



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:25 AM UTC

PDB ID : 4FFH / pdb_00004ffh
Title : Crystal Structure of Levan Fructotransferase D54N mutant from *Arthrobacter ureafaciens* in complex with sucrose
Authors : Park, J.; Rhee, S.
Deposited on : 2012-06-01
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

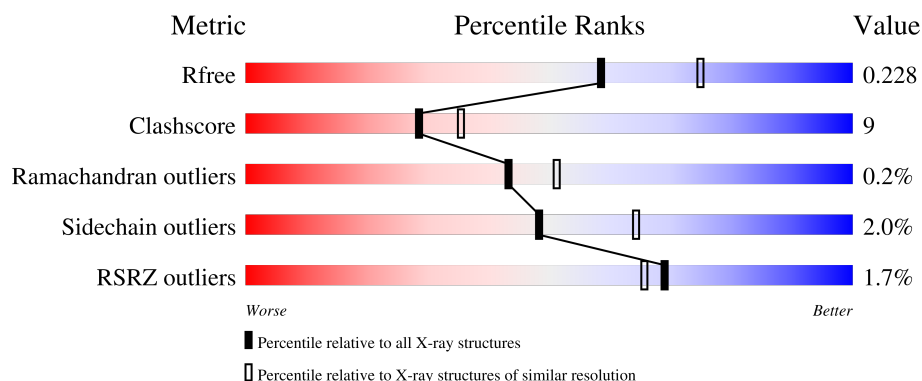
1 Overall quality at a glance

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	492	2% 76% 21% ..
1	B	492	3% 74% 21% ..
1	C	492	% 81% 15% ..
1	D	492	% 79% 16% ..
2	E	2	100%

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

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15917 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 Levan fructotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	480	Total	C	N	O	S	0	0	0
			3739	2375	646	710	8			
1	B	480	Total	C	N	O	S	0	0	0
			3739	2375	646	710	8			
1	C	480	Total	C	N	O	S	0	0	0
			3739	2375	646	710	8			
1	D	478	Total	C	N	O	S	0	0	0
			3725	2367	643	707	8			

There are 52 discrepancies between the modelled and reference sequences:

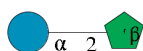
Chain	Residue	Modelled	Actual	Comment	Reference
A	40	MET	-	expression tag	UNP Q9KJD0
A	54	ASN	ASP	engineered mutation	UNP Q9KJD0
A	115	ASP	GLY	conflict	UNP Q9KJD0
A	522	LEU	-	expression tag	UNP Q9KJD0
A	523	GLU	-	expression tag	UNP Q9KJD0
A	524	HIS	-	expression tag	UNP Q9KJD0
A	525	HIS	-	expression tag	UNP Q9KJD0
A	526	HIS	-	expression tag	UNP Q9KJD0
A	527	HIS	-	expression tag	UNP Q9KJD0
A	528	HIS	-	expression tag	UNP Q9KJD0
A	529	HIS	-	expression tag	UNP Q9KJD0
A	530	HIS	-	expression tag	UNP Q9KJD0
A	531	HIS	-	expression tag	UNP Q9KJD0
B	40	MET	-	expression tag	UNP Q9KJD0
B	54	ASN	ASP	engineered mutation	UNP Q9KJD0
B	115	ASP	GLY	conflict	UNP Q9KJD0
B	522	LEU	-	expression tag	UNP Q9KJD0
B	523	GLU	-	expression tag	UNP Q9KJD0
B	524	HIS	-	expression tag	UNP Q9KJD0
B	525	HIS	-	expression tag	UNP Q9KJD0
B	526	HIS	-	expression tag	UNP Q9KJD0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	527	HIS	-	expression tag	UNP Q9KJD0
B	528	HIS	-	expression tag	UNP Q9KJD0
B	529	HIS	-	expression tag	UNP Q9KJD0
B	530	HIS	-	expression tag	UNP Q9KJD0
B	531	HIS	-	expression tag	UNP Q9KJD0
C	40	MET	-	expression tag	UNP Q9KJD0
C	54	ASN	ASP	engineered mutation	UNP Q9KJD0
C	115	ASP	GLY	conflict	UNP Q9KJD0
C	522	LEU	-	expression tag	UNP Q9KJD0
C	523	GLU	-	expression tag	UNP Q9KJD0
C	524	HIS	-	expression tag	UNP Q9KJD0
C	525	HIS	-	expression tag	UNP Q9KJD0
C	526	HIS	-	expression tag	UNP Q9KJD0
C	527	HIS	-	expression tag	UNP Q9KJD0
C	528	HIS	-	expression tag	UNP Q9KJD0
C	529	HIS	-	expression tag	UNP Q9KJD0
C	530	HIS	-	expression tag	UNP Q9KJD0
C	531	HIS	-	expression tag	UNP Q9KJD0
D	40	MET	-	expression tag	UNP Q9KJD0
D	54	ASN	ASP	engineered mutation	UNP Q9KJD0
D	115	ASP	GLY	conflict	UNP Q9KJD0
D	522	LEU	-	expression tag	UNP Q9KJD0
D	523	GLU	-	expression tag	UNP Q9KJD0
D	524	HIS	-	expression tag	UNP Q9KJD0
D	525	HIS	-	expression tag	UNP Q9KJD0
D	526	HIS	-	expression tag	UNP Q9KJD0
D	527	HIS	-	expression tag	UNP Q9KJD0
D	528	HIS	-	expression tag	UNP Q9KJD0
D	529	HIS	-	expression tag	UNP Q9KJD0
D	530	HIS	-	expression tag	UNP Q9KJD0
D	531	HIS	-	expression tag	UNP Q9KJD0

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



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

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

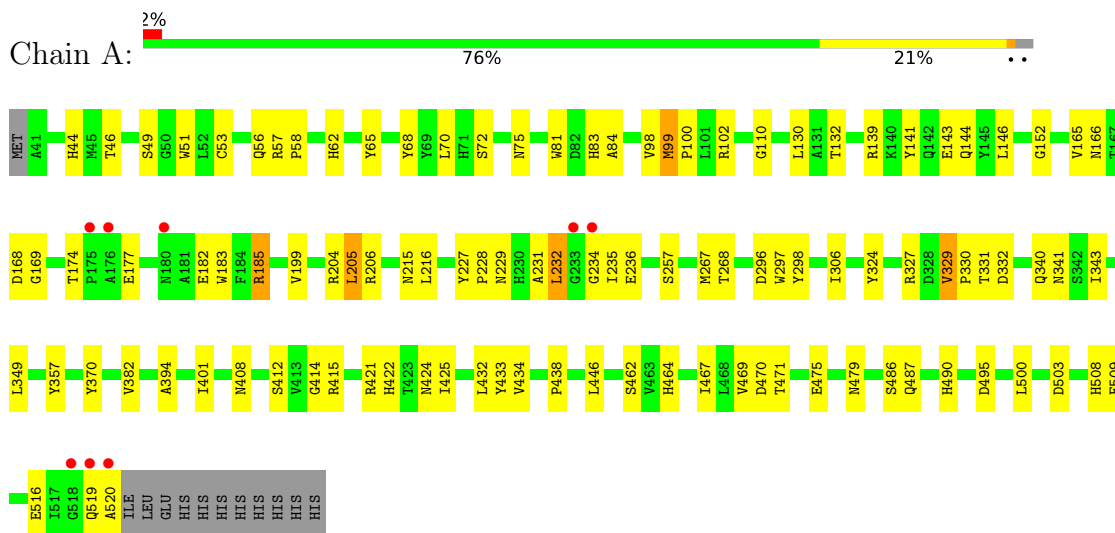
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	203	Total O 203 203	0	0
3	B	205	Total O 205 205	0	0
3	C	205	Total O 205 205	0	0
3	D	224	Total O 224 224	0	0

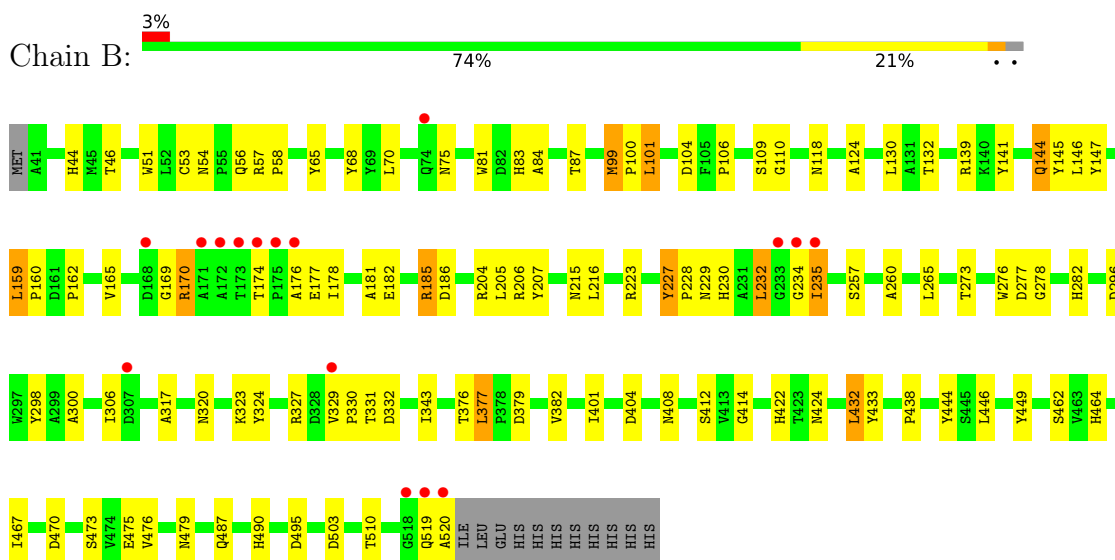
3 Residue-property plots

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.

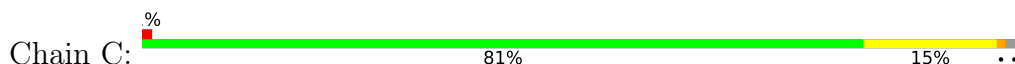
• Molecule 1: Levan fructotransferase

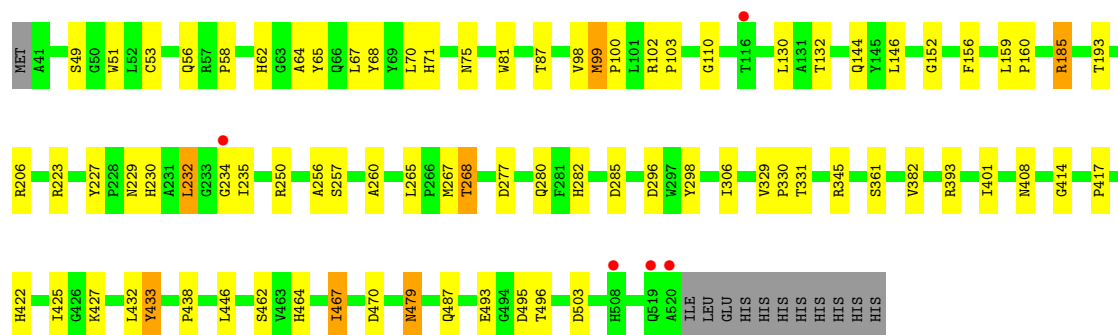


• Molecule 1: Levan fructotransferase

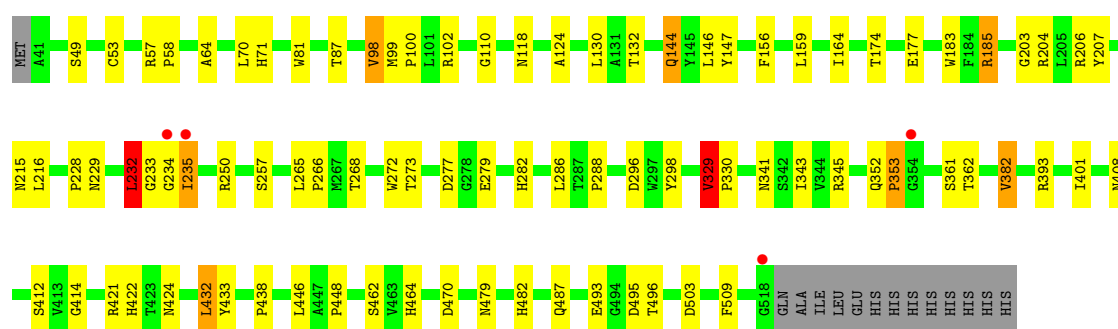
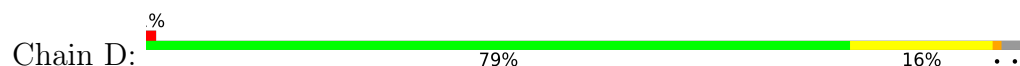


• Molecule 1: Levan fructotransferase





- Molecule 1: Levan fructotransferase



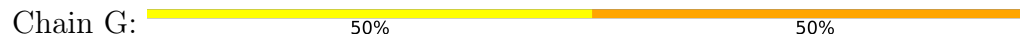
- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



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



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

Chain I:  50% 50%

GLC1
FRU2

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

Chain J:  50% 50%

GLC1
FRU2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.28Å 167.00Å 261.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	83.0 (50.00-2.20) 90.2 (50.00-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.190 , 0.218 0.201 , 0.228	Depositor DCC
R_{free} test set	16915 reflections (9.92%)	wwPDB-VP
Wilson B-factor (Å ²)	26.9	Xtriage
Anisotropy	0.403	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15917	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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: FRU, GLC

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	0.37	0/3863	0.91	15/5312 (0.3%)
1	B	0.37	0/3863	0.92	22/5312 (0.4%)
1	C	0.38	0/3863	0.91	16/5312 (0.3%)
1	D	0.38	0/3849	0.94	11/5293 (0.2%)
All	All	0.37	0/15438	0.92	64/21229 (0.3%)

There are no bond length outliers.

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	234	GLY	N-CA-C	8.81	129.10	112.62
1	B	227	TYR	CA-C-N	7.85	127.41	119.24
1	B	227	TYR	C-N-CA	7.85	127.41	119.24
1	A	228	PRO	N-CA-C	7.58	123.50	113.57
1	D	185	ARG	N-CA-C	7.18	118.65	108.74
1	D	432	LEU	N-CA-C	-7.18	93.48	107.62
1	A	99	MET	CA-C-N	7.17	127.17	119.78
1	A	99	MET	C-N-CA	7.17	127.17	119.78
1	B	343	ILE	N-CA-C	-6.93	102.38	110.21
1	B	432	LEU	N-CA-C	-6.86	94.11	107.62
1	A	432	LEU	N-CA-C	-6.77	94.28	107.62
1	D	343	ILE	N-CA-C	-6.68	100.92	109.80
1	B	185	ARG	N-CA-C	6.60	118.17	108.86
1	D	232	LEU	N-CA-C	-6.59	104.50	112.54
1	C	185	ARG	N-CA-C	6.52	117.73	108.74
1	B	99	MET	CA-C-N	6.47	126.44	119.78
1	B	99	MET	C-N-CA	6.47	126.44	119.78
1	B	144	GLN	N-CA-C	6.31	119.01	108.73
1	D	329	VAL	N-CA-CB	-6.30	107.48	111.83
1	A	343	ILE	N-CA-C	-6.29	101.44	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	144	GLN	N-CA-C	6.26	118.94	108.73
1	D	144	GLN	N-CA-C	6.25	118.90	108.96
1	C	296	ASP	N-CA-C	6.12	119.34	107.71
1	C	100	PRO	N-CA-C	6.02	120.67	111.34
1	A	227	TYR	CA-C-N	5.95	125.50	119.19
1	A	227	TYR	C-N-CA	5.95	125.50	119.19
1	C	159	LEU	N-CA-C	-5.93	101.00	109.24
1	D	159	LEU	N-CA-C	-5.83	101.13	109.24
1	C	99	MET	CA-C-N	5.78	126.10	119.92
1	C	99	MET	C-N-CA	5.78	126.10	119.92
1	A	185	ARG	N-CA-C	5.77	116.70	108.74
1	C	267	MET	N-CA-C	-5.76	103.06	111.30
1	C	268	THR	N-CA-C	5.73	116.77	108.34
1	A	296	ASP	N-CA-C	5.71	119.81	107.49
1	B	165	VAL	N-CA-C	5.70	116.95	109.21
1	B	159	LEU	CA-C-N	5.65	125.76	119.32
1	B	159	LEU	C-N-CA	5.65	125.76	119.32
1	B	100	PRO	N-CA-C	5.59	120.10	111.21
1	A	267	MET	N-CA-C	-5.57	103.33	111.30
1	A	100	PRO	N-CA-C	5.56	120.05	111.21
1	B	101	LEU	N-CA-C	-5.55	102.68	110.50
1	C	432	LEU	N-CA-C	-5.47	95.67	107.49
1	B	377	LEU	CA-C-N	5.45	125.46	119.90
1	B	377	LEU	C-N-CA	5.45	125.46	119.90
1	A	471	THR	N-CA-C	5.40	117.92	111.71
1	B	273	THR	N-CA-C	-5.36	102.94	110.50
1	A	165	VAL	N-CA-C	5.34	116.47	109.21
1	B	296	ASP	N-CA-C	5.33	118.99	107.49
1	D	100	PRO	N-CA-C	5.27	119.76	111.38
1	B	467	ILE	N-CA-C	5.25	115.42	107.75
1	A	329	VAL	N-CA-CB	-5.22	108.22	111.83
1	D	296	ASP	N-CA-C	5.19	118.70	107.49
1	D	273	THR	N-CA-C	-5.19	102.80	110.48
1	C	268	THR	CB-CA-C	-5.18	108.98	116.54
1	B	476	VAL	N-CA-C	5.16	115.28	107.80
1	C	479	ASN	CB-CA-C	-5.16	110.61	116.54
1	B	473	SER	N-CA-C	5.15	116.35	108.42
1	C	433	TYR	N-CA-C	5.14	118.38	110.42
1	B	235	ILE	N-CA-C	5.11	119.97	109.34
1	C	227	TYR	CA-C-N	5.05	124.65	119.05
1	C	227	TYR	C-N-CA	5.05	124.65	119.05
1	A	231	ALA	N-CA-C	-5.04	107.19	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	467	ILE	N-CA-C	5.03	115.10	107.80
1	B	433	TYR	N-CA-C	5.03	118.22	110.42

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	3739	0	3491	73	0
1	B	3739	0	3491	74	0
1	C	3739	0	3491	57	0
1	D	3725	0	3478	53	0
2	E	23	0	19	4	0
2	F	23	0	19	3	0
2	G	23	0	19	2	0
2	H	23	0	19	0	0
2	I	23	0	19	1	0
2	J	23	0	19	1	0
3	A	203	0	0	5	0
3	B	205	0	0	3	0
3	C	205	0	0	6	0
3	D	224	0	0	3	0
All	All	15917	0	14065	256	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 (256) 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:A:139:ARG:HH22	2:E:1:GLC:H61	1.27	0.97
1:B:174:THR:HB	1:B:177:GLU:HG3	1.46	0.95
1:B:139:ARG:HH22	2:F:1:GLC:H61	1.33	0.90
1:A:329:VAL:HG13	1:A:330:PRO:HD2	1.55	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:425:ILE:HD13	1:C:467:ILE:HD13	1.61	0.82
1:A:434:VAL:HB	1:A:487:GLN:HE22	1.44	0.81
1:B:408:ASN:HB3	1:B:503:ASP:HB2	1.65	0.79
1:C:329:VAL:HG13	1:C:330:PRO:HD2	1.66	0.78
1:A:174:THR:OG1	1:A:177:GLU:HG3	1.85	0.77
1:B:329:VAL:HG13	1:B:330:PRO:HD2	1.66	0.76
1:B:206:ARG:HH11	1:B:234:GLY:HA3	1.52	0.73
1:D:203:GLY:HA2	1:D:235:ILE:HG22	1.68	0.73
1:C:417:PRO:HG2	3:C:612:HOH:O	1.88	0.73
1:A:139:ARG:NH2	2:E:1:GLC:H61	2.03	0.73
1:D:329:VAL:HG22	1:D:330:PRO:HD2	1.73	0.70
1:A:206:ARG:HH11	1:A:234:GLY:HA3	1.57	0.69
1:A:139:ARG:HH22	2:E:1:GLC:C6	2.03	0.69
1:A:434:VAL:CB	1:A:487:GLN:HE22	2.06	0.69
1:A:141:TYR:O	1:A:143:GLU:HG2	1.92	0.69
1:B:145:TYR:CZ	1:B:162:PRO:HG3	2.29	0.68
1:D:464:HIS:H	1:D:479:ASN:ND2	1.91	0.67
1:B:54:ASN:HD21	2:F:2:FRU:H11	1.60	0.67
1:C:464:HIS:H	1:C:479:ASN:ND2	1.92	0.67
1:C:408:ASN:HB3	1:C:503:ASP:HB2	1.76	0.66
1:D:207:TYR:O	1:D:235:ILE:HG21	1.96	0.66
1:D:174:THR:OG1	1:D:177:GLU:HG3	1.96	0.65
1:D:53:CYS:HB3	1:D:70:LEU:HB2	1.78	0.65
1:A:464:HIS:H	1:A:479:ASN:ND2	1.95	0.65
1:C:393:ARG:HD3	1:C:496:THR:HG22	1.80	0.64
1:B:206:ARG:HD3	1:B:234:GLY:HA2	1.77	0.64
1:D:393:ARG:HD3	1:D:496:THR:HG22	1.80	0.63
1:C:206:ARG:NH1	1:C:234:GLY:N	2.47	0.63
1:B:145:TYR:CE2	1:B:162:PRO:HG3	2.34	0.63
1:A:44:HIS:HD2	1:A:470:ASP:OD2	1.81	0.62
1:B:464:HIS:H	1:B:479:ASN:ND2	1.97	0.62
1:A:206:ARG:HD3	1:A:234:GLY:HA2	1.80	0.62
1:A:229:ASN:O	1:A:232:LEU:HB2	1.99	0.62
1:B:159:LEU:HD22	1:B:160:PRO:HD2	1.81	0.62
1:A:102:ARG:HD3	3:A:608:HOH:O	2.00	0.62
1:C:81:TRP:HB2	1:C:99:MET:HB2	1.82	0.61
1:C:53:CYS:HB3	1:C:70:LEU:HB2	1.81	0.61
1:B:81:TRP:HB2	1:B:99:MET:HB2	1.83	0.61
1:C:206:ARG:HH11	1:C:234:GLY:CA	2.12	0.61
1:A:44:HIS:HE1	1:A:475:GLU:OE1	1.84	0.61
1:D:464:HIS:H	1:D:479:ASN:HD21	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:TYR:O	1:A:327:ARG:HG2	2.02	0.60
1:B:87:THR:HG22	3:B:721:HOH:O	2.01	0.60
1:B:329:VAL:HG12	1:B:331:THR:H	1.67	0.60
1:C:193:THR:HG22	3:C:637:HOH:O	2.01	0.59
1:A:229:ASN:HB3	1:A:232:LEU:HD22	1.82	0.59
1:B:229:ASN:O	1:B:232:LEU:HB2	2.02	0.59
1:A:166:ASN:C	1:A:166:ASN:HD22	2.11	0.58
1:C:229:ASN:O	1:C:232:LEU:HB2	2.04	0.58
1:A:434:VAL:HB	1:A:487:GLN:NE2	2.17	0.58
1:A:81:TRP:HB2	1:A:99:MET:HB2	1.85	0.58
1:D:257:SER:HA	1:D:268:THR:O	2.03	0.58
1:C:422:HIS:O	1:C:438:PRO:HB2	2.04	0.57
1:D:203:GLY:CA	1:D:235:ILE:HG22	2.34	0.57
1:C:49:SER:O	1:C:71:HIS:HE1	1.87	0.57
1:B:206:ARG:NH1	1:B:234:GLY:HA3	2.20	0.57
1:D:49:SER:O	1:D:71:HIS:HE1	1.87	0.57
1:B:519:GLN:N	1:B:519:GLN:OE1	2.36	0.57
1:D:229:ASN:HB3	1:D:232:LEU:HD22	1.86	0.57
1:C:56:GLN:HB2	1:C:68:TYR:HB2	1.87	0.56
1:D:206:ARG:NE	1:D:233:GLY:HA2	2.20	0.56
1:A:519:GLN:O	1:A:520:ALA:C	2.48	0.56
1:A:329:VAL:HG13	1:A:330:PRO:CD	2.31	0.56
1:D:64:ALA:HB2	1:D:87:THR:HG22	1.87	0.56
1:A:215:ASN:O	1:A:216:LEU:HB2	2.05	0.56
1:B:44:HIS:HD2	1:B:470:ASP:OD2	1.88	0.56
1:D:414:GLY:O	1:D:495:ASP:HB3	2.05	0.56
1:B:204:ARG:O	1:B:234:GLY:O	2.24	0.56
1:A:408:ASN:HB3	1:A:503:ASP:HB2	1.87	0.56
1:B:146:LEU:HD23	1:B:147:TYR:N	2.21	0.56
1:C:64:ALA:HB2	1:C:87:THR:HG22	1.88	0.55
1:A:72:SER:HB3	3:A:696:HOH:O	2.06	0.55
1:B:54:ASN:HD21	2:F:2:FRU:C1	2.19	0.55
1:B:53:CYS:HB3	1:B:70:LEU:HB2	1.87	0.55
1:C:464:HIS:H	1:C:479:ASN:HD21	1.54	0.55
1:B:146:LEU:HD23	1:B:146:LEU:C	2.32	0.55
1:B:174:THR:HG22	1:B:176:ALA:H	1.70	0.55
1:B:404:ASP:HB3	3:B:730:HOH:O	2.07	0.55
1:C:206:ARG:NH1	1:C:234:GLY:H	2.03	0.55
1:A:433:TYR:CE2	2:G:2:FRU:H12	2.41	0.55
1:B:519:GLN:O	1:B:520:ALA:HB3	2.07	0.55
1:A:53:CYS:HB3	1:A:70:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:ASN:HB2	1:B:124:ALA:HA	1.90	0.54
1:C:285:ASP:HB3	3:C:795:HOH:O	2.08	0.54
1:B:446:LEU:HD21	1:B:490:HIS:CD2	2.43	0.54
1:C:277:ASP:OD1	1:C:282:HIS:HE1	1.90	0.54
1:A:204:ARG:O	1:A:234:GLY:O	2.26	0.54
1:C:257:SER:HB3	1:C:298:TYR:CE2	2.43	0.54
1:D:228:PRO:HD3	1:D:286:LEU:HD13	1.90	0.53
1:D:81:TRP:HB2	1:D:99:MET:HB2	1.90	0.53
1:B:324:TYR:O	1:B:327:ARG:HG2	2.09	0.53
1:A:236:GLU:OE2	2:E:2:FRU:H12	2.07	0.53
1:C:146:LEU:C	1:C:146:LEU:HD23	2.34	0.52
1:C:206:ARG:HD3	1:C:234:GLY:HA2	1.89	0.52
1:D:412:SER:OG	1:D:424:ASN:ND2	2.41	0.52
1:D:329:VAL:HG22	1:D:330:PRO:CD	2.39	0.52
1:D:257:SER:HB3	1:D:298:TYR:CE2	2.43	0.52
1:A:486:SER:C	1:A:487:GLN:HG3	2.34	0.52
1:D:146:LEU:HD23	1:D:146:LEU:C	2.35	0.52
1:A:139:ARG:HG2	1:A:182:GLU:HG2	1.91	0.52
1:B:51:TRP:HB2	1:B:75:ASN:HD22	1.74	0.51
1:D:422:HIS:O	1:D:438:PRO:HB2	2.09	0.51
1:A:486:SER:O	1:A:487:GLN:HG3	2.10	0.51
1:A:464:HIS:H	1:A:479:ASN:HD21	1.59	0.51
1:D:433:TYR:CE2	2:J:2:FRU:H12	2.46	0.51
1:C:250:ARG:NH1	3:C:602:HOH:O	2.43	0.51
1:A:206:ARG:NH1	1:A:234:GLY:HA3	2.24	0.50
1:C:62:HIS:HE1	1:C:152:GLY:HA3	1.75	0.50
1:B:401:ILE:O	1:B:462:SER:HA	2.11	0.50
1:C:433:TYR:CE2	2:I:2:FRU:H12	2.47	0.50
1:D:132:THR:HG21	1:D:185:ARG:HB3	1.92	0.50
1:B:215:ASN:O	1:B:216:LEU:HB2	2.10	0.50
1:C:257:SER:HA	1:C:268:THR:O	2.12	0.50
1:B:110:GLY:HA3	1:B:130:LEU:O	2.12	0.49
1:D:393:ARG:HH11	1:D:393:ARG:HG3	1.78	0.49
1:C:110:GLY:HA3	1:C:130:LEU:O	2.13	0.49
1:A:62:HIS:HE1	1:A:152:GLY:HA3	1.76	0.49
1:C:98:VAL:HG13	1:C:99:MET:HE3	1.94	0.49
1:D:118:ASN:HB2	1:D:124:ALA:HA	1.95	0.49
1:C:329:VAL:HG13	1:C:330:PRO:CD	2.40	0.49
1:B:206:ARG:HD3	1:B:234:GLY:CA	2.42	0.49
1:D:352:GLN:OE1	1:D:482:HIS:HE1	1.94	0.49
1:B:141:TYR:CE1	1:B:170:ARG:HD3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:TRP:HB2	1:C:75:ASN:HD22	1.78	0.49
1:A:146:LEU:C	1:A:146:LEU:HD23	2.37	0.48
1:C:345:ARG:HD3	1:C:361:SER:HB3	1.95	0.48
1:C:393:ARG:CD	1:C:496:THR:HG22	2.43	0.48
1:C:414:GLY:O	1:C:495:ASP:HB3	2.13	0.48
1:A:206:ARG:HH11	1:A:234:GLY:CA	2.26	0.48
1:B:276:TRP:NE1	1:B:278:GLY:HA2	2.29	0.48
1:C:65:TYR:OH	1:C:306:ILE:HG13	2.12	0.48
1:C:160:PRO:HG2	3:C:716:HOH:O	2.14	0.48
1:D:470:ASP:HB3	3:D:722:HOH:O	2.12	0.48
1:A:49:SER:HB2	3:A:715:HOH:O	2.13	0.48
1:A:257:SER:HA	1:A:268:THR:O	2.14	0.48
1:C:65:TYR:CZ	1:C:306:ILE:HG13	2.48	0.48
1:C:329:VAL:HG12	1:C:331:THR:H	1.78	0.48
1:B:101:LEU:HD12	1:B:106:PRO:HA	1.96	0.47
1:B:412:SER:OG	1:B:424:ASN:ND2	2.47	0.47
1:B:414:GLY:O	1:B:495:ASP:HB3	2.14	0.47
1:A:62:HIS:CE1	1:A:152:GLY:HA3	2.49	0.47
1:A:433:TYR:CZ	2:G:2:FRU:H12	2.50	0.47
1:D:408:ASN:HB3	1:D:503:ASP:HB2	1.97	0.47
1:A:44:HIS:CE1	1:A:475:GLU:OE1	2.65	0.47
1:A:183:TRP:O	1:A:204:ARG:HD2	2.14	0.47
1:B:44:HIS:HE1	1:B:475:GLU:OE2	1.97	0.47
1:A:132:THR:HG21	1:A:185:ARG:HB3	1.95	0.47
1:A:370:TYR:HE2	1:A:520:ALA:HA	1.79	0.47
1:D:393:ARG:CD	1:D:496:THR:HG22	2.44	0.47
1:B:323:LYS:HD3	1:B:449:TYR:CZ	2.50	0.47
1:C:98:VAL:HG22	1:C:156:PHE:HD1	1.80	0.47
1:B:178:ILE:O	1:B:182:GLU:HG3	2.15	0.47
1:B:118:ASN:HB2	1:B:124:ALA:CA	2.45	0.47
1:C:223:ARG:HB2	1:C:280:GLN:HB3	1.97	0.46
1:D:204:ARG:O	1:D:235:ILE:HB	2.15	0.46
1:D:99:MET:HG2	1:D:147:TYR:CD1	2.50	0.46
1:B:464:HIS:H	1:B:479:ASN:HD21	1.62	0.46
1:A:401:ILE:O	1:A:462:SER:HA	2.15	0.46
1:C:493:GLU:HG2	1:D:493:GLU:HG2	1.96	0.46
1:A:425:ILE:HD13	1:A:467:ILE:HD13	1.98	0.46
1:A:166:ASN:ND2	1:A:169:GLY:H	2.13	0.46
1:B:56:GLN:HB2	1:B:68:TYR:HB2	1.97	0.46
1:D:215:ASN:O	1:D:216:LEU:HB2	2.15	0.46
1:B:257:SER:HB3	1:B:298:TYR:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:421:ARG:O	1:D:422:HIS:HB3	2.16	0.46
1:B:44:HIS:CE1	1:B:475:GLU:OE2	2.70	0.45
1:C:206:ARG:NH1	1:C:234:GLY:CA	2.78	0.45
1:A:422:HIS:O	1:A:438:PRO:HB2	2.17	0.45
1:B:109:SER:HB2	1:B:186:ASP:OD1	2.15	0.45
1:B:230:HIS:C	1:B:232:LEU:H	2.25	0.45
1:B:277:ASP:OD1	1:B:282:HIS:HE1	1.99	0.45
1:B:379:ASP:HB3	1:B:510:THR:HG22	1.99	0.45
1:D:362:THR:HG22	3:D:757:HOH:O	2.17	0.45
1:B:206:ARG:HA	1:B:234:GLY:HA2	1.99	0.45
1:A:65:TYR:CE1	1:A:306:ILE:HG13	2.52	0.45
1:C:98:VAL:CG1	1:C:99:MET:HE3	2.47	0.45
1:C:260:ALA:CB	1:C:265:LEU:HB2	2.47	0.45
1:D:277:ASP:OD1	1:D:282:HIS:HE1	1.99	0.45
1:D:345:ARG:HD3	1:D:361:SER:HB3	1.99	0.45
1:A:46:THR:HG22	1:A:340:GLN:HB3	1.99	0.44
1:A:434:VAL:CG1	1:A:487:GLN:HE22	2.30	0.44
1:B:227:TYR:HA	1:B:228:PRO:HD3	1.83	0.44
1:C:230:HIS:C	1:C:232:LEU:H	2.25	0.44
1:D:99:MET:HE3	1:D:147:TYR:CD2	2.52	0.44
1:A:51:TRP:HB2	1:A:75:ASN:HA	1.99	0.44
1:B:223:ARG:HG2	1:B:223:ARG:HH11	1.83	0.44
1:D:203:GLY:HA2	1:D:235:ILE:CG2	2.42	0.44
1:A:508:HIS:HB2	3:A:761:HOH:O	2.16	0.44
1:B:169:GLY:HA2	1:B:181:ALA:CB	2.48	0.44
1:B:206:ARG:HH11	1:B:234:GLY:CA	2.23	0.44
1:D:110:GLY:HA3	1:D:130:LEU:O	2.18	0.44
1:B:65:TYR:CE1	1:B:306:ILE:HG13	2.53	0.44
1:D:204:ARG:HB2	1:D:207:TYR:O	2.18	0.44
1:C:427:LYS:HD3	1:C:427:LYS:C	2.43	0.44
1:A:414:GLY:O	1:A:495:ASP:HB3	2.18	0.44
1:B:260:ALA:HB1	1:B:265:LEU:HB2	1.99	0.43
1:C:206:ARG:HH11	1:C:234:GLY:HA3	1.80	0.43
1:D:144:GLN:HG2	1:D:164:ILE:HB	2.00	0.43
1:B:422:HIS:O	1:B:438:PRO:HB2	2.18	0.43
1:A:56:GLN:HB2	1:A:68:TYR:HB2	2.01	0.43
1:A:500:LEU:HD13	1:A:509:PHE:CG	2.54	0.43
1:B:376:THR:C	1:B:377:LEU:HD12	2.43	0.43
1:D:57:ARG:HA	1:D:58:PRO:HD3	1.89	0.43
1:B:329:VAL:HG13	1:B:330:PRO:CD	2.41	0.43
1:C:99:MET:HE2	1:C:156:PHE:CG	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:GLY:HA3	1:A:130:LEU:O	2.18	0.42
1:A:470:ASP:HB3	3:A:633:HOH:O	2.18	0.42
1:A:57:ARG:HA	1:A:58:PRO:HD3	1.91	0.42
1:A:83:HIS:CD2	1:A:84:ALA:N	2.87	0.42
1:A:166:ASN:HD21	1:A:168:ASP:HB2	1.84	0.42
1:B:330:PRO:HD3	1:B:444:TYR:CD1	2.54	0.42
1:C:401:ILE:O	1:C:462:SER:HA	2.19	0.42
1:D:183:TRP:O	1:D:204:ARG:HD2	2.19	0.42
1:D:118:ASN:HB2	1:D:124:ALA:CA	2.49	0.42
1:D:265:LEU:HB3	1:D:266:PRO:CD	2.50	0.42
1:C:206:ARG:HD3	1:C:234:GLY:CA	2.49	0.42
1:C:132:THR:HG21	1:C:185:ARG:HB3	2.01	0.42
1:D:382:VAL:HG13	1:D:509:PHE:CE2	2.55	0.42
1:C:102:ARG:O	1:C:103:PRO:C	2.63	0.42
1:A:257:SER:HB3	1:A:298:TYR:CE2	2.55	0.41
1:A:415:ARG:HA	1:A:421:ARG:O	2.20	0.41
1:B:377:LEU:HD12	1:B:377:LEU:N	2.35	0.41
1:C:235:ILE:HG23	1:C:256:ALA:CB	2.49	0.41
1:A:205:LEU:CD2	1:A:206:ARG:HG2	2.50	0.41
1:A:446:LEU:HD21	1:A:490:HIS:CD2	2.55	0.41
1:B:470:ASP:HB3	3:B:674:HOH:O	2.19	0.41
1:C:260:ALA:HB1	1:C:265:LEU:HB2	2.02	0.41
1:D:98:VAL:HG13	1:D:156:PHE:CD1	2.55	0.41
1:B:132:THR:HG21	1:B:185:ARG:HB3	2.00	0.41
1:B:169:GLY:HA2	1:B:181:ALA:HB1	2.02	0.41
1:A:349:LEU:HG	1:A:357:TYR:HB3	2.01	0.41
1:B:205:LEU:O	1:B:207:TYR:HD2	2.03	0.41
1:A:329:VAL:O	1:A:332:ASP:HB2	2.21	0.41
1:B:300:ALA:HB2	1:B:317:ALA:HB2	2.03	0.41
1:B:83:HIS:CD2	1:B:84:ALA:N	2.89	0.41
1:B:329:VAL:O	1:B:332:ASP:HB2	2.21	0.41
1:B:519:GLN:H	1:B:519:GLN:CD	2.28	0.41
1:C:58:PRO:HB3	1:C:67:LEU:HA	2.01	0.41
1:C:229:ASN:HB3	1:C:232:LEU:HD22	2.03	0.41
1:C:470:ASP:HB3	3:C:714:HOH:O	2.20	0.41
1:D:102:ARG:HD3	3:D:675:HOH:O	2.20	0.41
1:D:341:ASN:HD22	1:D:341:ASN:HA	1.76	0.41
1:A:329:VAL:HG12	1:A:331:THR:H	1.86	0.41
1:A:412:SER:OG	1:A:424:ASN:ND2	2.54	0.41
1:B:432:LEU:HA	1:B:432:LEU:HD22	1.87	0.41
1:A:341:ASN:HD22	1:A:341:ASN:HA	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:ALA:HA	1:A:469:VAL:O	2.22	0.40
1:A:206:ARG:HD3	1:A:234:GLY:CA	2.47	0.40
1:D:401:ILE:O	1:D:462:SER:HA	2.22	0.40
1:D:272:TRP:CE2	1:D:288:PRO:HB3	2.56	0.40
1:B:57:ARG:HA	1:B:58:PRO:HD3	1.89	0.40
1:B:99:MET:HE3	1:B:147:TYR:CD2	2.57	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	478/492 (97%)	454 (95%)	23 (5%)	1 (0%)	43	51
1	B	478/492 (97%)	454 (95%)	23 (5%)	1 (0%)	43	51
1	C	478/492 (97%)	454 (95%)	24 (5%)	0	100	100
1	D	476/492 (97%)	454 (95%)	20 (4%)	2 (0%)	30	34
All	All	1910/1968 (97%)	1816 (95%)	90 (5%)	4 (0%)	43	51

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	235	ILE
1	D	353	PRO
1	A	235	ILE
1	B	235	ILE

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	381/393 (97%)	373 (98%)	8 (2%)	47	63
1	B	381/393 (97%)	373 (98%)	8 (2%)	47	63
1	C	381/393 (97%)	377 (99%)	4 (1%)	68	81
1	D	380/393 (97%)	369 (97%)	11 (3%)	37	51
All	All	1523/1572 (97%)	1492 (98%)	31 (2%)	48	64

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

Mol	Chain	Res	Type
1	A	98	VAL
1	A	144	GLN
1	A	199	VAL
1	A	205	LEU
1	A	232	LEU
1	A	297	TRP
1	A	382	VAL
1	A	516	GLU
1	B	46	THR
1	B	104	ASP
1	B	144	GLN
1	B	170	ARG
1	B	232	LEU
1	B	320	ASN
1	B	382	VAL
1	B	487	GLN
1	C	232	LEU
1	C	382	VAL
1	C	446	LEU
1	C	487	GLN
1	D	98	VAL
1	D	232	LEU
1	D	250	ARG
1	D	279	GLU
1	D	329	VAL
1	D	353	PRO
1	D	382	VAL
1	D	432	LEU

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Mol	Chain	Res	Type
1	D	446	LEU
1	D	448	PRO
1	D	487	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	HIS
1	A	54	ASN
1	A	62	HIS
1	A	76	ASN
1	A	133	GLN
1	A	144	GLN
1	A	166	ASN
1	A	289	GLN
1	A	340	GLN
1	A	341	ASN
1	A	424	ASN
1	A	479	ASN
1	A	487	GLN
1	A	508	HIS
1	B	44	HIS
1	B	54	ASN
1	B	62	HIS
1	B	75	ASN
1	B	144	GLN
1	B	280	GLN
1	B	282	HIS
1	B	320	ASN
1	B	341	ASN
1	B	391	ASN
1	B	424	ASN
1	B	479	ASN
1	C	62	HIS
1	C	71	HIS
1	C	75	ASN
1	C	94	HIS
1	C	144	GLN
1	C	282	HIS
1	C	289	GLN
1	C	340	GLN
1	C	341	ASN

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Mol	Chain	Res	Type
1	C	424	ASN
1	C	479	ASN
1	C	508	HIS
1	D	71	HIS
1	D	133	GLN
1	D	144	GLN
1	D	282	HIS
1	D	289	GLN
1	D	341	ASN
1	D	408	ASN
1	D	424	ASN
1	D	479	ASN
1	D	482	HIS
1	D	508	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 ⓘ

12 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	E	1	2	11,11,12	2.40	5 (45%)	15,15,17	1.07	1 (6%)
2	FRU	E	2	2	11,12,12	1.59	3 (27%)	10,18,18	1.25	2 (20%)
2	GLC	F	1	2	11,11,12	2.38	5 (45%)	15,15,17	1.20	1 (6%)
2	FRU	F	2	2	11,12,12	1.51	2 (18%)	10,18,18	1.40	2 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	G	1	2	11,11,12	2.44	5 (45%)	15,15,17	1.08	0
2	FRU	G	2	2	11,12,12	1.57	2 (18%)	10,18,18	1.12	2 (20%)
2	GLC	H	1	2	11,11,12	2.40	5 (45%)	15,15,17	1.43	3 (20%)
2	FRU	H	2	2	11,12,12	1.52	2 (18%)	10,18,18	0.99	0
2	GLC	I	1	2	11,11,12	2.51	5 (45%)	15,15,17	1.16	1 (6%)
2	FRU	I	2	2	11,12,12	1.51	3 (27%)	10,18,18	1.12	1 (10%)
2	GLC	J	1	2	11,11,12	2.43	5 (45%)	15,15,17	1.04	1 (6%)
2	FRU	J	2	2	11,12,12	1.60	3 (27%)	10,18,18	1.22	2 (20%)

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	E	1	2	-	2/2/19/22	0/1/1/1
2	FRU	E	2	2	-	5/5/24/24	0/1/1/1
2	GLC	F	1	2	-	2/2/19/22	0/1/1/1
2	FRU	F	2	2	-	5/5/24/24	0/1/1/1
2	GLC	G	1	2	-	2/2/19/22	0/1/1/1
2	FRU	G	2	2	-	0/5/24/24	0/1/1/1
2	GLC	H	1	2	-	2/2/19/22	0/1/1/1
2	FRU	H	2	2	-	0/5/24/24	0/1/1/1
2	GLC	I	1	2	-	2/2/19/22	0/1/1/1
2	FRU	I	2	2	-	3/5/24/24	0/1/1/1
2	GLC	J	1	2	-	2/2/19/22	0/1/1/1
2	FRU	J	2	2	-	1/5/24/24	0/1/1/1

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	1	GLC	C4-C3	-4.33	1.41	1.52
2	E	1	GLC	C4-C3	-4.22	1.41	1.52
2	F	1	GLC	C4-C3	-4.13	1.41	1.52
2	I	1	GLC	C2-C3	-4.04	1.46	1.52
2	J	1	GLC	C4-C3	-4.01	1.41	1.52
2	F	1	GLC	O2-C2	-3.99	1.35	1.43
2	H	1	GLC	C4-C3	-3.98	1.42	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1	GLC	C4-C3	-3.98	1.42	1.52
2	G	1	GLC	O2-C2	-3.88	1.35	1.43
2	H	1	GLC	O2-C2	-3.84	1.35	1.43
2	J	1	GLC	C2-C3	-3.84	1.46	1.52
2	F	1	GLC	C2-C3	-3.80	1.46	1.52
2	G	1	GLC	C2-C3	-3.76	1.46	1.52
2	I	1	GLC	O2-C2	-3.76	1.35	1.43
2	E	1	GLC	O2-C2	-3.73	1.35	1.43
2	J	1	GLC	O2-C2	-3.55	1.35	1.43
2	H	1	GLC	C2-C3	-3.52	1.47	1.52
2	E	1	GLC	C2-C3	-3.52	1.47	1.52
2	H	1	GLC	O5-C5	3.12	1.49	1.43
2	I	1	GLC	O5-C1	-3.11	1.38	1.43
2	E	1	GLC	O5-C5	3.07	1.49	1.43
2	J	1	GLC	O5-C5	3.06	1.49	1.43
2	J	1	GLC	O5-C1	-3.06	1.38	1.43
2	G	1	GLC	O5-C1	-3.05	1.38	1.43
2	I	1	GLC	O5-C5	2.87	1.49	1.43
2	G	1	GLC	O5-C5	2.73	1.48	1.43
2	H	1	GLC	O5-C1	-2.69	1.39	1.43
2	F	1	GLC	O5-C5	2.52	1.48	1.43
2	J	2	FRU	C4-C3	-2.41	1.43	1.53
2	I	2	FRU	C4-C3	-2.38	1.43	1.53
2	E	1	GLC	O5-C1	-2.35	1.39	1.43
2	G	2	FRU	O5-C5	-2.34	1.38	1.43
2	J	2	FRU	O5-C5	-2.34	1.38	1.43
2	F	1	GLC	O5-C1	-2.33	1.39	1.43
2	H	2	FRU	C4-C3	-2.25	1.44	1.53
2	E	2	FRU	C4-C3	-2.24	1.44	1.53
2	G	2	FRU	C4-C3	-2.19	1.44	1.53
2	J	2	FRU	O4-C4	-2.16	1.37	1.43
2	F	2	FRU	C4-C3	-2.12	1.44	1.53
2	F	2	FRU	O5-C2	2.09	1.46	1.43
2	I	2	FRU	O5-C5	-2.09	1.39	1.43
2	I	2	FRU	O4-C4	-2.05	1.37	1.43
2	E	2	FRU	O5-C5	-2.05	1.39	1.43
2	E	2	FRU	O5-C2	2.03	1.46	1.43
2	H	2	FRU	O5-C5	-2.01	1.39	1.43

All (16) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	FRU	O1-C1-C2	2.99	118.29	111.67
2	F	1	GLC	C1-O5-C5	2.80	115.94	112.19
2	E	2	FRU	O1-C1-C2	2.79	117.84	111.67
2	J	2	FRU	O3-C3-C4	-2.70	103.71	113.25
2	H	1	GLC	O5-C5-C6	2.56	112.64	107.66
2	G	2	FRU	O1-C1-C2	2.50	117.20	111.67
2	I	2	FRU	O1-C1-C2	2.40	116.99	111.67
2	J	2	FRU	O1-C1-C2	2.37	116.92	111.67
2	I	1	GLC	C3-C4-C5	2.32	114.43	110.23
2	G	2	FRU	O3-C3-C4	-2.20	105.47	113.25
2	J	1	GLC	O5-C5-C6	2.20	111.94	107.66
2	H	1	GLC	O3-C3-C4	-2.20	105.19	110.38
2	H	1	GLC	C3-C4-C5	2.11	114.07	110.23
2	E	2	FRU	O3-C3-C4	-2.11	105.79	113.25
2	E	1	GLC	O5-C5-C6	2.10	111.76	107.66
2	F	2	FRU	O3-C3-C4	-2.06	105.98	113.25

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	FRU	O1-C1-C2-C3
2	E	2	FRU	O1-C1-C2-O2
2	E	2	FRU	O1-C1-C2-O5
2	F	2	FRU	O1-C1-C2-C3
2	F	2	FRU	O1-C1-C2-O2
2	F	2	FRU	O1-C1-C2-O5
2	H	1	GLC	O5-C5-C6-O6
2	F	1	GLC	O5-C5-C6-O6
2	G	1	GLC	O5-C5-C6-O6
2	G	1	GLC	C4-C5-C6-O6
2	J	1	GLC	O5-C5-C6-O6
2	H	1	GLC	C4-C5-C6-O6
2	F	1	GLC	C4-C5-C6-O6
2	I	1	GLC	C4-C5-C6-O6
2	J	1	GLC	C4-C5-C6-O6
2	I	1	GLC	O5-C5-C6-O6
2	E	1	GLC	C4-C5-C6-O6
2	F	2	FRU	O5-C5-C6-O6
2	I	2	FRU	O1-C1-C2-O5

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Mol	Chain	Res	Type	Atoms
2	E	1	GLC	O5-C5-C6-O6
2	E	2	FRU	O5-C5-C6-O6
2	E	2	FRU	C4-C5-C6-O6
2	F	2	FRU	C4-C5-C6-O6
2	I	2	FRU	O1-C1-C2-C3
2	J	2	FRU	C4-C5-C6-O6
2	I	2	FRU	O1-C1-C2-O2

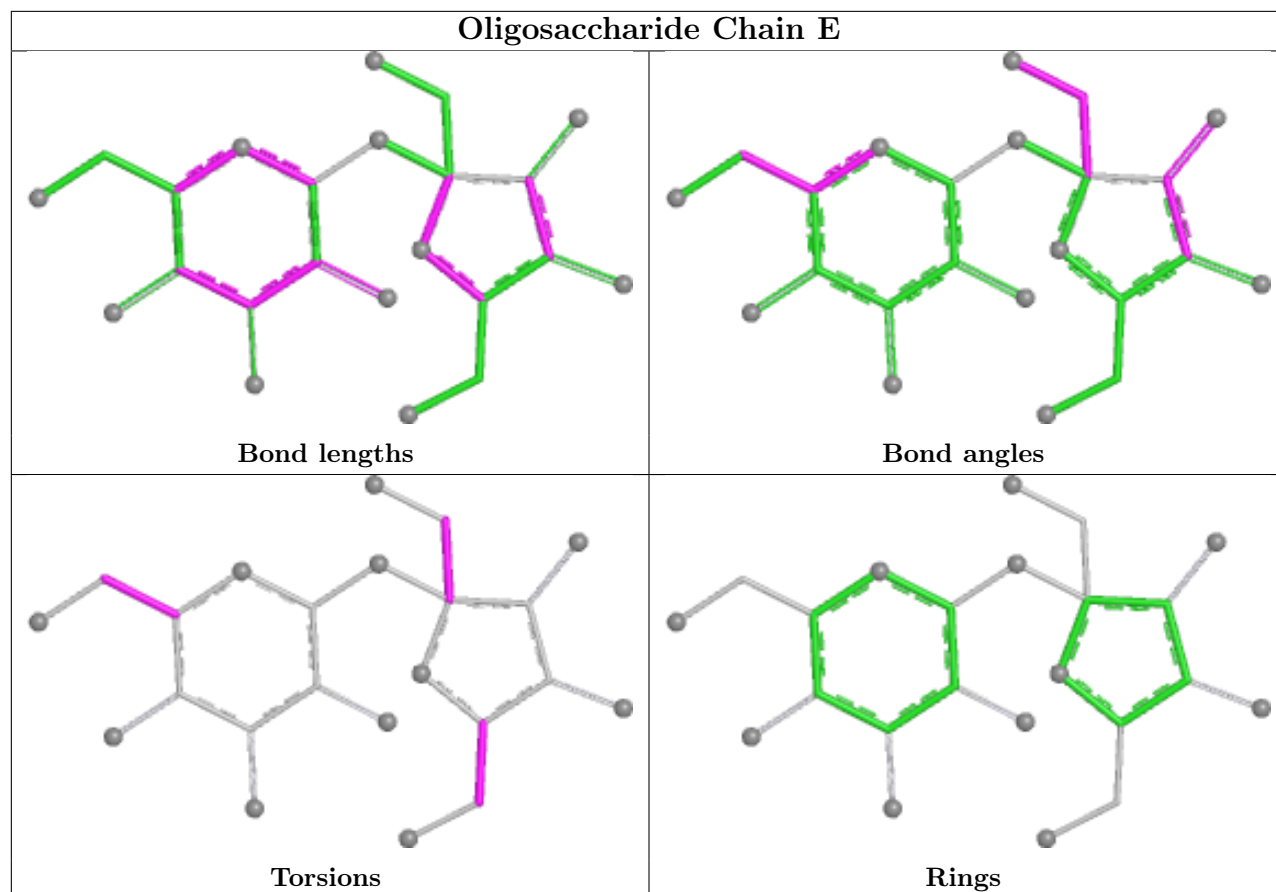
There are no ring outliers.

7 monomers are involved in 11 short contacts:

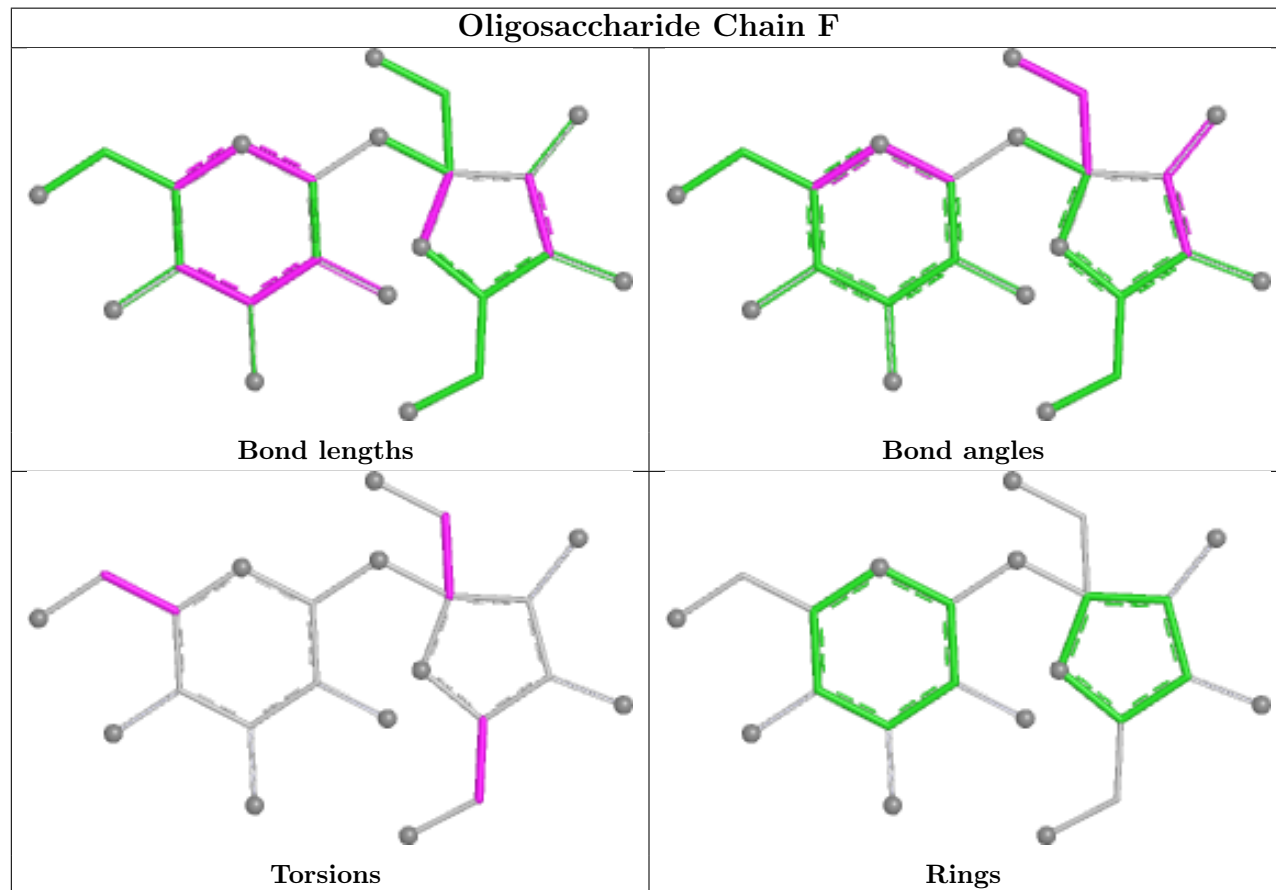
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	2	FRU	1	0
2	F	1	GLC	1	0
2	J	2	FRU	1	0
2	E	2	FRU	1	0
2	F	2	FRU	2	0
2	G	2	FRU	2	0
2	E	1	GLC	3	0

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

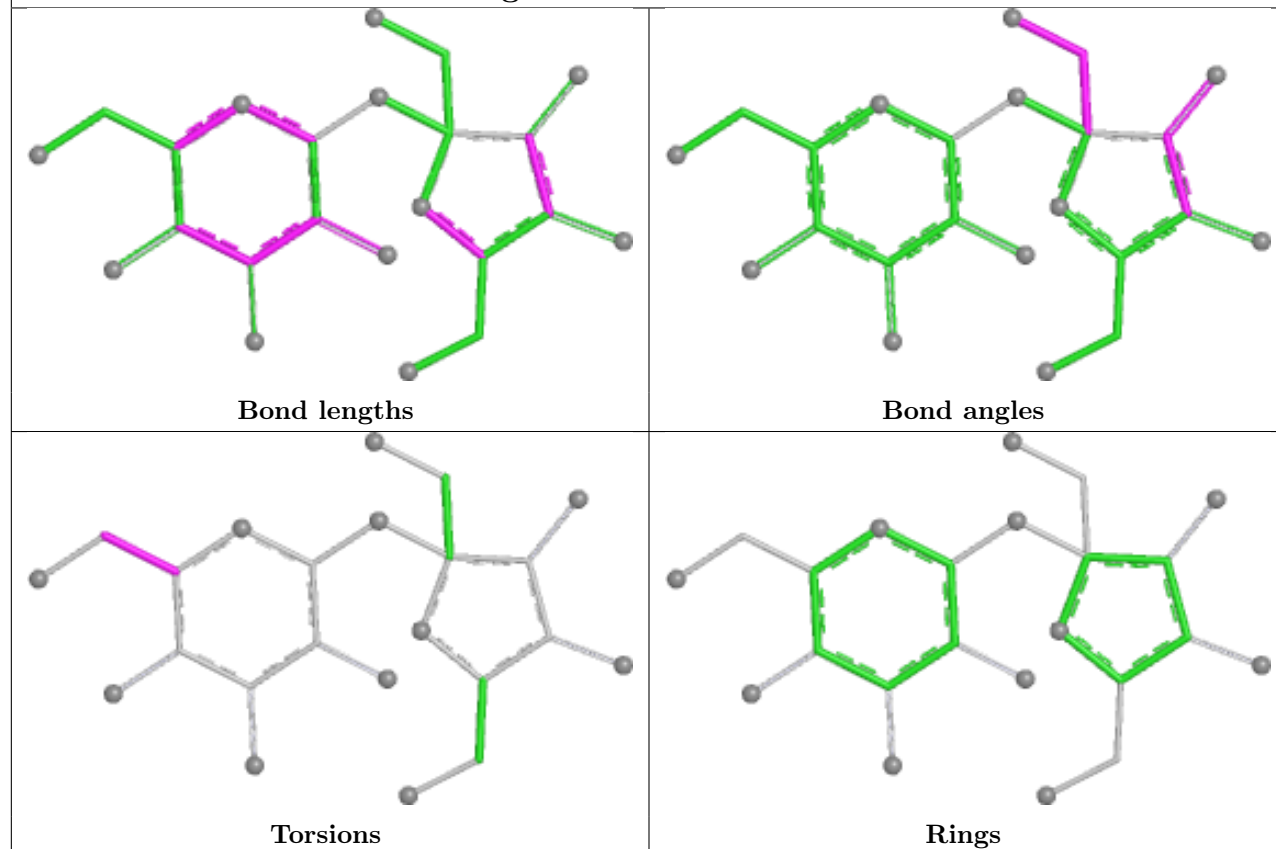
Oligosaccharide Chain E



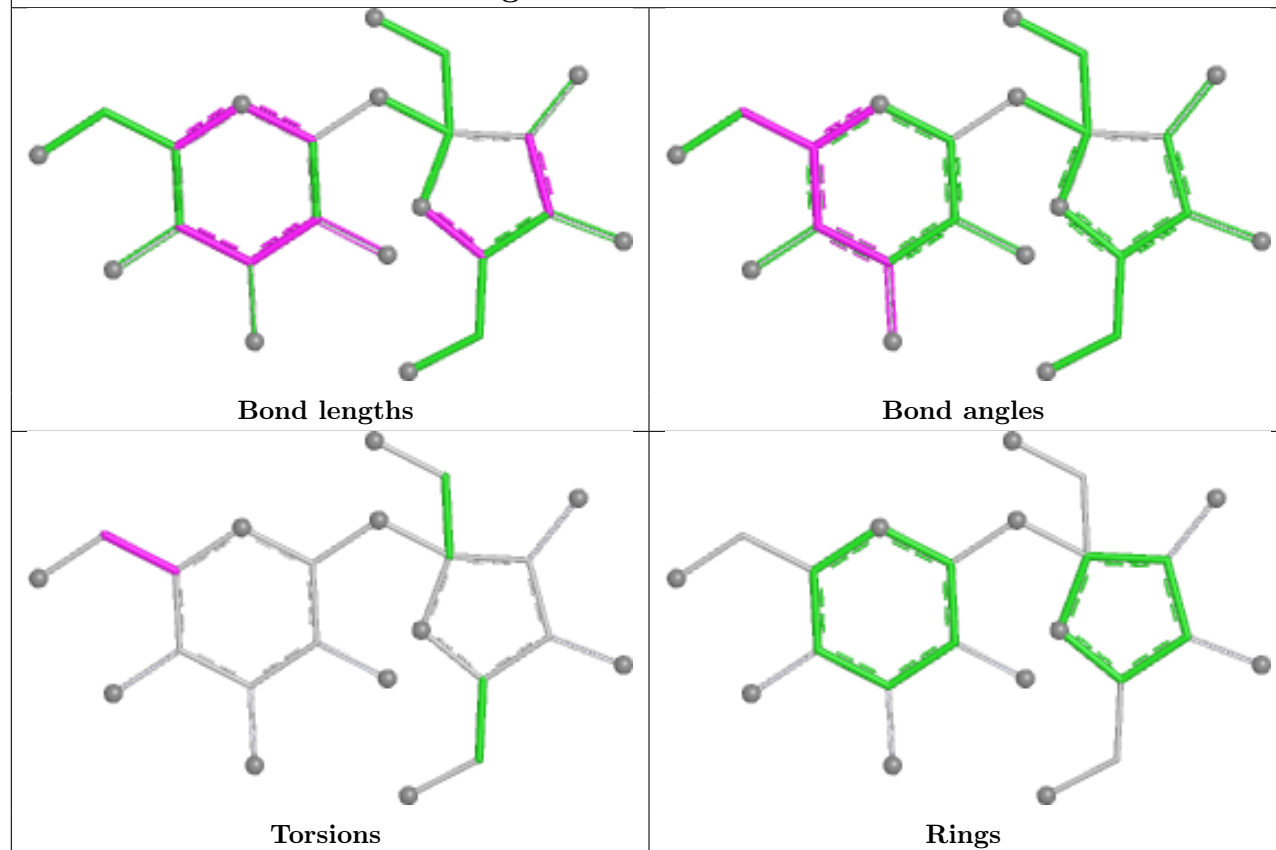
Oligosaccharide Chain F

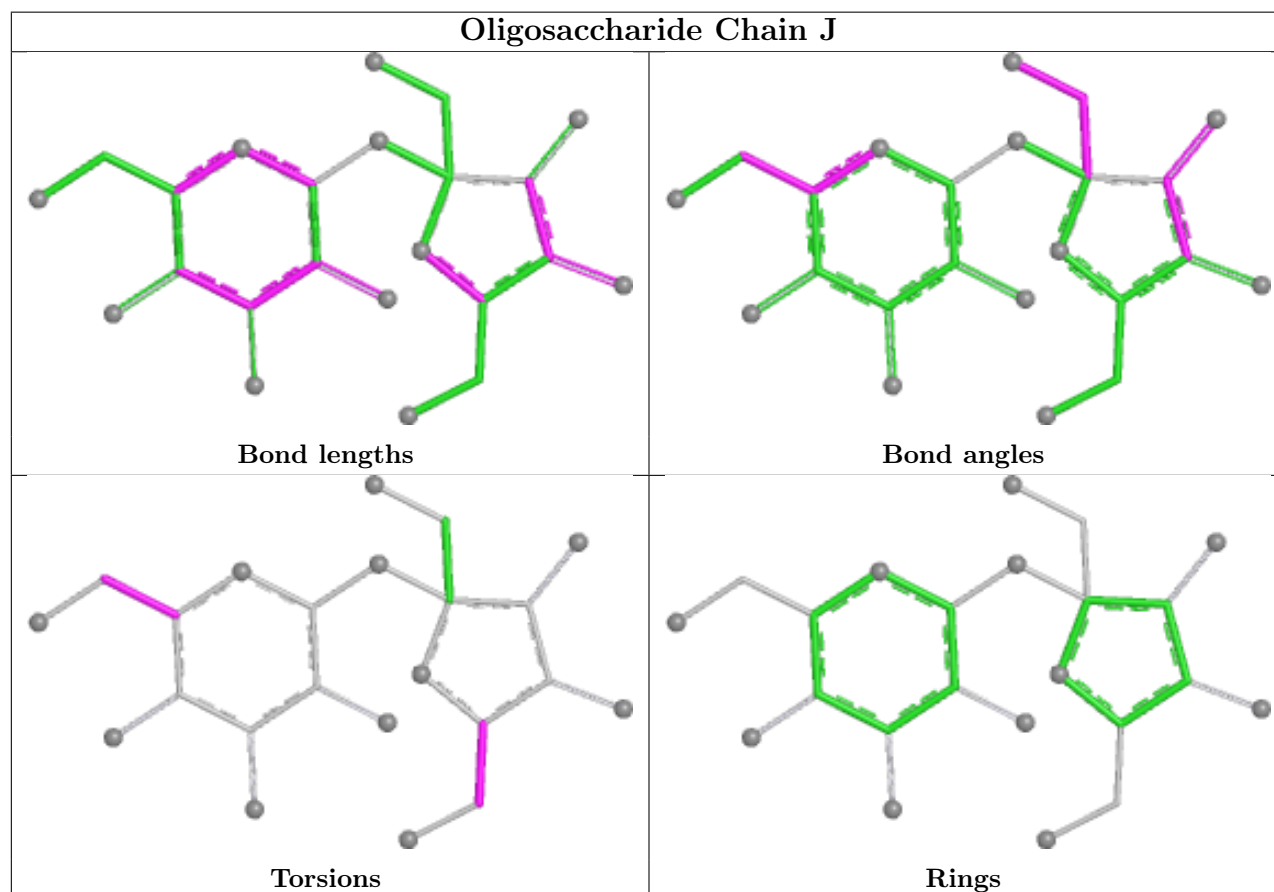
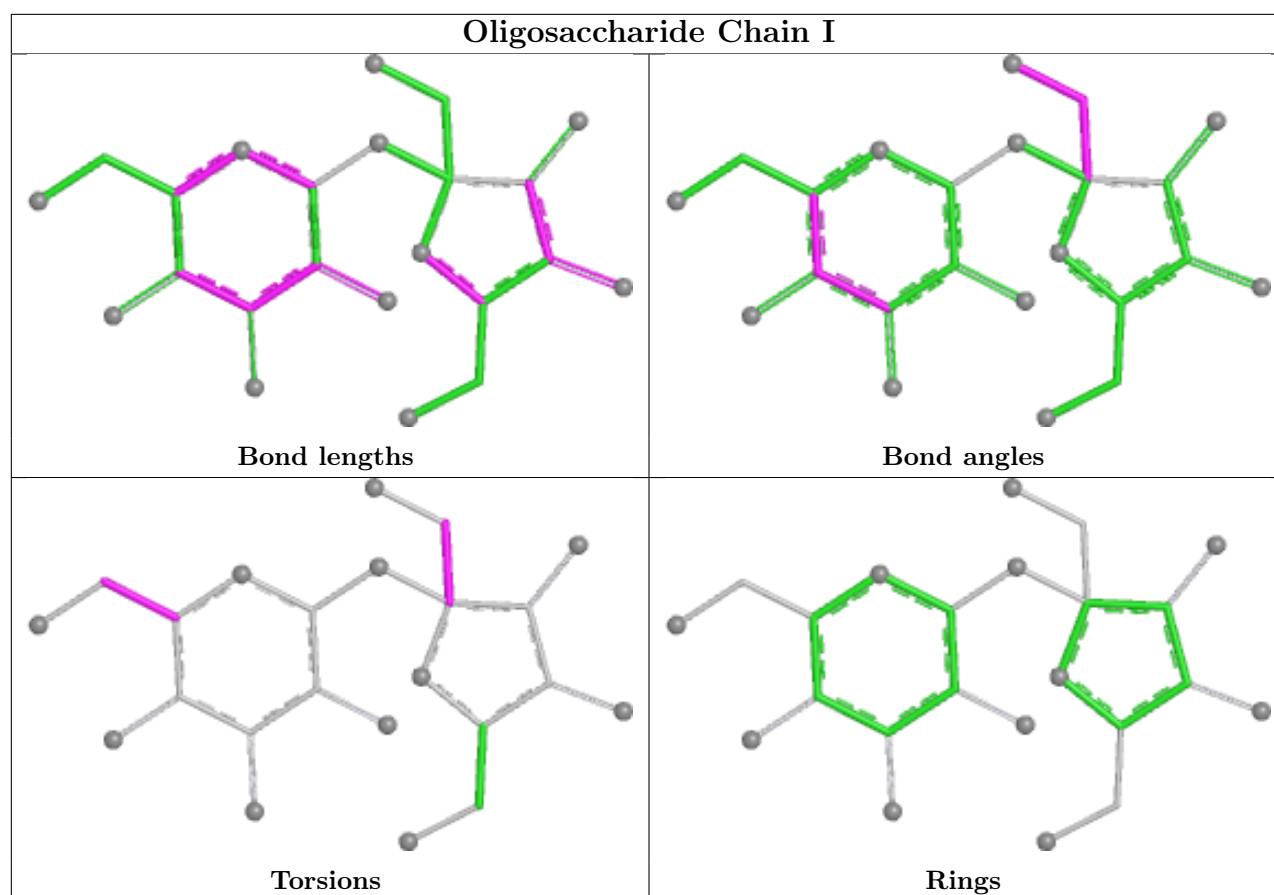


Oligosaccharide Chain G



Oligosaccharide Chain H





5.6 Ligand geometry

There are no ligands in this entry.

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

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	480/492 (97%)	-0.07	8 (1%) 69 66	18, 28, 42, 66	0
1	B	480/492 (97%)	-0.12	16 (3%) 49 46	17, 28, 42, 63	0
1	C	480/492 (97%)	-0.20	5 (1%) 79 77	17, 26, 39, 65	0
1	D	478/492 (97%)	-0.23	4 (0%) 82 80	17, 26, 36, 45	0
All	All	1918/1968 (97%)	-0.15	33 (1%) 69 66	17, 27, 39, 66	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	520	ALA	11.7
1	C	520	ALA	8.0
1	B	520	ALA	7.6
1	A	234	GLY	6.1
1	C	234	GLY	5.7
1	B	234	GLY	4.8
1	D	235	ILE	4.7
1	B	518	GLY	3.9
1	C	519	GLN	3.9
1	B	173	THR	3.7
1	A	519	GLN	3.6
1	B	519	GLN	3.3
1	A	233	GLY	3.2
1	D	354	GLY	3.1
1	D	518	GLY	3.0
1	D	234	GLY	2.9
1	B	174	THR	2.9
1	B	74	GLN	2.7
1	C	508	HIS	2.7
1	A	175	PRO	2.6
1	B	171	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	176	ALA	2.5
1	B	172	ALA	2.5
1	B	175	PRO	2.5
1	B	233	GLY	2.3
1	B	168	ASP	2.2
1	B	307	ASP	2.1
1	A	518	GLY	2.1
1	A	180	ASN	2.1
1	C	116	THR	2.0
1	B	329	VAL	2.0
1	B	176	ALA	2.0
1	B	235	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

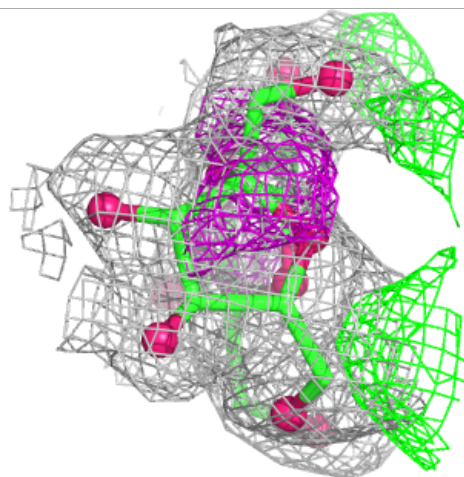
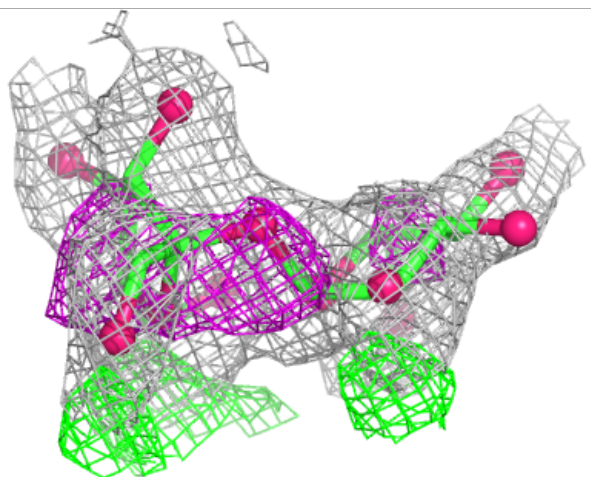
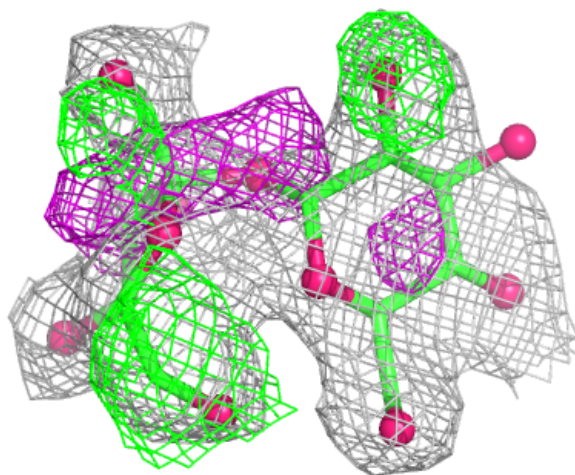
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FRU	E	2	12/12	0.69	0.23	57,60,62,64	0
2	FRU	F	2	12/12	0.72	0.20	54,58,60,62	0
2	GLC	F	1	11/12	0.76	0.18	63,64,64,65	0
2	GLC	E	1	11/12	0.76	0.18	63,65,66,67	0
2	GLC	I	1	11/12	0.81	0.14	42,45,50,53	0
2	GLC	J	1	11/12	0.83	0.14	39,43,47,51	0
2	GLC	H	1	11/12	0.84	0.13	35,41,44,48	0
2	GLC	G	1	11/12	0.91	0.11	39,41,45,47	0
2	FRU	I	2	12/12	0.93	0.08	28,33,37,39	0
2	FRU	G	2	12/12	0.95	0.07	23,31,33,36	0
2	FRU	H	2	12/12	0.96	0.06	25,29,33,34	0
2	FRU	J	2	12/12	0.97	0.05	23,30,32,36	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.

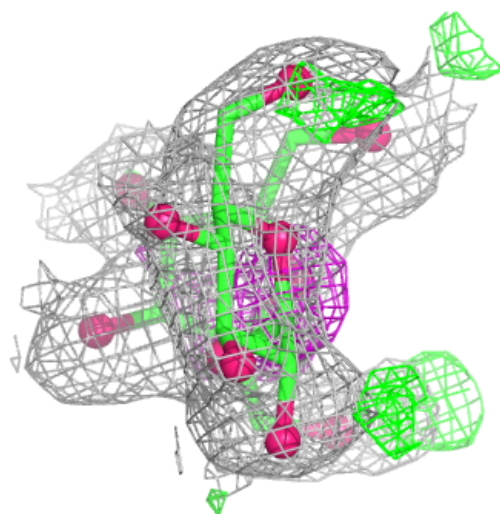
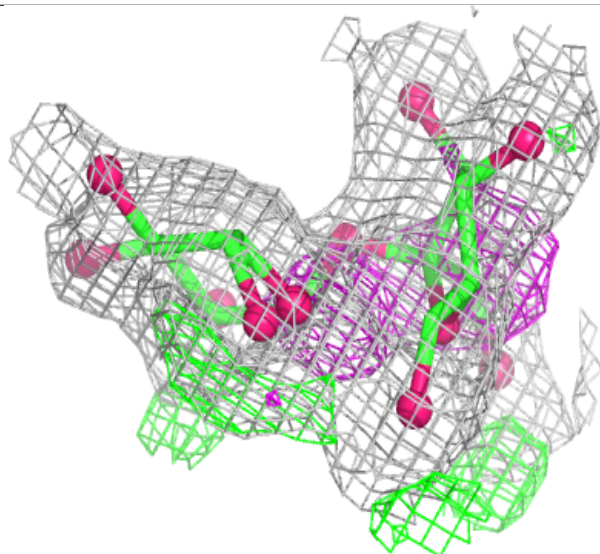
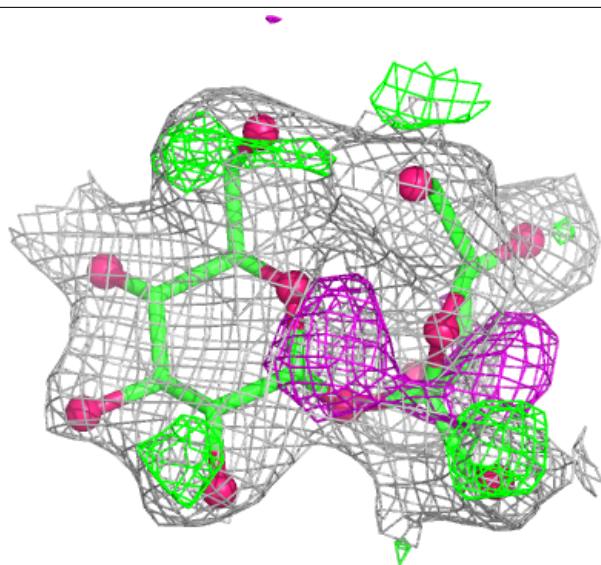
Electron density around Chain E:

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



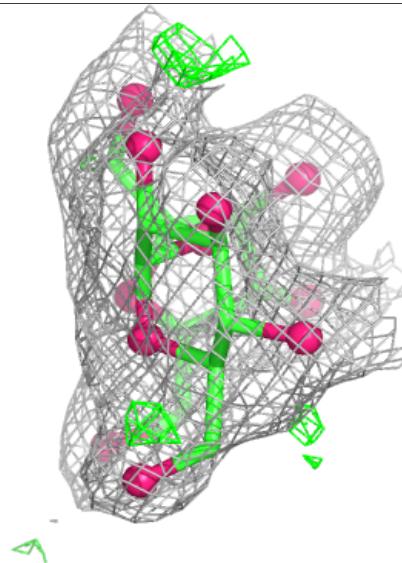
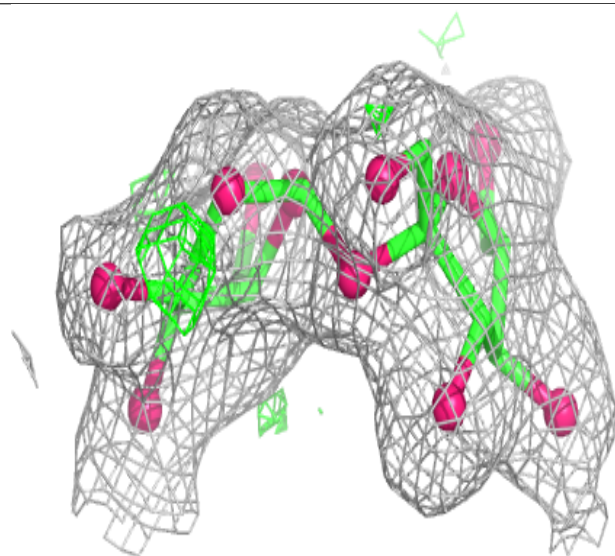
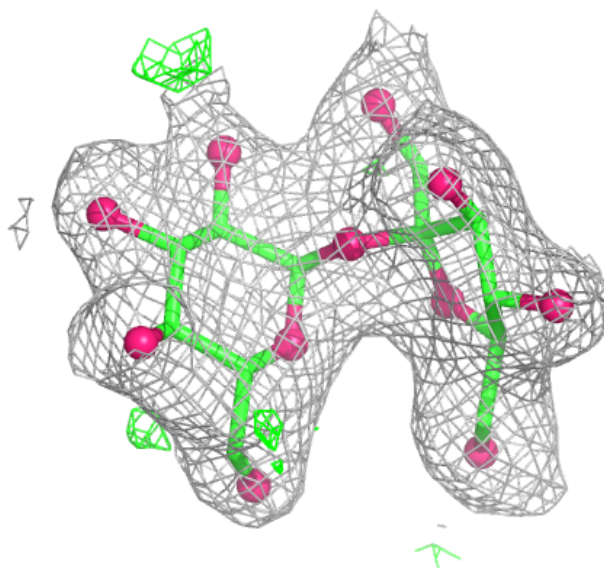
Electron density around Chain F:

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



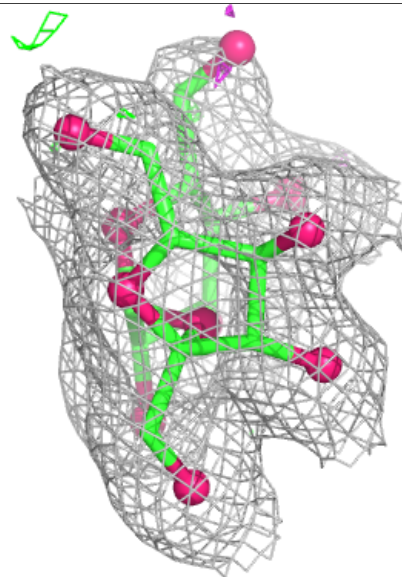
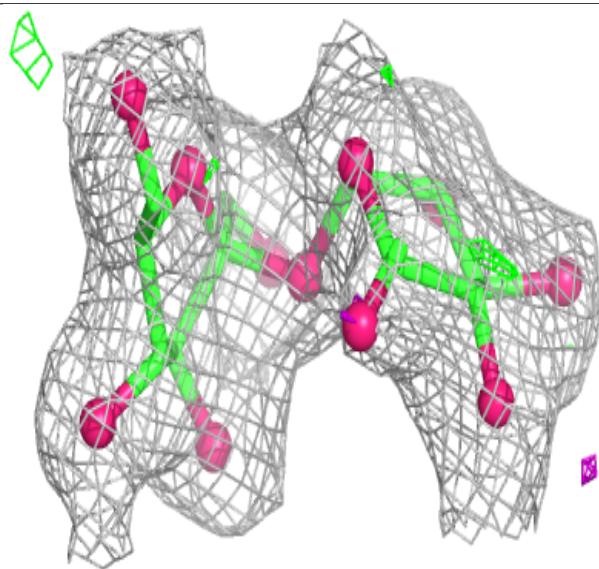
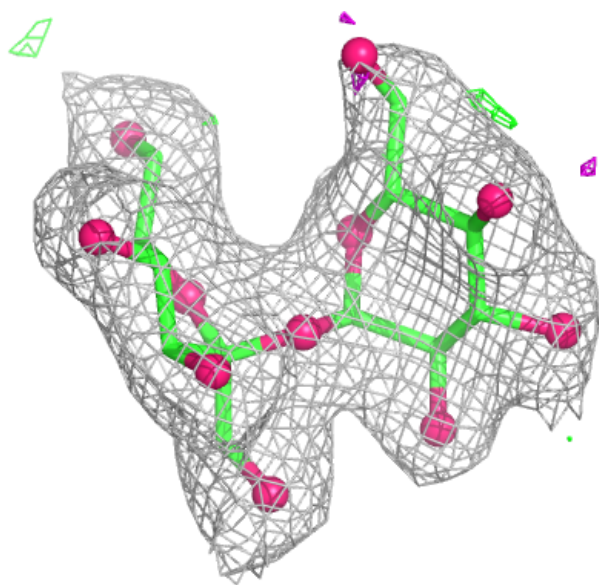
Electron density around Chain G:

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



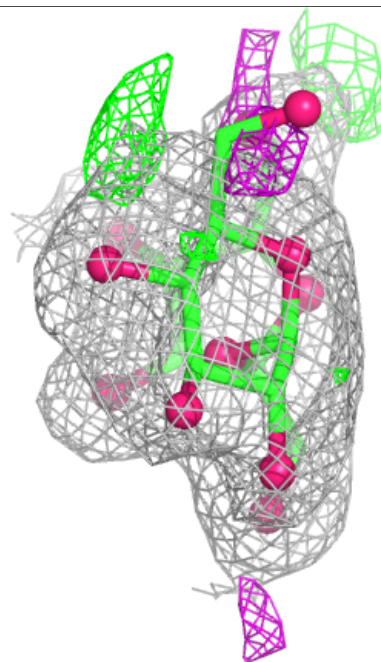
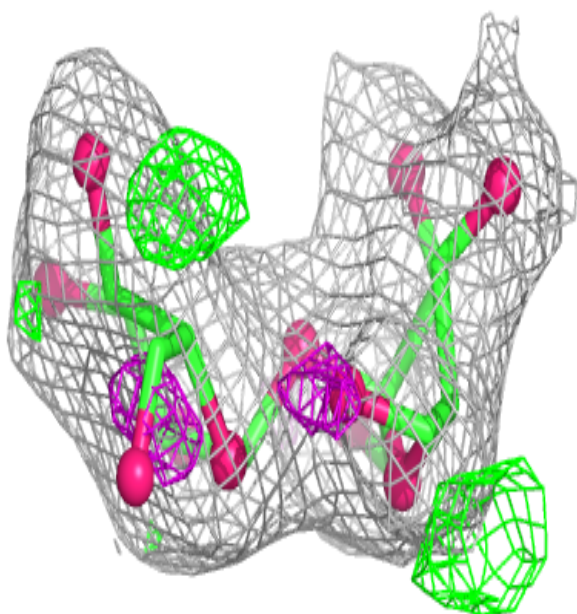
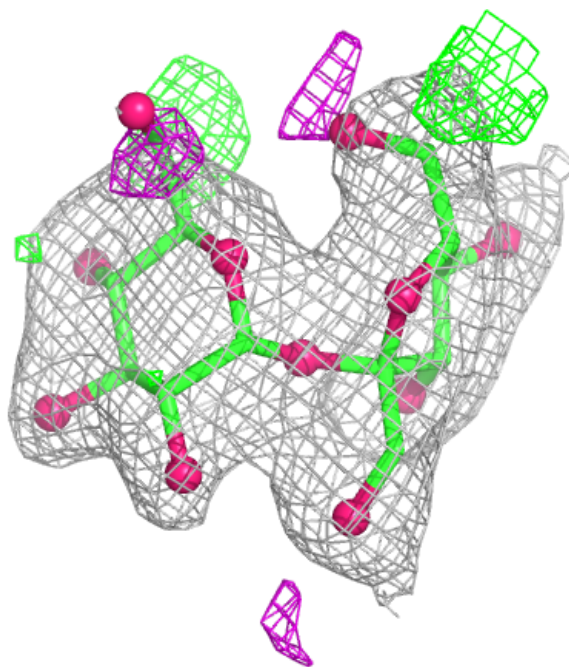
Electron density around Chain H:

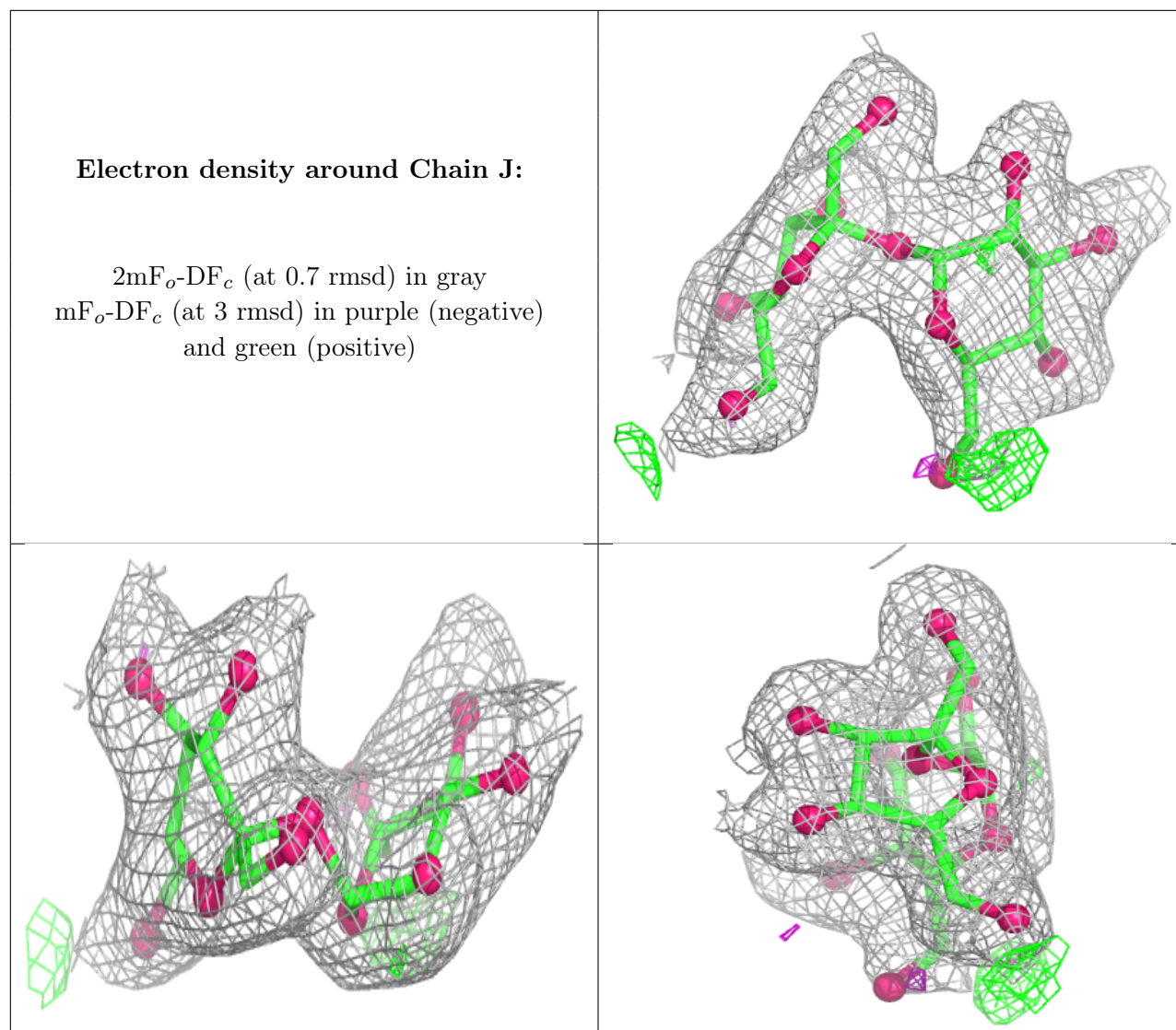
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain 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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.