA-C	7.17	119.96	111.71
1	D	277	ASP	N-CA-C	6.86	119.39	111.02
1	C	442	ASN	N-CA-C	6.83	118.72	111.28
1	C	55	MET	N-CA-C	6.82	119.55	111.71
1	B	414	LEU	N-CA-C	6.63	119.85	111.69
1	B	58	ASN	N-CA-C	6.57	120.55	112.54
1	B	57	LYS	N-CA-C	6.56	118.09	111.07
1	D	55	MET	N-CA-C	6.34	120.28	112.54
1	D	442	ASN	N-CA-C	6.25	118.09	111.28
1	D	297	ASN	CA-C-N	6.24	125.46	118.97
1	D	297	ASN	C-N-CA	6.24	125.46	118.97
1	A	58	ASN	N-CA-C	6.14	118.94	111.82
1	C	168	GLY	CA-C-N	5.96	125.90	119.76
1	C	168	GLY	C-N-CA	5.96	125.90	119.76
1	C	454	TYR	N-CA-C	5.95	122.96	109.81

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	141	GLU	N-CA-C	5.90	117.52	111.14
1	B	196	THR	N-CA-C	-5.88	102.61	110.55
1	C	57	LYS	N-CA-C	5.88	117.37	110.97
1	D	196	THR	N-CA-C	-5.82	101.86	110.48
1	D	292	HIS	N-CA-C	5.81	119.63	112.54
1	A	342	GLU	N-CA-C	5.79	117.67	111.36
1	A	196	THR	N-CA-C	-5.65	102.12	110.48
1	A	505	VAL	N-CA-C	-5.56	103.50	108.95
1	D	342	GLU	N-CA-C	5.55	117.42	111.36
1	A	55	MET	N-CA-C	5.53	119.29	112.54
1	D	389	ASN	N-CA-C	5.53	119.21	111.74
1	C	141	GLU	N-CA-C	5.50	116.96	111.07
1	B	345	MET	CA-C-N	5.42	124.60	118.97
1	B	345	MET	C-N-CA	5.42	124.60	118.97
1	D	414	LEU	N-CA-C	5.39	117.97	111.40
1	C	389	ASN	N-CA-C	5.38	119.01	111.74
1	B	141	GLU	N-CA-C	5.35	116.79	111.07
1	C	63	PHE	N-CA-C	5.25	117.64	110.55
1	D	141	GLU	N-CA-C	5.18	116.62	111.07
1	C	414	LEU	N-CA-C	5.18	118.06	111.69
1	B	292	HIS	N-CA-C	5.11	119.23	112.89
1	C	304	ALA	N-CA-C	-5.07	107.64	113.88
1	B	87	SER	N-CA-C	5.07	117.55	108.17
1	B	399	GLN	N-CA-C	5.03	118.19	111.75
1	A	287	LYS	N-CA-C	5.02	117.67	109.59

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4119	0	3984	48	0
1	B	4119	0	3984	59	0
1	C	4119	0	3984	37	0
1	D	4119	0	3984	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	23	0	21	0	0
2	F	23	0	21	0	0
2	G	23	0	21	0	0
2	H	23	0	21	0	0
2	J	23	0	21	0	0
2	L	23	0	21	0	0
3	I	23	0	21	0	0
3	K	23	0	21	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	145	0	0	0	0
5	B	104	0	0	1	0
5	C	130	0	0	1	0
5	D	94	0	0	1	0
All	All	17137	0	16104	192	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 (192) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:337:LYS:HD3	1:D:344:SER:HB2	1.66	0.77
1:D:498:ILE:H	1:D:498:ILE:HD13	1.53	0.73
1:C:372:ILE:HG23	1:C:377:GLU:HB2	1.73	0.71
1:A:47:THR:HG22	1:A:83:ILE:HB	1.74	0.70
1:D:198:PHE:O	1:D:202:LYS:HG2	1.91	0.70
1:C:375:GLU:HB3	1:C:410:LYS:HD3	1.72	0.70
1:C:2:VAL:O	1:C:5:LYS:HG2	1.92	0.69
1:B:11:TYR:HA	1:B:391:ALA:O	1.94	0.68
1:C:421:MET:SD	1:C:470:ASN:HB3	2.33	0.68
1:A:103:ILE:HD11	1:A:108:TRP:CZ2	2.30	0.67
1:B:498:ILE:HD13	1:B:498:ILE:H	1.60	0.66
1:D:226:ILE:HD13	1:D:226:ILE:H	1.60	0.66
1:D:16:MET:HG2	5:D:793:HOH:O	1.96	0.66
1:A:1:ALA:HB3	1:A:5:LYS:HG3	1.78	0.64
1:B:383:GLU:O	1:B:387:ASN:HB2	1.96	0.64
1:B:372:ILE:HG23	1:B:377:GLU:HB2	1.77	0.64
1:C:432:THR:HG22	1:C:433:ILE:H	1.62	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:498:ILE:HG12	1:D:500:GLN:NE2	2.14	0.62
1:B:41:ASN:HA	1:B:412:LYS:HD3	1.81	0.61
1:B:21:LYS:O	1:B:24:GLU:HG2	2.01	0.60
1:A:92:GLY:HA2	1:A:97:ASP:HB3	1.82	0.60
1:B:2:VAL:O	1:B:5:LYS:HG2	2.02	0.60
1:C:352:ASN:O	1:C:356:LEU:HD23	2.01	0.60
1:D:482:LYS:HE2	1:D:496:GLN:O	2.02	0.59
1:C:103:ILE:HD11	1:C:108:TRP:CZ2	2.37	0.59
1:C:134:ALA:O	1:C:138:ILE:HG12	2.02	0.59
1:A:399:GLN:NE2	1:A:399:GLN:H	2.01	0.59
1:A:21:LYS:HB3	1:A:23:PRO:HD2	1.84	0.59
1:A:452:LYS:HE3	1:A:452:LYS:H	1.68	0.58
1:D:2:VAL:O	1:D:5:LYS:HG2	2.03	0.58
1:B:7:MET:HE2	1:B:419:PRO:HG3	1.85	0.58
1:C:482:LYS:HG2	1:C:499:GLN:HA	1.86	0.58
1:A:2:VAL:O	1:A:5:LYS:HG2	2.04	0.57
1:A:375:GLU:HB3	1:A:410:LYS:HD3	1.85	0.57
1:C:104:PRO:HB2	1:C:107:VAL:HG23	1.86	0.57
1:C:126:ASN:OD1	1:C:128:GLU:HG2	2.04	0.57
1:A:202:LYS:HA	1:A:202:LYS:HE2	1.87	0.57
1:D:189:ARG:HD2	1:D:241:LEU:HD12	1.87	0.57
1:A:104:PRO:O	1:A:107:VAL:HG12	2.05	0.56
1:C:92:GLY:HA2	1:C:97:ASP:HB3	1.86	0.56
1:D:103:ILE:HD11	1:D:108:TRP:CZ2	2.41	0.56
1:B:461:ASP:O	1:B:465:ASN:N	2.40	0.54
1:D:356:LEU:HB3	1:D:360:LYS:NZ	2.22	0.54
1:A:55:MET:O	1:A:63:PHE:HA	2.08	0.53
1:D:300:ILE:HG13	1:D:300:ILE:O	2.07	0.53
1:B:103:ILE:HD11	1:B:108:TRP:CZ2	2.44	0.53
1:D:498:ILE:HD13	1:D:498:ILE:N	2.24	0.53
1:B:425:VAL:HB	1:B:513:THR:HA	1.90	0.53
1:B:344:SER:C	1:B:346:PRO:HD3	2.34	0.53
1:A:22:ILE:HB	1:A:23:PRO:HD3	1.91	0.52
1:A:485:ILE:HG13	1:A:516:TRP:CH2	2.44	0.52
1:B:454:TYR:N	1:B:455:PRO:HD2	2.24	0.52
1:B:116:LEU:HD21	1:B:137:VAL:HG21	1.92	0.52
1:B:498:ILE:HD13	1:B:498:ILE:N	2.24	0.52
1:A:454:TYR:N	1:A:455:PRO:HD2	2.25	0.52
1:D:372:ILE:HG23	1:D:377:GLU:HB2	1.90	0.52
1:D:454:TYR:N	1:D:455:PRO:HD2	2.25	0.52
1:B:429:VAL:HG12	1:B:431:THR:HG23	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:453:GLN:C	1:C:455:PRO:HD2	2.34	0.52
1:D:55:MET:O	1:D:63:PHE:HA	2.09	0.52
1:B:154:LYS:HB3	1:B:155:PRO:HD3	1.92	0.51
1:D:487:SER:OG	1:D:491:THR:HG22	2.11	0.51
1:B:51:TRP:CZ2	1:B:91:CYS:SG	3.03	0.51
1:C:300:ILE:HG13	1:C:300:ILE:O	2.09	0.51
1:B:16:MET:HE1	1:B:396:LEU:HD12	1.92	0.51
1:D:118:PHE:HB2	1:D:126:ASN:HB3	1.92	0.51
1:B:475:ALA:HB1	1:B:507:LEU:HD23	1.93	0.50
1:B:225:LEU:HD22	1:B:230:ALA:HB1	1.93	0.50
1:A:104:PRO:HB3	1:A:106:TRP:NE1	2.26	0.50
1:C:201:SER:O	1:C:205:LEU:HG	2.10	0.50
1:B:427:LYS:HG2	1:B:466:ASP:CB	2.42	0.50
1:B:426:VAL:HA	1:B:514:SER:O	2.11	0.49
1:B:55:MET:O	1:B:63:PHE:HA	2.13	0.49
1:D:104:PRO:HB2	1:D:107:VAL:HG23	1.94	0.49
1:D:351:GLN:HG2	1:D:384:MET:HE1	1.95	0.49
1:A:213:SER:O	1:A:217:VAL:HG23	2.12	0.48
1:A:300:ILE:O	1:A:300:ILE:HG13	2.12	0.48
1:B:454:TYR:N	1:B:455:PRO:CD	2.76	0.48
1:B:427:LYS:HG2	1:B:466:ASP:HB3	1.95	0.48
1:B:134:ALA:O	1:B:138:ILE:HG12	2.13	0.48
1:D:356:LEU:O	1:D:360:LYS:HG3	2.14	0.48
1:B:107:VAL:O	1:B:110:GLN:HB2	2.14	0.48
1:B:348:THR:HA	1:B:351:GLN:HE21	1.79	0.48
1:B:474:PRO:HB2	1:B:477:ARG:HG3	1.96	0.48
1:B:485:ILE:HG13	1:B:516:TRP:CH2	2.48	0.48
1:C:399:GLN:H	1:C:399:GLN:CD	2.21	0.48
1:A:63:PHE:HB3	1:A:65:PHE:CE1	2.49	0.48
1:D:238:GLU:HG2	1:D:242:MET:HE2	1.95	0.48
1:A:367:GLU:HG2	1:A:394:THR:HB	1.96	0.47
1:B:63:PHE:HB3	1:B:65:PHE:CE1	2.50	0.47
1:C:344:SER:C	1:C:346:PRO:HD3	2.40	0.47
1:D:16:MET:O	1:D:398:TYR:HB2	2.14	0.47
1:A:454:TYR:N	1:A:455:PRO:CD	2.78	0.47
1:B:330:THR:O	1:B:331:CYS:HB2	2.15	0.47
1:C:317:LEU:HD12	1:C:356:LEU:HB3	1.96	0.47
1:A:510:THR:HB	1:A:511:SER:H	1.59	0.46
1:B:85:ILE:HG12	1:B:164:TYR:HB2	1.97	0.46
1:A:482:LYS:HE2	1:A:496:GLN:O	2.14	0.46
1:B:104:PRO:HB3	1:B:106:TRP:NE1	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:MET:O	1:C:63:PHE:HA	2.16	0.46
1:B:16:MET:HE3	1:B:396:LEU:HB2	1.97	0.46
1:D:238:GLU:O	1:D:242:MET:HG3	2.16	0.46
1:A:306:LYS:HB2	1:A:307:PRO:HD3	1.97	0.45
1:B:336:ASP:HA	1:B:346:PRO:HD2	1.98	0.45
1:C:365:ASN:HB3	5:C:718:HOH:O	2.16	0.45
1:A:90:GLN:HG3	1:A:102:PRO:HA	1.98	0.45
1:C:397:ARG:HG2	1:C:398:TYR:N	2.32	0.45
1:B:47:THR:HG22	1:B:83:ILE:HB	1.99	0.45
1:A:421:MET:SD	1:A:470:ASN:HB3	2.56	0.45
1:B:433:ILE:HD12	1:B:433:ILE:O	2.17	0.45
1:B:482:LYS:HG3	1:B:496:GLN:HB3	1.98	0.45
1:D:51:TRP:CZ2	1:D:91:CYS:SG	3.10	0.45
1:A:329:PHE:CE2	1:A:350:VAL:HG22	2.51	0.45
1:D:484:PHE:HB3	1:D:495:TRP:CE3	2.52	0.45
1:A:273:HIS:O	1:A:277:ASP:HB2	2.17	0.44
1:B:104:PRO:HB2	1:B:107:VAL:HG23	1.99	0.44
1:C:104:PRO:HB3	1:C:106:TRP:NE1	2.33	0.44
1:A:240:PHE:HE1	1:A:250:GLY:HA2	1.82	0.44
1:B:157:LYS:HE3	1:B:157:LYS:HB2	1.83	0.44
1:C:422:GLN:HB2	1:C:473:LEU:HD23	1.99	0.44
1:A:329:PHE:HE2	1:A:350:VAL:HG22	1.82	0.44
1:A:383:GLU:O	1:A:387:ASN:HB2	2.17	0.44
1:D:454:TYR:N	1:D:455:PRO:CD	2.80	0.44
1:D:92:GLY:HA2	1:D:97:ASP:HB3	2.00	0.44
1:C:1:ALA:HB3	1:C:5:LYS:HG3	1.99	0.44
1:A:429:VAL:HG12	1:A:431:THR:HG23	1.99	0.44
1:B:90:GLN:HB3	1:B:128:GLU:HB2	1.99	0.44
1:A:498:ILE:HD12	1:A:498:ILE:H	1.82	0.43
1:C:51:TRP:CZ2	1:C:91:CYS:SG	3.12	0.43
1:D:47:THR:HG22	1:D:83:ILE:HB	2.00	0.43
1:D:324:LYS:HE2	1:D:324:LYS:HB3	1.73	0.43
1:A:240:PHE:CE1	1:A:250:GLY:HA2	2.52	0.43
1:B:156:TYR:O	1:B:159:VAL:HG22	2.17	0.43
1:A:452:LYS:HE3	1:A:452:LYS:N	2.31	0.43
1:D:19:LEU:HD12	1:D:19:LEU:HA	1.86	0.43
1:D:226:ILE:H	1:D:226:ILE:CD1	2.28	0.43
1:A:7:MET:HE2	1:A:419:PRO:HB3	2.00	0.43
1:B:407:LEU:HD23	1:B:407:LEU:HA	1.86	0.43
1:C:11:TYR:HA	1:C:391:ALA:O	2.19	0.43
1:C:86:ILE:HD12	1:C:86:ILE:N	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:MET:O	1:A:398:TYR:HB2	2.18	0.43
1:B:302:HIS:HB2	1:B:306:LYS:HE3	2.01	0.43
1:C:262:GLU:OE1	1:C:315:HIS:HD2	2.02	0.43
1:A:154:LYS:HB3	1:A:155:PRO:HD3	2.01	0.43
1:D:16:MET:HB2	1:D:395:LEU:O	2.19	0.42
1:C:108:TRP:CZ2	1:C:127:LYS:HB3	2.55	0.42
1:D:270:GLU:HG3	1:D:271:LEU:N	2.34	0.42
1:A:424:ILE:O	1:A:468:ARG:HA	2.20	0.42
1:A:19:LEU:HG	1:A:91:CYS:SG	2.60	0.42
1:A:256:TRP:O	1:A:260:ILE:HG12	2.19	0.42
1:B:16:MET:HG2	5:B:737:HOH:O	2.19	0.42
1:D:213:SER:OG	1:D:216:GLU:HG2	2.20	0.42
1:A:85:ILE:HG12	1:A:164:TYR:HB2	2.01	0.42
1:A:118:PHE:HB2	1:A:126:ASN:HB3	2.00	0.42
1:D:356:LEU:HB3	1:D:360:LYS:HZ2	1.83	0.42
1:D:498:ILE:HG12	1:D:500:GLN:HE22	1.82	0.42
1:A:443:ARG:HB3	1:A:445:GLU:OE1	2.19	0.42
1:B:498:ILE:HG12	1:B:500:GLN:HE22	1.85	0.42
1:D:85:ILE:HG12	1:D:164:TYR:HB2	2.01	0.42
1:B:21:LYS:HG2	1:B:67:TYR:CZ	2.55	0.41
1:B:306:LYS:HB2	1:B:307:PRO:HD3	2.01	0.41
1:C:140:LYS:O	1:C:144:GLU:HG3	2.20	0.41
1:B:300:ILE:HG13	1:B:300:ILE:O	2.20	0.41
1:C:454:TYR:N	1:C:455:PRO:HD2	2.34	0.41
1:D:154:LYS:HB3	1:D:155:PRO:HD3	2.03	0.41
1:D:383:GLU:O	1:D:387:ASN:HB2	2.20	0.41
1:B:1:ALA:HA	1:B:387:ASN:OD1	2.20	0.41
1:D:346:PRO:O	1:D:350:VAL:HG23	2.20	0.41
1:B:399:GLN:H	1:B:399:GLN:CD	2.29	0.41
1:D:186:TYR:HD1	1:D:293:TRP:CD2	2.38	0.41
1:B:229:LEU:HD22	1:B:229:LEU:N	2.35	0.41
1:C:19:LEU:HD12	1:C:19:LEU:HA	1.88	0.41
1:A:329:PHE:O	1:A:366:GLY:HA2	2.21	0.41
1:B:424:ILE:O	1:B:468:ARG:HA	2.21	0.41
1:C:1:ALA:HA	1:C:387:ASN:OD1	2.21	0.41
1:D:119:LYS:HE3	1:D:196:THR:HG22	2.01	0.41
1:D:184:THR:CG2	1:D:191:LYS:HG3	2.51	0.41
1:B:39:LYS:HE2	1:B:39:LYS:HB3	1.87	0.41
1:D:117:TYR:CD1	1:D:125:VAL:HG13	2.56	0.41
1:D:215:ASN:ND2	1:D:219:LYS:HE3	2.36	0.41
1:D:432:THR:HG22	1:D:435:ASP:OD2	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:TYR:CD1	1:A:125:VAL:HG13	2.57	0.40
1:C:22:ILE:N	1:C:23:PRO:HD2	2.36	0.40
1:C:76:LYS:HB2	1:C:159:VAL:HG11	2.03	0.40
1:C:329:PHE:O	1:C:366:GLY:HA2	2.22	0.40
1:C:377:GLU:O	1:C:381:VAL:HG23	2.22	0.40
1:B:422:GLN:HB2	1:B:473:LEU:HD23	2.04	0.40
1:A:8:ASN:HA	1:A:9:PRO:HD3	1.95	0.40
1:A:84:PRO:HD2	1:A:162:LYS:O	2.21	0.40
1:B:15:LEU:HD11	1:B:398:TYR:HA	2.03	0.40
1:B:35:LEU:HB3	1:B:80:MET:HG3	2.03	0.40
1:D:429:VAL:HG12	1:D:431:THR:HG23	2.03	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	514/516 (100%)	488 (95%)	25 (5%)	1 (0%)	43	51
1	B	514/516 (100%)	484 (94%)	29 (6%)	1 (0%)	43	51
1	C	514/516 (100%)	486 (95%)	27 (5%)	1 (0%)	43	51
1	D	514/516 (100%)	488 (95%)	25 (5%)	1 (0%)	43	51
All	All	2056/2064 (100%)	1946 (95%)	106 (5%)	4 (0%)	43	51

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	398	TYR
1	B	398	TYR
1	D	398	TYR
1	C	398	TYR

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	440/440 (100%)	426 (97%)	14 (3%)	34	47
1	B	440/440 (100%)	427 (97%)	13 (3%)	36	49
1	C	440/440 (100%)	432 (98%)	8 (2%)	51	68
1	D	440/440 (100%)	429 (98%)	11 (2%)	42	56
All	All	1760/1760 (100%)	1714 (97%)	46 (3%)	40	55

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	21	LYS
1	A	24	GLU
1	A	173	LEU
1	A	332	LEU
1	A	349	LEU
1	A	377	GLU
1	A	399	GLN
1	A	452	LYS
1	A	473	LEU
1	A	504	PRO
1	A	507	LEU
1	A	508	LYS
1	A	510	THR
1	B	19	LEU
1	B	109	ASN
1	B	110	GLN
1	B	181	SER
1	B	228	GLU
1	B	349	LEU
1	B	377	GLU
1	B	399	GLN
1	B	405	ASN
1	B	412	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	498	ILE
1	B	504	PRO
1	B	508	LYS
1	C	19	LEU
1	C	332	LEU
1	C	349	LEU
1	C	399	GLN
1	C	473	LEU
1	C	502	TRP
1	C	504	PRO
1	C	508	LYS
1	D	16	MET
1	D	19	LEU
1	D	46	ILE
1	D	187	PRO
1	D	226	ILE
1	D	349	LEU
1	D	399	GLN
1	D	421	MET
1	D	488	LYS
1	D	498	ILE
1	D	504	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	315	HIS
1	A	351	GLN
1	A	352	ASN
1	A	399	GLN
1	A	470	ASN
1	B	239	GLN
1	B	263	ASN
1	B	315	HIS
1	B	351	GLN
1	B	453	GLN
1	B	500	GLN
1	C	33	ASN
1	C	77	ASN
1	C	274	ASN
1	C	315	HIS
1	C	352	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	457	GLN
1	D	73	GLN
1	D	215	ASN
1	D	239	GLN
1	D	274	ASN
1	D	281	GLN
1	D	292	HIS
1	D	351	GLN
1	D	352	ASN
1	D	453	GLN
1	D	478	ASN
1	D	503	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

16 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BGC	E	1	2	12,12,12	0.35	0	17,17,17	0.51	0
2	GLC	E	2	2	11,11,12	0.41	0	15,15,17	0.73	1 (6%)
2	BGC	F	1	2	12,12,12	0.30	0	17,17,17	0.51	0
2	GLC	F	2	2	11,11,12	0.32	0	15,15,17	0.76	1 (6%)
2	BGC	G	1	2	12,12,12	0.49	0	17,17,17	0.45	0
2	GLC	G	2	2	11,11,12	0.40	0	15,15,17	0.60	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BGC	H	1	2	12,12,12	0.38	0	17,17,17	0.49	0
2	GLC	H	2	2	11,11,12	0.38	0	15,15,17	0.65	1 (6%)
3	GLC	I	1	3	12,12,12	0.42	0	17,17,17	0.41	0
3	GLC	I	2	3	11,11,12	0.45	0	15,15,17	0.60	0
2	BGC	J	1	2	12,12,12	0.31	0	17,17,17	0.50	0
2	GLC	J	2	2	11,11,12	0.37	0	15,15,17	0.54	0
3	GLC	K	1	3	12,12,12	0.35	0	17,17,17	0.52	0
3	GLC	K	2	3	11,11,12	0.42	0	15,15,17	0.59	0
2	BGC	L	1	2	12,12,12	0.36	0	17,17,17	0.48	0
2	GLC	L	2	2	11,11,12	0.30	0	15,15,17	0.68	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	BGC	E	1	2	-	0/2/22/22	0/1/1/1
2	GLC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	1	2	-	1/2/22/22	0/1/1/1
2	GLC	F	2	2	-	0/2/19/22	0/1/1/1
2	BGC	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	BGC	H	1	2	-	0/2/22/22	0/1/1/1
2	GLC	H	2	2	-	0/2/19/22	0/1/1/1
3	GLC	I	1	3	1/1/5/5	0/2/22/22	0/1/1/1
3	GLC	I	2	3	-	0/2/19/22	0/1/1/1
2	BGC	J	1	2	-	2/2/22/22	0/1/1/1
2	GLC	J	2	2	-	0/2/19/22	0/1/1/1
3	GLC	K	1	3	1/1/5/5	0/2/22/22	0/1/1/1
3	GLC	K	2	3	-	0/2/19/22	0/1/1/1
2	BGC	L	1	2	-	1/2/22/22	0/1/1/1
2	GLC	L	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	GLC	C1-O5-C5	2.41	115.42	112.19
2	F	2	GLC	C1-O5-C5	2.33	115.30	112.19
2	G	2	GLC	C1-O5-C5	2.08	114.98	112.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	2	GLC	C1-O5-C5	2.06	114.94	112.19
2	L	2	GLC	C1-O5-C5	2.02	114.89	112.19

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	I	1	GLC	C1
3	K	1	GLC	C1

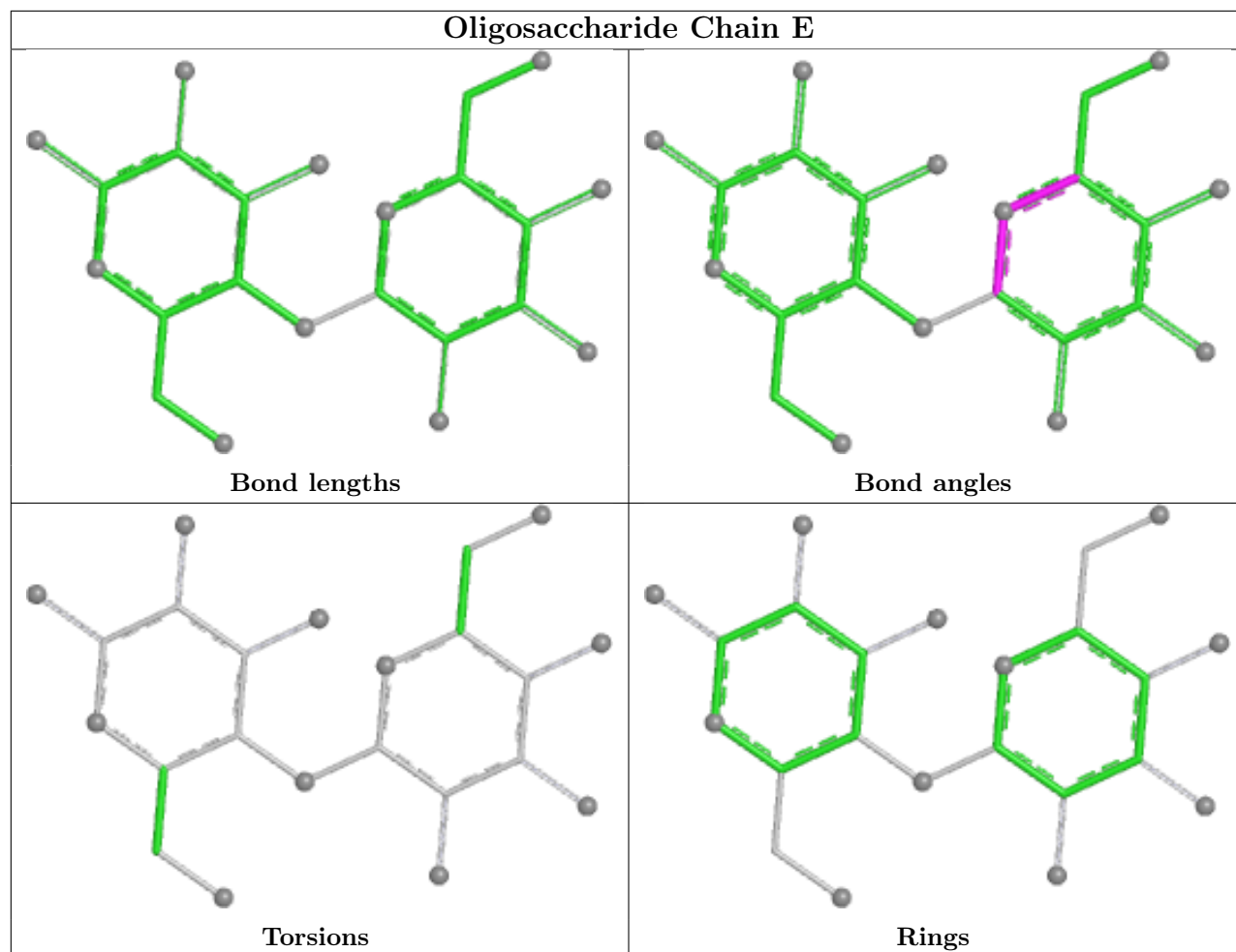
All (4) torsion outliers are listed below:

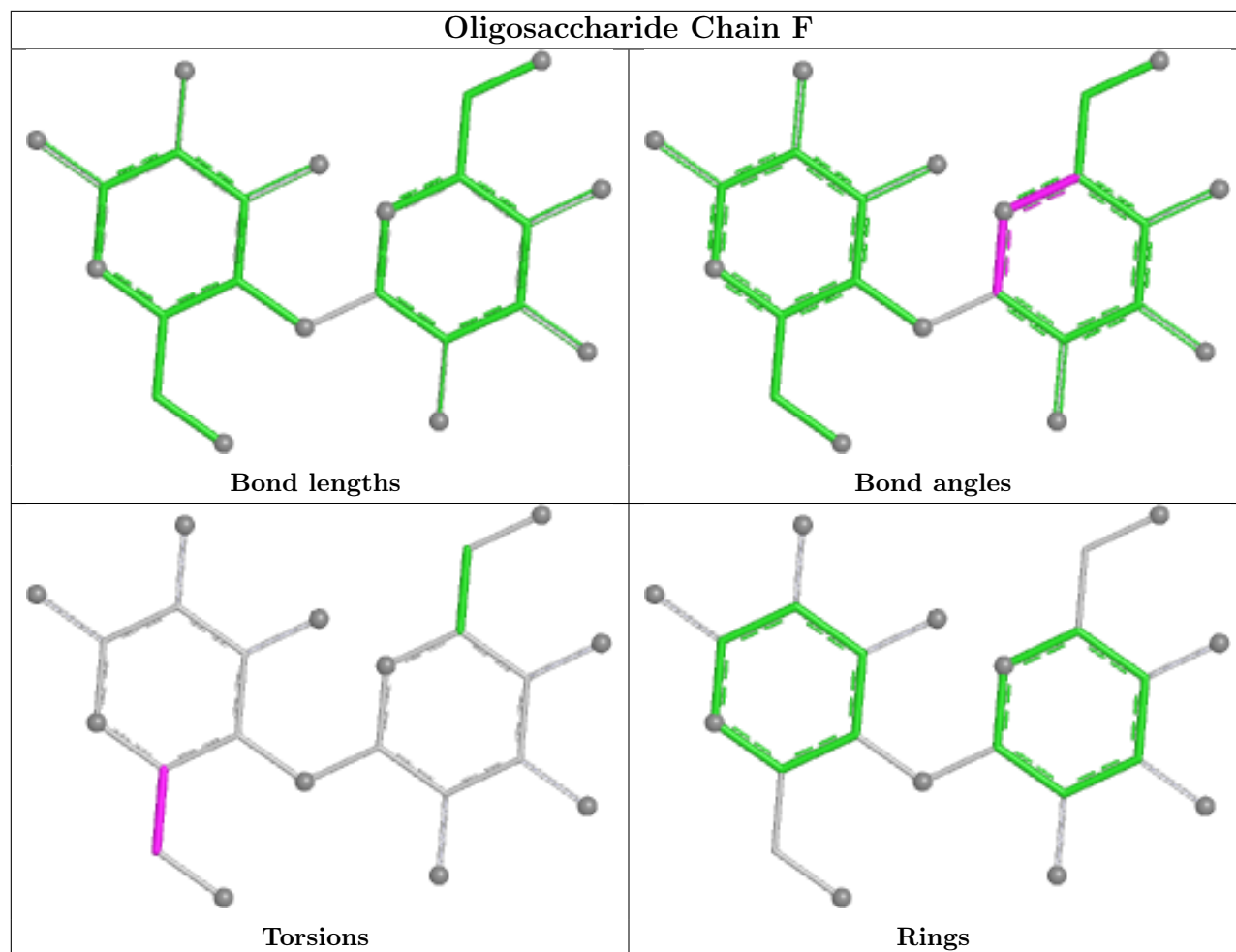
Mol	Chain	Res	Type	Atoms
2	J	1	BGC	O5-C5-C6-O6
2	F	1	BGC	O5-C5-C6-O6
2	L	1	BGC	O5-C5-C6-O6
2	J	1	BGC	C4-C5-C6-O6

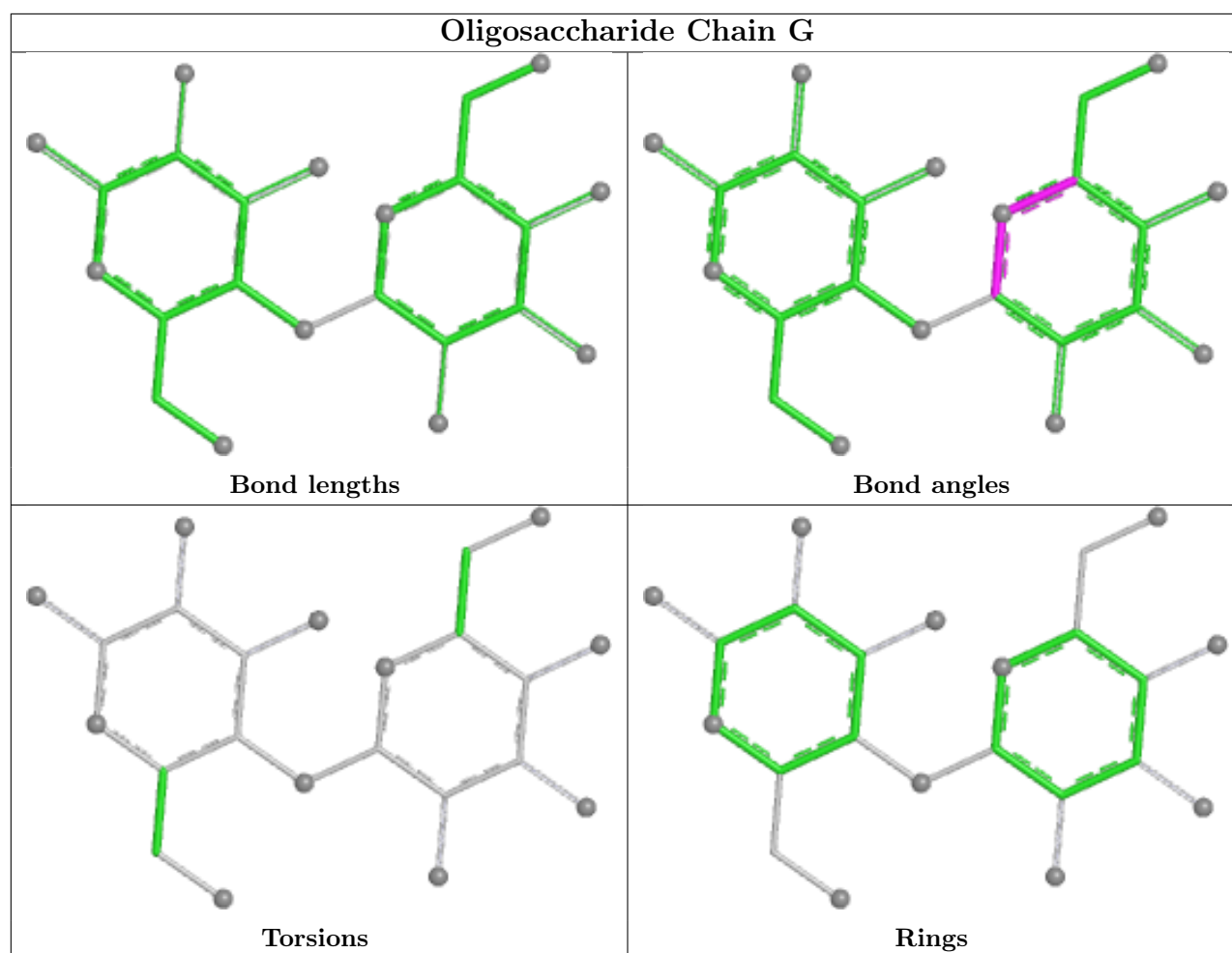
There are no ring outliers.

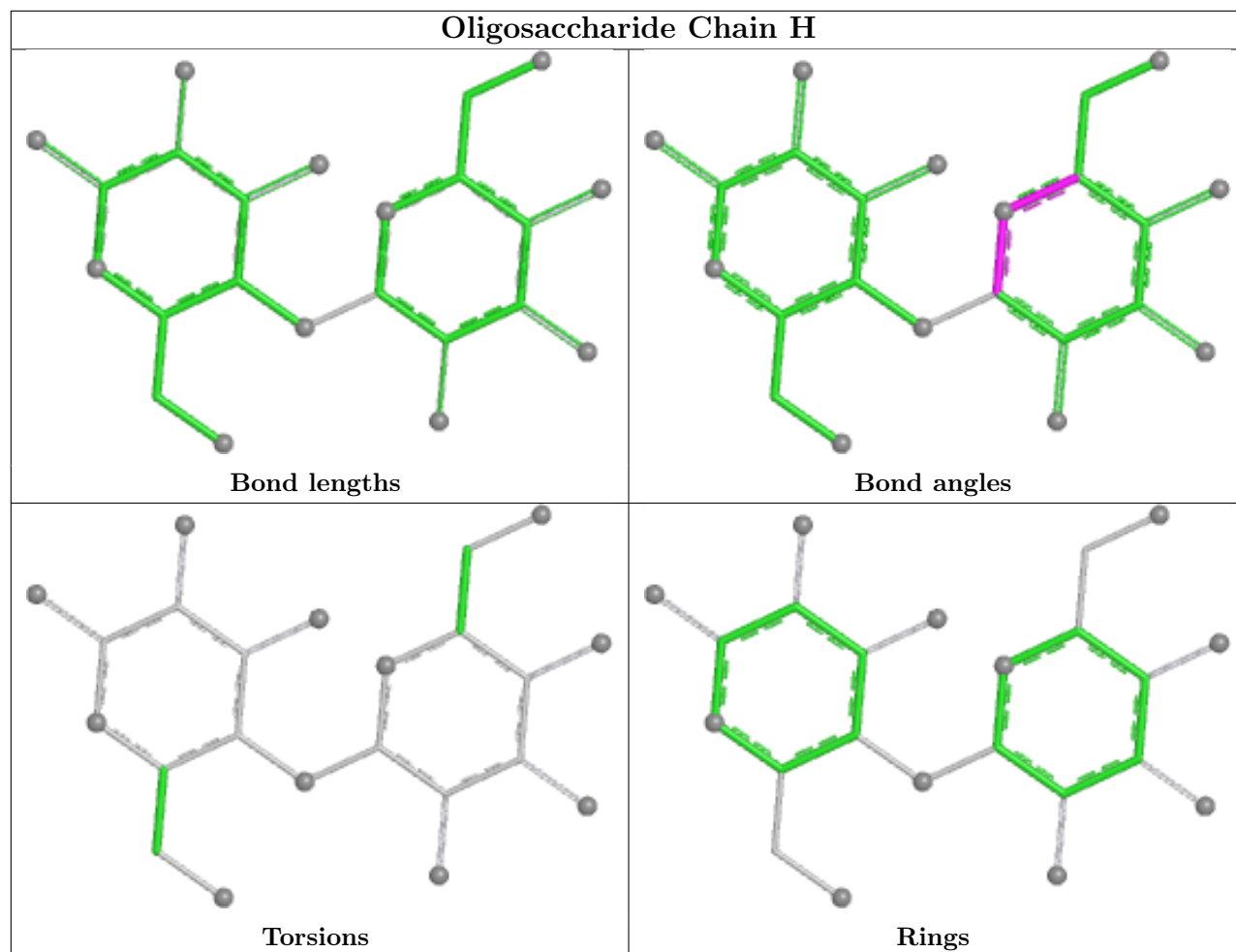
No monomer is involved in short contacts.

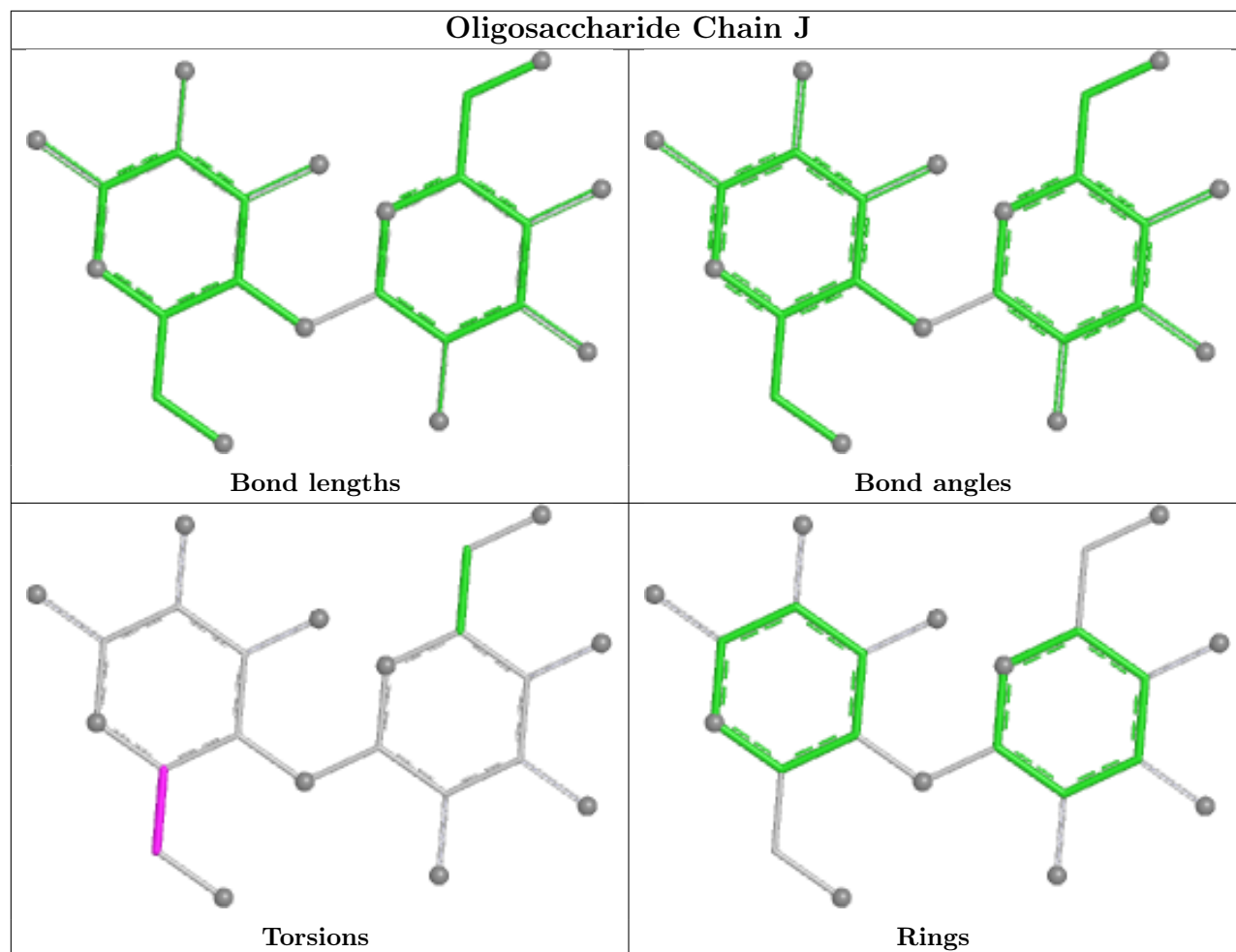
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

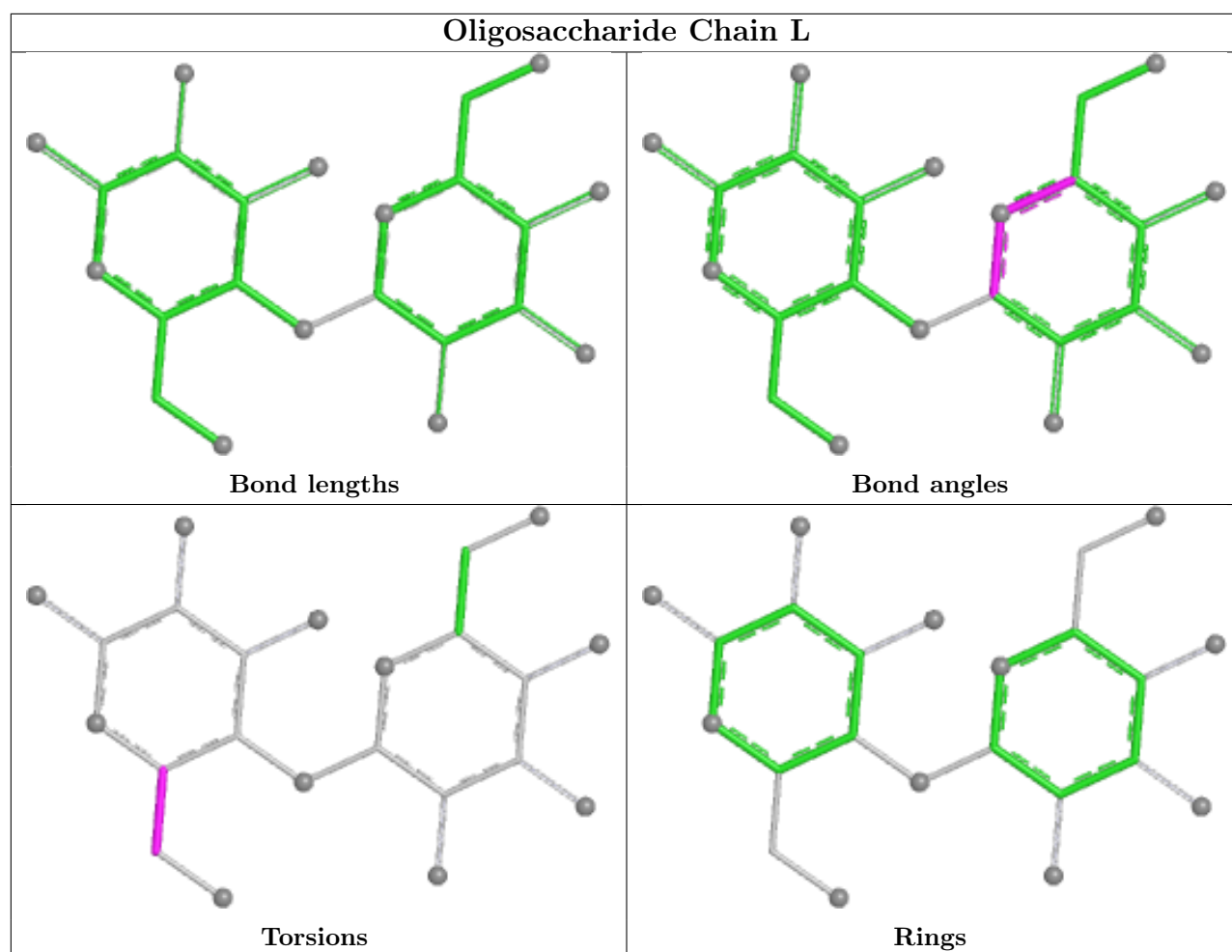


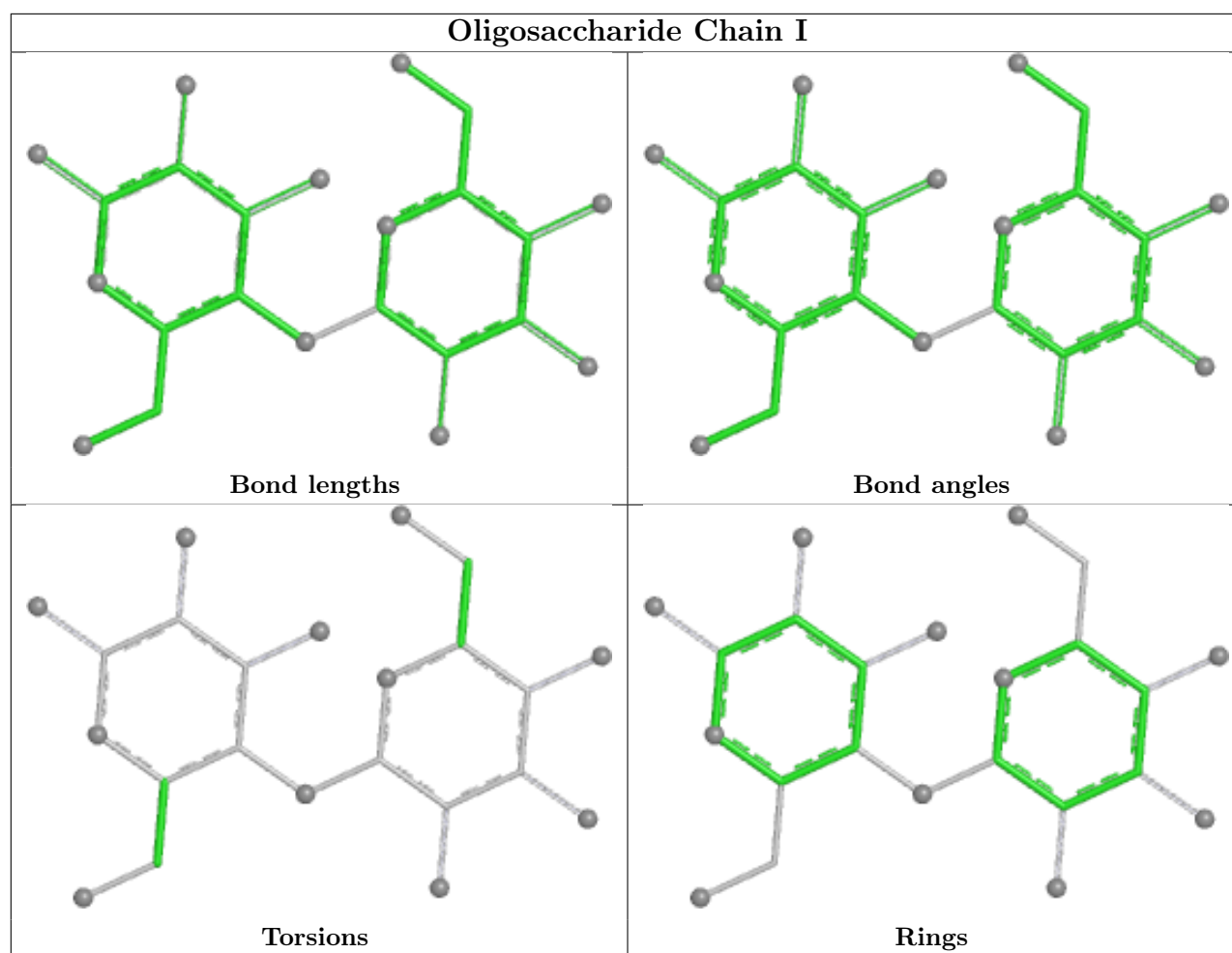


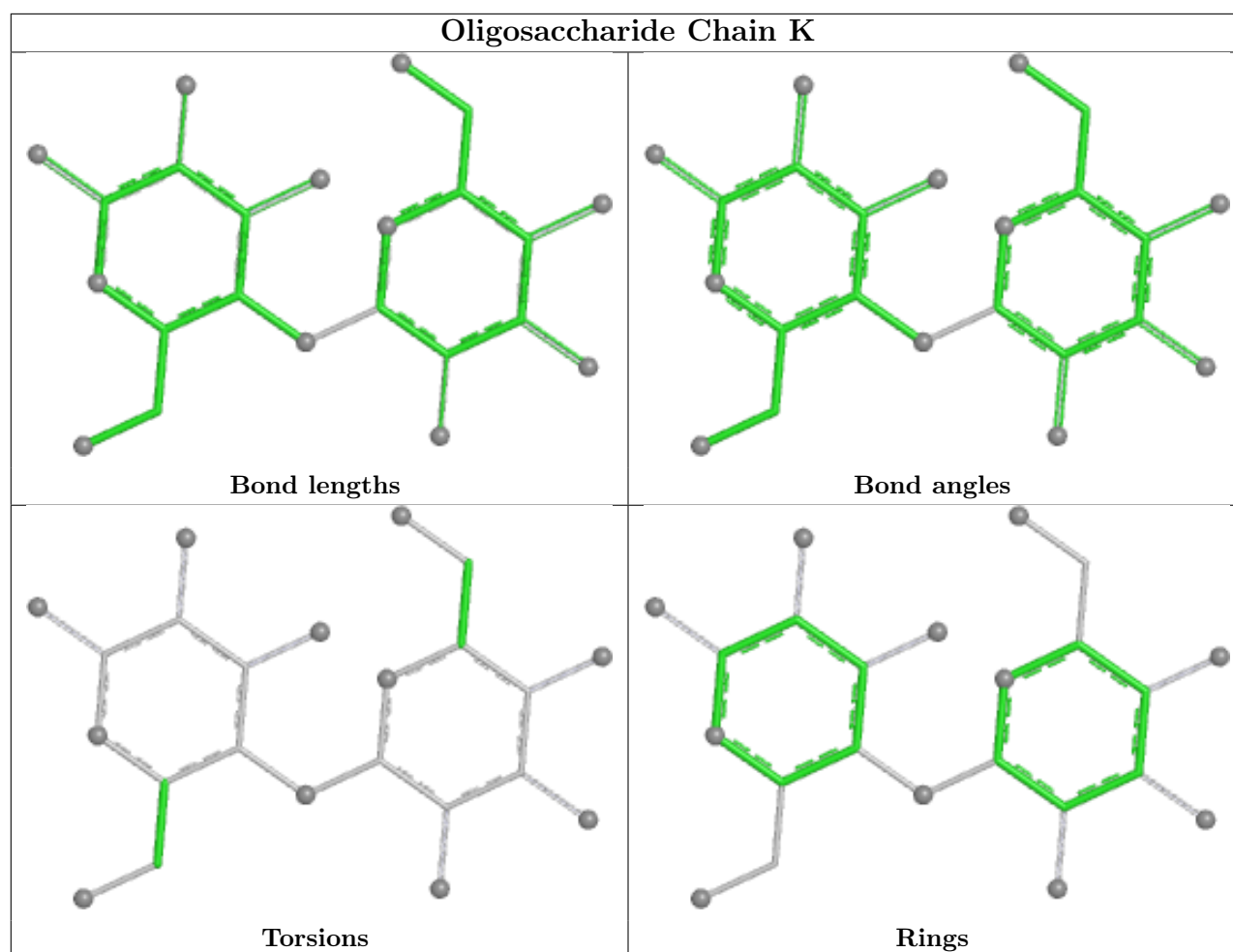












5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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	516/516 (100%)	-0.90	0 100 100	6, 17, 36, 57	0
1	B	516/516 (100%)	-0.72	2 (0%) 88 87	6, 19, 52, 69	0
1	C	516/516 (100%)	-0.81	0 100 100	5, 19, 43, 70	0
1	D	516/516 (100%)	-0.78	0 100 100	6, 19, 43, 60	0
All	All	2064/2064 (100%)	-0.80	2 (0%) 92 90	5, 18, 45, 70	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	514	SER	2.3
1	B	432	THR	2.2

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.

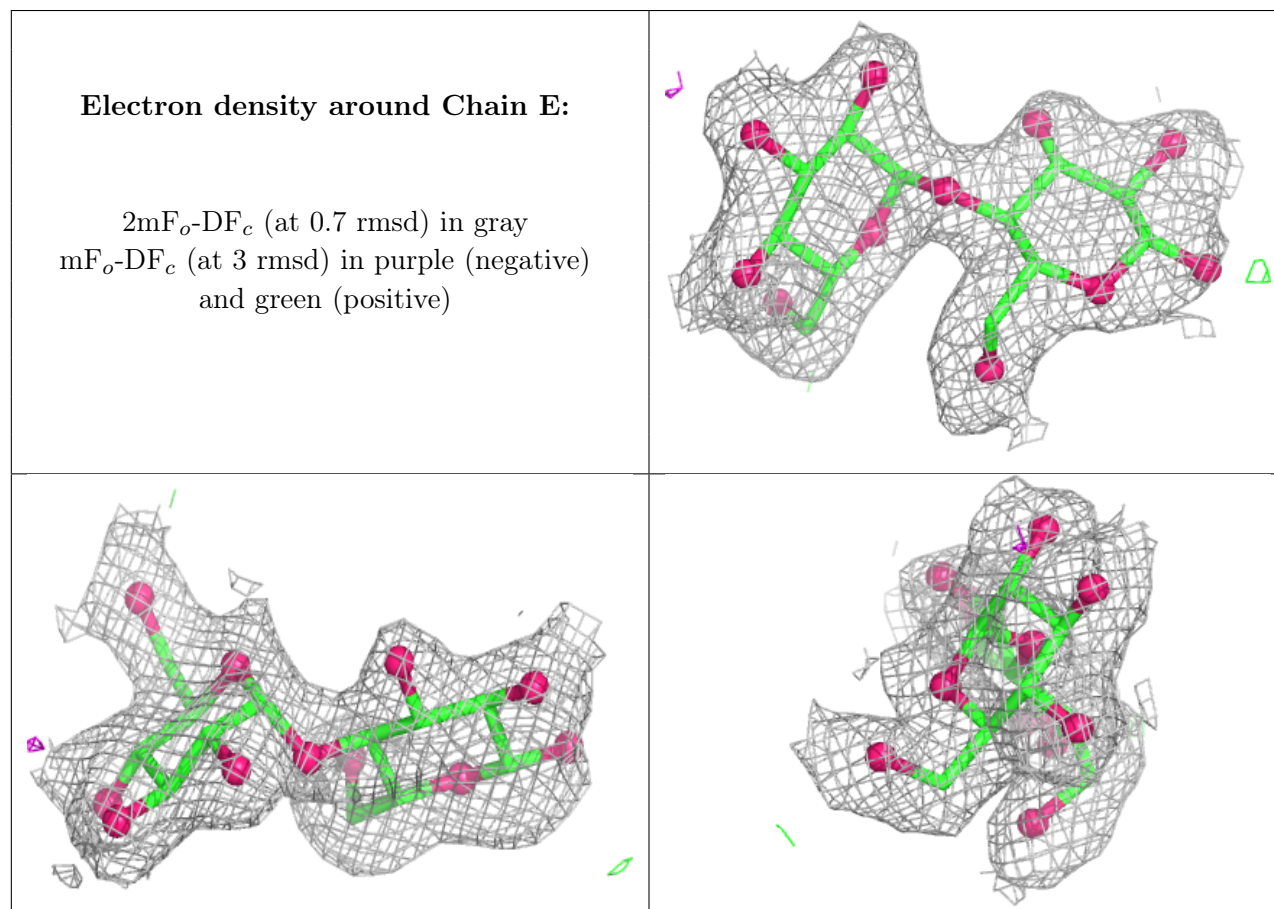
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BGC	L	1	12/12	0.85	0.08	37,49,55,59	0
2	BGC	H	1	12/12	0.90	0.07	28,32,44,47	0
2	BGC	F	1	12/12	0.90	0.07	28,35,40,45	0
3	GLC	K	1	12/12	0.90	0.07	22,25,29,39	0
3	GLC	I	1	12/12	0.91	0.06	16,24,29,39	0

Continued on next page...

Continued from previous page...

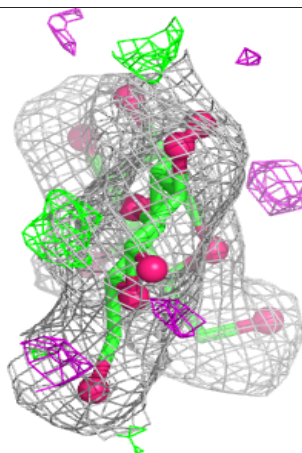
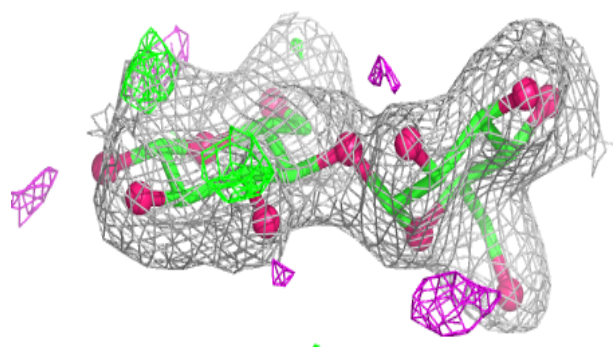
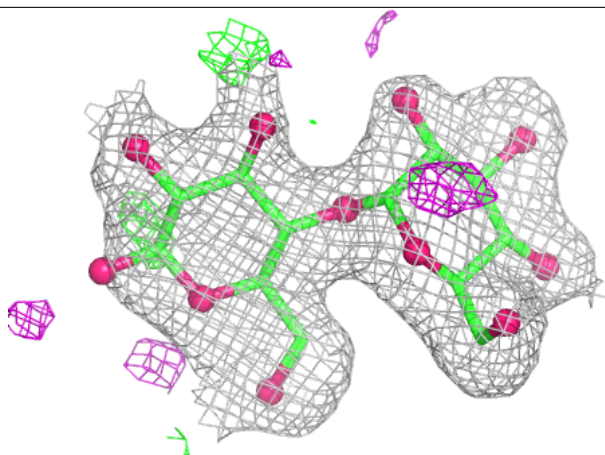
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BGC	E	1	12/12	0.93	0.07	15,23,31,38	0
2	GLC	G	2	11/12	0.94	0.06	11,16,20,21	0
2	GLC	F	2	11/12	0.95	0.06	19,22,25,26	0
2	GLC	L	2	11/12	0.95	0.06	26,29,31,37	0
2	GLC	H	2	11/12	0.96	0.05	16,22,26,26	0
2	BGC	J	1	12/12	0.96	0.05	19,23,30,39	0
2	GLC	E	2	11/12	0.96	0.04	12,15,17,18	0
2	BGC	G	1	12/12	0.97	0.05	14,25,28,31	0
3	GLC	I	2	11/12	0.97	0.04	10,13,17,17	0
2	GLC	J	2	11/12	0.97	0.05	14,18,20,20	0
3	GLC	K	2	11/12	0.97	0.04	15,17,19,20	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.



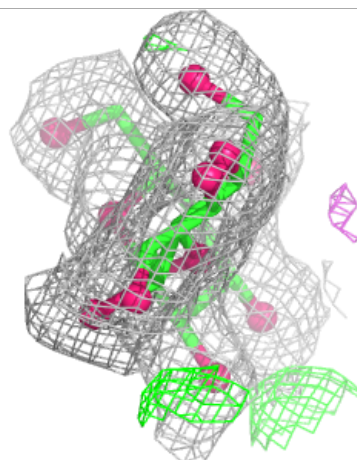
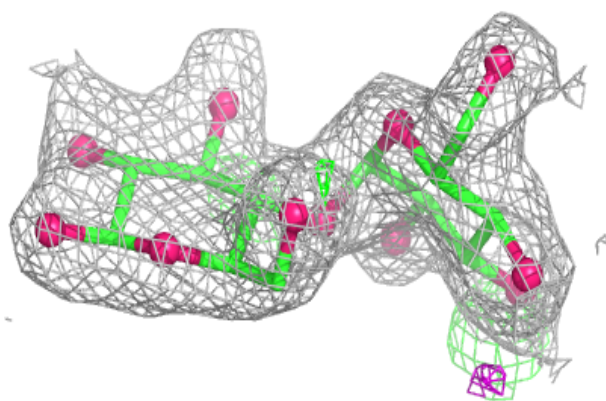
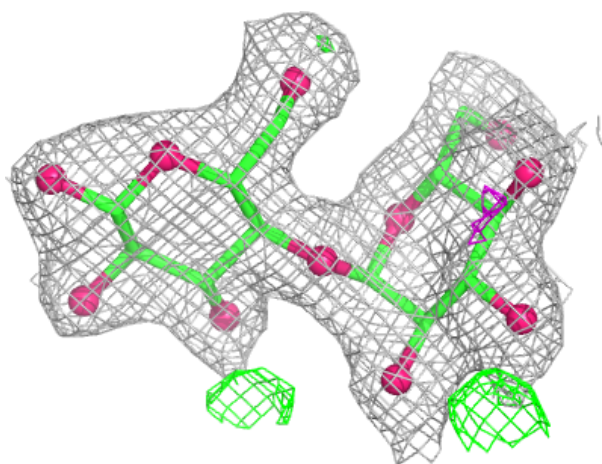
Electron density around Chain F:

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



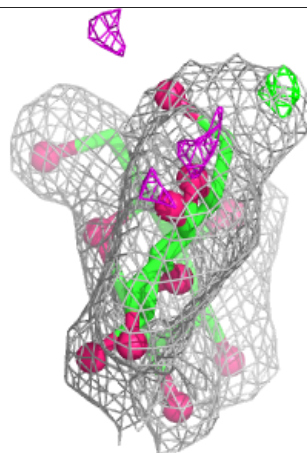
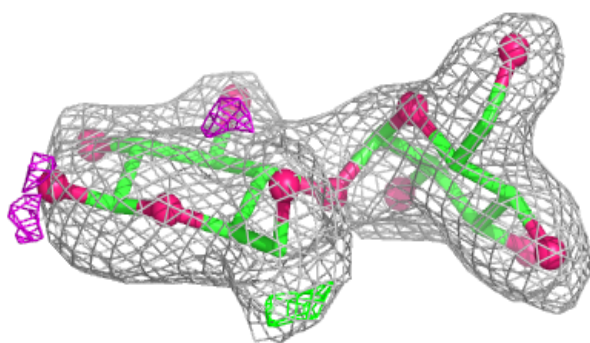
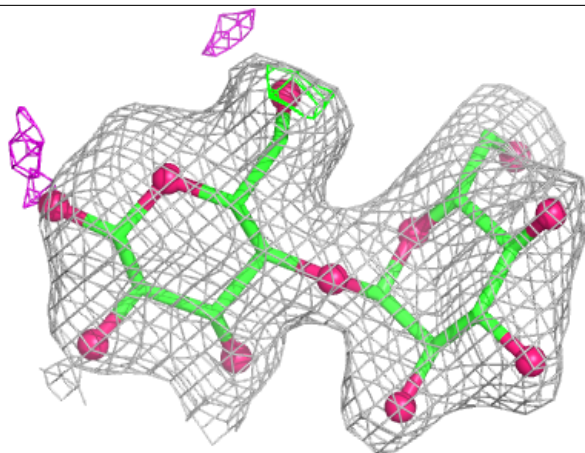
Electron density around Chain G:

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



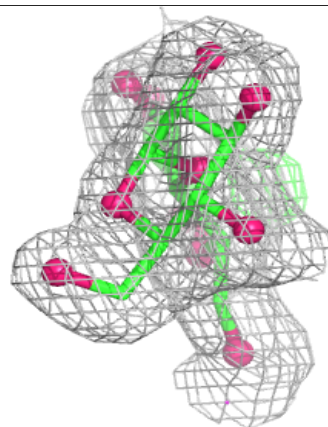
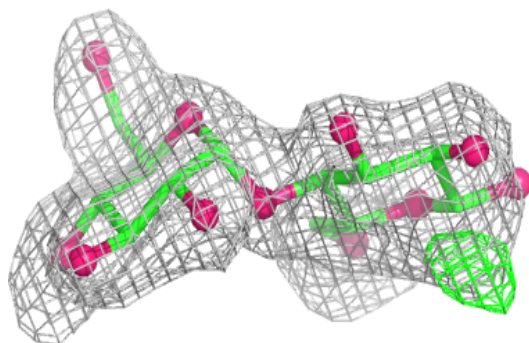
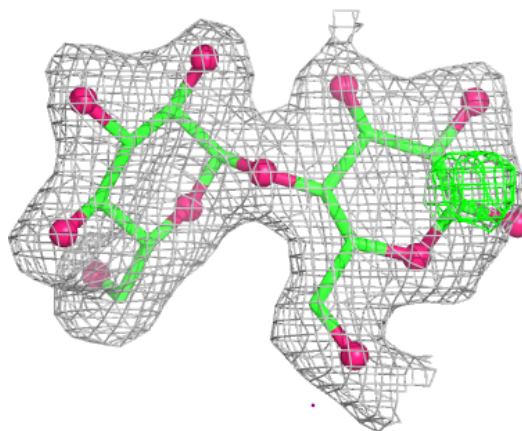
Electron density around Chain H:

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



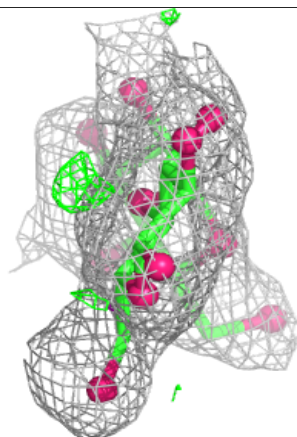
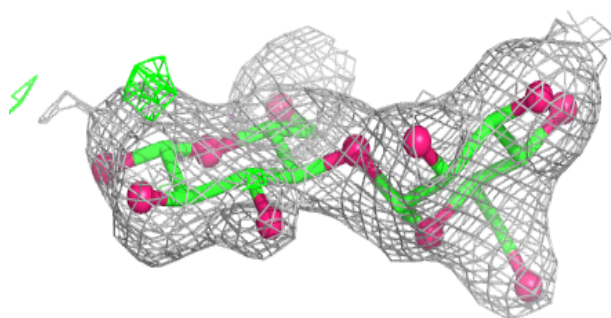
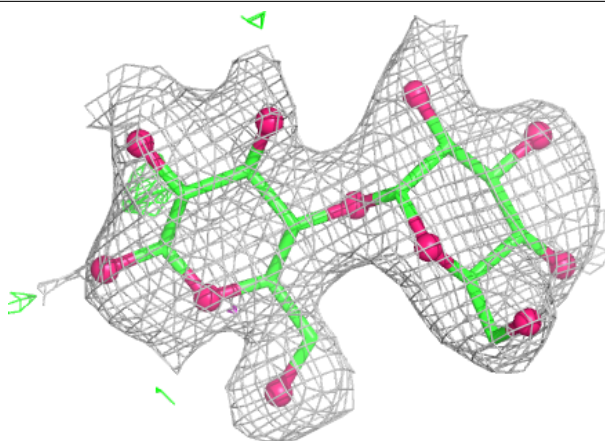
Electron density around Chain J:

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



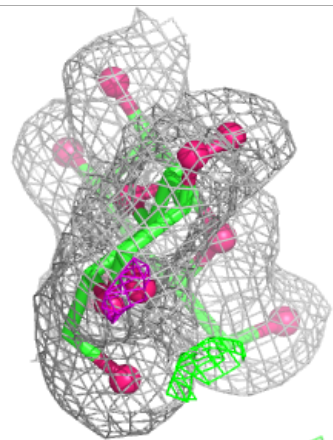
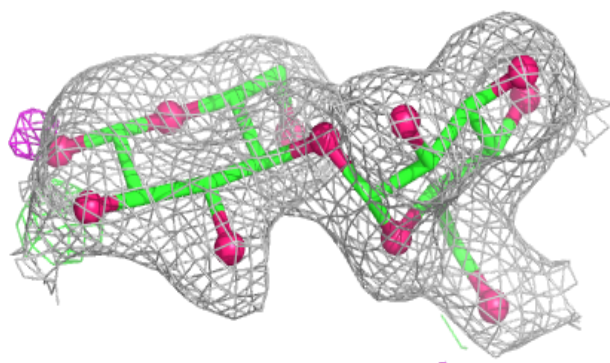
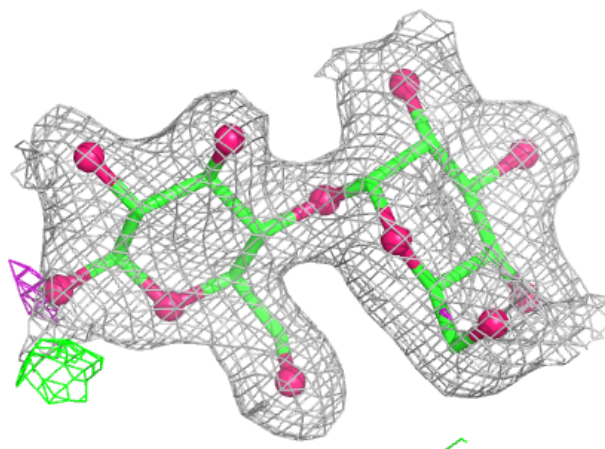
Electron density around Chain L:

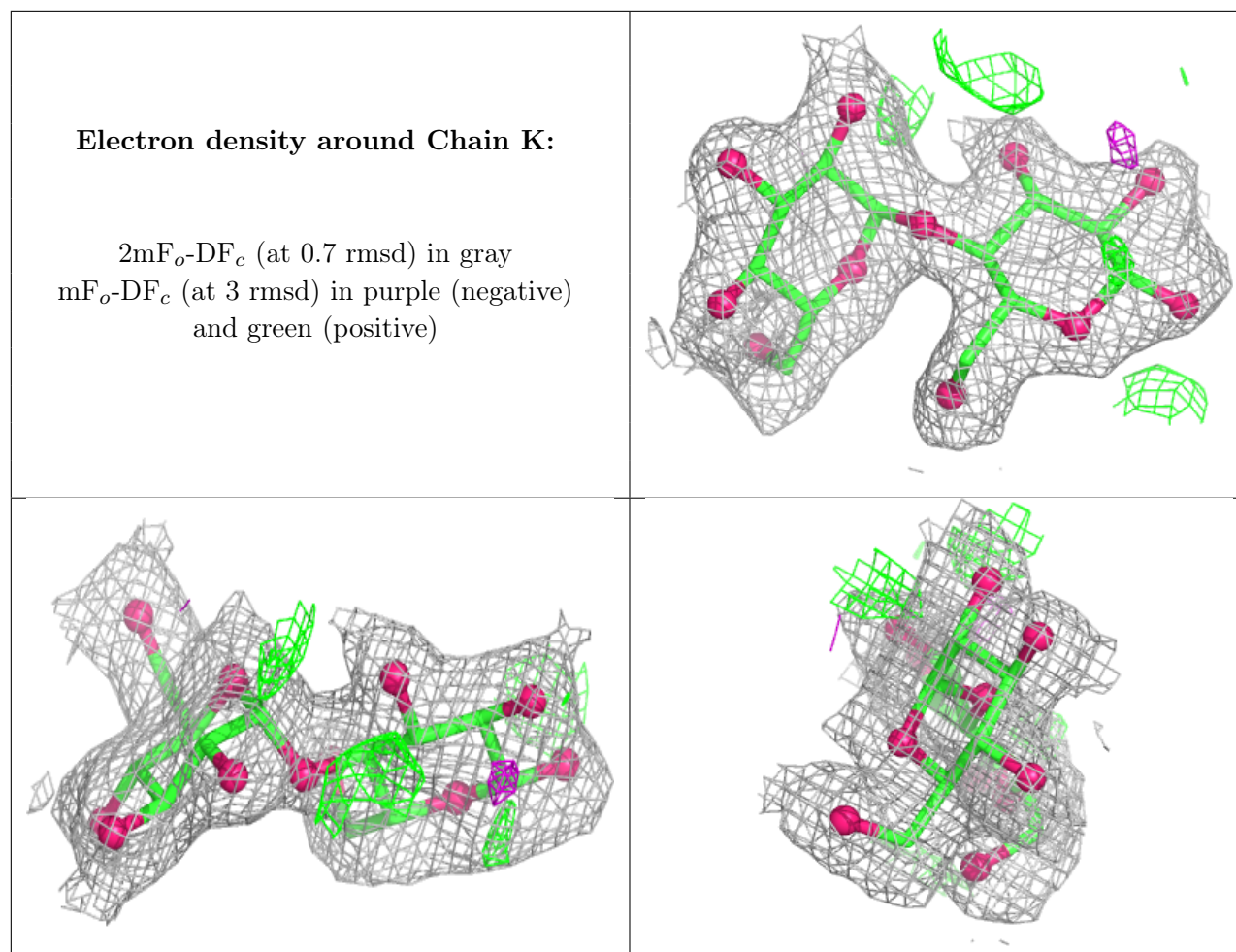
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
4	CA	D	701	1/1	0.97	0.03	20,20,20,20	0
4	CA	C	701	1/1	0.98	0.02	8,8,8,8	0
4	CA	A	701	1/1	0.98	0.02	14,14,14,14	0
4	CA	B	701	1/1	0.99	0.04	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.