



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:17 PM UTC

PDB ID : 4UTC / pdb_00004utc
Title : Crystal structure of dengue 2 virus envelope glycoprotein
Authors : Kikuti, C.; Rouvinski, A.; Guardado-Calvo, P.; Barba-Spaeth, G.; Duquerroy, S.; Vaney, M.C.; Rey, F.A.
Deposited on : 2014-07-18
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

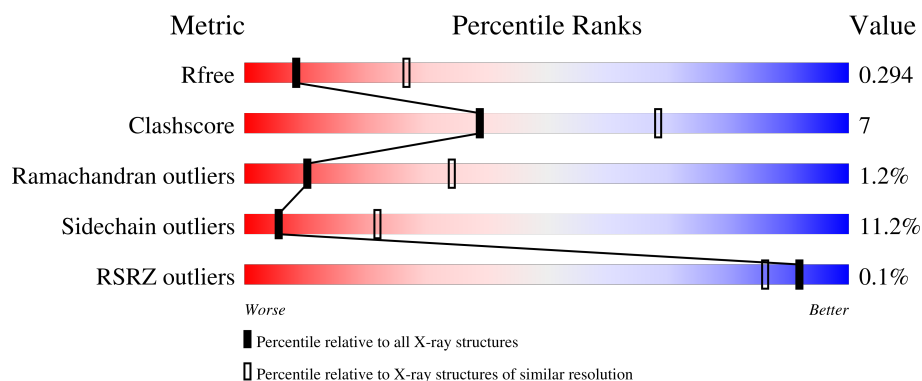
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

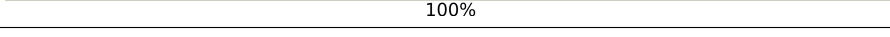
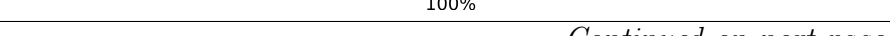
The reported resolution of this entry is 3.08 Å.

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	422	
1	B	422	
2	C	3	
3	D	2	
3	F	2	

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Mol	Chain	Length	Quality of chain
4	E	6	 50%50%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6243 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 ENVELOPE GLYCOPROTEIN E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	0	0	0
			3035	1912	521	578	24			
1	B	390	Total	C	N	O	S	0	0	0
			3037	1914	523	576	24			

There are 64 discrepancies between the modelled and reference sequences:

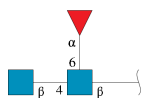
Chain	Residue	Modelled	Actual	Comment	Reference
A	392	LEU	-	expression tag	UNP Q68Y26
A	393	ARG	-	expression tag	UNP Q68Y26
A	394	PRO	-	expression tag	UNP Q68Y26
A	395	LEU	-	expression tag	UNP Q68Y26
A	396	GLU	-	expression tag	UNP Q68Y26
A	397	SER	-	expression tag	UNP Q68Y26
A	398	ARG	-	expression tag	UNP Q68Y26
A	399	GLY	-	expression tag	UNP Q68Y26
A	400	PRO	-	expression tag	UNP Q68Y26
A	401	PHE	-	expression tag	UNP Q68Y26
A	402	GLU	-	expression tag	UNP Q68Y26
A	403	GLY	-	expression tag	UNP Q68Y26
A	404	LYS	-	expression tag	UNP Q68Y26
A	405	PRO	-	expression tag	UNP Q68Y26
A	406	ILE	-	expression tag	UNP Q68Y26
A	407	PRO	-	expression tag	UNP Q68Y26
A	408	ASN	-	expression tag	UNP Q68Y26
A	409	PRO	-	expression tag	UNP Q68Y26
A	410	LEU	-	expression tag	UNP Q68Y26
A	411	LEU	-	expression tag	UNP Q68Y26
A	412	GLY	-	expression tag	UNP Q68Y26
A	413	LEU	-	expression tag	UNP Q68Y26
A	414	ASP	-	expression tag	UNP Q68Y26
A	415	SER	-	expression tag	UNP Q68Y26
A	416	THR	-	expression tag	UNP Q68Y26

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Chain	Residue	Modelled	Actual	Comment	Reference
A	417	ARG	-	expression tag	UNP Q68Y26
A	418	THR	-	expression tag	UNP Q68Y26
A	419	GLY	-	expression tag	UNP Q68Y26
A	420	HIS	-	expression tag	UNP Q68Y26
A	421	HIS	-	expression tag	UNP Q68Y26
A	422	HIS	-	expression tag	UNP Q68Y26
A	118	LYS	MET	conflict	UNP Q68Y26
B	392	LEU	-	expression tag	UNP Q68Y26
B	393	ARG	-	expression tag	UNP Q68Y26
B	394	PRO	-	expression tag	UNP Q68Y26
B	395	LEU	-	expression tag	UNP Q68Y26
B	396	GLU	-	expression tag	UNP Q68Y26
B	397	SER	-	expression tag	UNP Q68Y26
B	398	ARG	-	expression tag	UNP Q68Y26
B	399	GLY	-	expression tag	UNP Q68Y26
B	400	PRO	-	expression tag	UNP Q68Y26
B	401	PHE	-	expression tag	UNP Q68Y26
B	402	GLU	-	expression tag	UNP Q68Y26
B	403	GLY	-	expression tag	UNP Q68Y26
B	404	LYS	-	expression tag	UNP Q68Y26
B	405	PRO	-	expression tag	UNP Q68Y26
B	406	ILE	-	expression tag	UNP Q68Y26
B	407	PRO	-	expression tag	UNP Q68Y26
B	408	ASN	-	expression tag	UNP Q68Y26
B	409	PRO	-	expression tag	UNP Q68Y26
B	410	LEU	-	expression tag	UNP Q68Y26
B	411	LEU	-	expression tag	UNP Q68Y26
B	412	GLY	-	expression tag	UNP Q68Y26
B	413	LEU	-	expression tag	UNP Q68Y26
B	414	ASP	-	expression tag	UNP Q68Y26
B	415	SER	-	expression tag	UNP Q68Y26
B	416	THR	-	expression tag	UNP Q68Y26
B	417	ARG	-	expression tag	UNP Q68Y26
B	418	THR	-	expression tag	UNP Q68Y26
B	419	GLY	-	expression tag	UNP Q68Y26
B	420	HIS	-	expression tag	UNP Q68Y26
B	421	HIS	-	expression tag	UNP Q68Y26
B	422	HIS	-	expression tag	UNP Q68Y26
B	118	LYS	MET	conflict	UNP Q68Y26

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



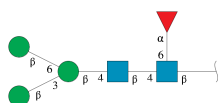
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			38	22	2	14			

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



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

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	6	Total	C	N	O	0	0	0
			71	40	2	29			

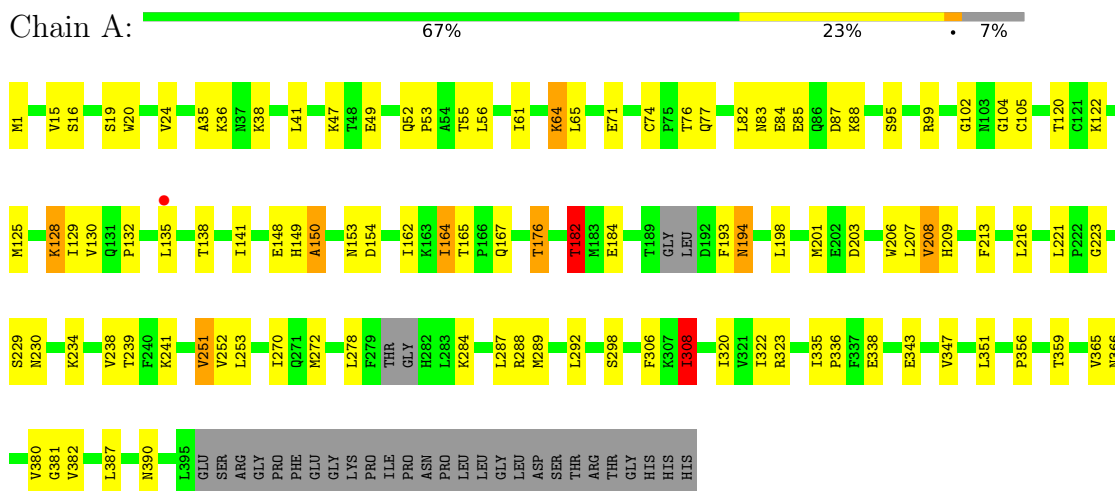
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	O	0	0
			3	3		
5	B	3	Total	O	0	0
			3	3		

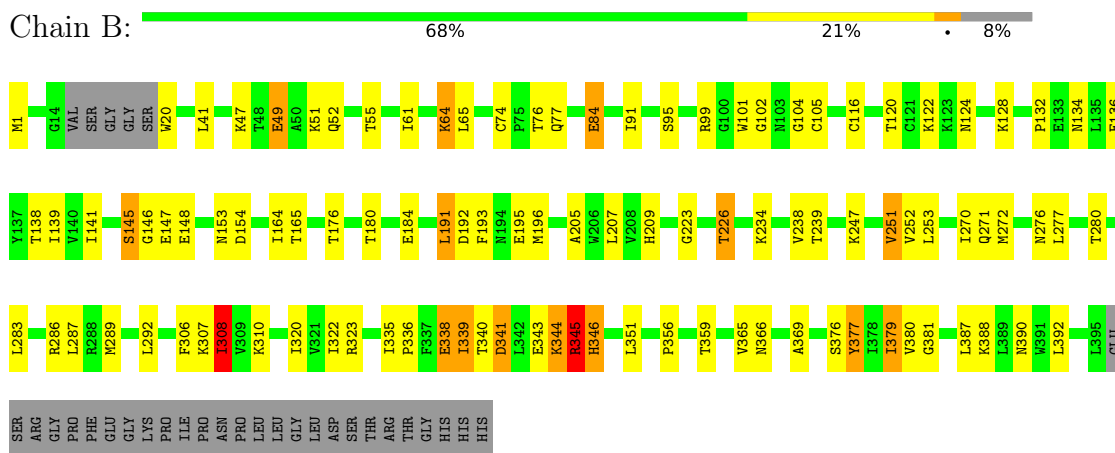
3 Residue-property plots

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: ENVELOPE GLYCOPROTEIN E



• Molecule 1: ENVELOPE GLYCOPROTEIN E



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2
FUC3

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

Chain D:  100%

MAG1
MAG2

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

Chain F:  100%

MAG1
MAG2

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

Chain E:  50%  50%

MAG1
MAG2
BMA3
BMA4
BMA5
FUC6

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.46Å 105.46Å 165.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.08 20.00 – 3.08	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-3.08) 97.4 (20.00-3.08)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 3.06Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.211 , 0.279 0.225 , 0.294	Depositor DCC
R_{free} test set	886 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	86.0	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 70.0	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	0.93	EDS
Total number of atoms	6243	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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: FUC, BMA, NAG

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	0.91	1/3095 (0.0%)	1.33	27/4183 (0.6%)
1	B	0.87	0/3098	1.33	17/4188 (0.4%)
All	All	0.89	1/6193 (0.0%)	1.33	44/8371 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	52	GLN	CA-C	5.06	1.59	1.52

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	101	TRP	N-CA-C	-8.73	98.19	110.50
1	B	124	ASN	CA-CB-CG	7.99	120.59	112.60
1	B	145	SER	N-CA-C	-7.40	94.90	107.99
1	A	87	ASP	CA-CB-CG	6.60	119.20	112.60
1	A	203	ASP	N-CA-C	-6.29	105.64	113.38
1	A	278	LEU	CA-C-N	6.27	132.98	121.70
1	A	278	LEU	C-N-CA	6.27	132.98	121.70
1	B	226	THR	CA-C-N	6.17	128.54	120.28
1	B	226	THR	C-N-CA	6.17	128.54	120.28
1	A	251	VAL	N-CA-C	6.13	116.69	108.11
1	A	234	LYS	CA-C-N	6.07	129.24	120.38
1	A	234	LYS	C-N-CA	6.07	129.24	120.38
1	A	308	ILE	CA-C-N	6.07	128.20	120.56
1	A	308	ILE	C-N-CA	6.07	128.20	120.56
1	B	308	ILE	CA-C-N	6.02	128.15	120.56
1	B	308	ILE	C-N-CA	6.02	128.15	120.56
1	A	208	VAL	CA-C-N	6.01	129.38	120.90
1	A	208	VAL	C-N-CA	6.01	129.38	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	83	ASN	CA-C-N	5.87	128.95	120.38
1	A	83	ASN	C-N-CA	5.87	128.95	120.38
1	A	154	ASP	CA-C-N	5.77	128.33	120.54
1	A	154	ASP	C-N-CA	5.77	128.33	120.54
1	B	153	ASN	CA-C-N	5.76	128.57	120.28
1	B	153	ASN	C-N-CA	5.76	128.57	120.28
1	B	346	HIS	CA-C-N	5.72	128.16	120.50
1	B	346	HIS	C-N-CA	5.72	128.16	120.50
1	A	15	VAL	CA-C-N	5.69	130.44	121.56
1	A	15	VAL	C-N-CA	5.69	130.44	121.56
1	A	194	ASN	CA-CB-CG	5.67	118.27	112.60
1	A	347	VAL	N-CA-CB	5.54	116.57	110.53
1	B	341	ASP	CA-CB-CG	5.52	118.12	112.60
1	A	164	ILE	CB-CA-C	5.47	118.94	110.96
1	B	154	ASP	CA-C-N	5.43	129.83	121.19
1	B	154	ASP	C-N-CA	5.43	129.83	121.19
1	A	85	GLU	CA-C-N	5.41	127.80	120.44
1	A	85	GLU	C-N-CA	5.41	127.80	120.44
1	A	104	GLY	N-CA-C	5.37	122.73	115.32
1	A	182	THR	CB-CA-C	5.34	118.56	109.80
1	B	359	THR	CB-CA-C	5.34	117.62	109.34
1	A	359	THR	CB-CA-C	5.14	117.31	109.34
1	B	104	GLY	N-CA-C	5.11	122.36	115.32
1	A	153	ASN	CA-C-N	5.10	127.12	120.28
1	A	153	ASN	C-N-CA	5.10	127.12	120.28
1	B	251	VAL	N-CA-C	5.08	115.43	108.12

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	3035	0	3021	35	0
1	B	3037	0	3032	41	0
2	C	38	0	34	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	28	0	25	0	0
3	F	28	0	25	0	0
4	E	71	0	61	6	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
All	All	6243	0	6198	84	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 7.

All (84) 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)
4:E:2:NAG:H3	4:E:6:FUC:H61	1.60	0.84
2:C:2:NAG:H3	2:C:3:FUC:H61	1.57	0.83
1:A:20:TRP:HA	1:A:287:LEU:O	1.82	0.79
1:B:195:GLU:HG2	1:B:209:HIS:CE1	2.20	0.76
1:A:239:THR:HB	1:A:251:VAL:HG23	1.76	0.66
1:A:213:PHE:O	1:A:216:LEU:HG	1.95	0.65
1:B:335:ILE:HD12	1:B:356:PRO:HB2	1.80	0.63
1:B:20:TRP:HD1	1:B:286:ARG:HH12	1.46	0.62
1:B:272:MET:HA	1:B:276:ASN:O	2.00	0.61
1:A:335:ILE:HD12	1:A:356:PRO:HB2	1.81	0.61
1:A:74:CYS:HB2	1:A:77:GLN:HG3	1.85	0.59
1:B:239:THR:HB	1:B:251:VAL:HG13	1.84	0.59
1:B:74:CYS:HB2	1:B:77:GLN:HG3	1.83	0.59
1:A:1:MET:HE1	1:A:366:ASN:HB2	1.86	0.58
1:B:339:ILE:HD11	1:B:369:ALA:HB1	1.85	0.58
1:A:64:LYS:HB2	1:A:122:LYS:HD2	1.86	0.56
1:A:55:THR:O	1:A:223:GLY:HA3	2.06	0.56
4:E:2:NAG:O3	4:E:3:BMA:H2	2.06	0.55
1:B:338:GLU:HG2	1:B:340:THR:HG23	1.88	0.54
1:B:191:LEU:HD23	1:B:192:ASP:H	1.72	0.54
1:B:51:LYS:HE2	1:B:136:GLU:HB2	1.91	0.53
1:B:64:LYS:HB2	1:B:122:LYS:HD2	1.90	0.53
1:A:102:GLY:HA2	4:E:1:NAG:H81	1.91	0.52
1:A:56:LEU:HB2	1:A:129:ILE:HG13	1.92	0.52
1:B:55:THR:O	1:B:223:GLY:HA3	2.09	0.52
1:B:102:GLY:HA2	2:C:1:NAG:H81	1.90	0.52
1:B:289:MET:HG2	1:B:292:LEU:HD12	1.91	0.52
1:B:139:ILE:HD11	1:B:283:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:SER:C	1:B:147:GLU:H	2.17	0.51
1:A:1:MET:CE	1:A:150:ALA:HB3	2.41	0.51
1:B:308:ILE:HG22	1:B:322:ILE:HD11	1.93	0.51
1:A:16:SER:HB3	1:A:36:LYS:HB3	1.93	0.50
1:B:49:GLU:HG2	1:B:277:LEU:HD12	1.94	0.50
1:B:306:PHE:CZ	1:B:335:ILE:HG23	2.47	0.49
1:A:308:ILE:HG22	1:A:322:ILE:HD11	1.94	0.49
1:A:182:THR:HG22	1:A:288:ARG:CB	2.43	0.48
1:A:289:MET:HG2	1:A:292:LEU:HD12	1.95	0.47
1:A:41:LEU:HD11	1:A:292:LEU:HD11	1.95	0.47
1:B:99:ARG:HB3	1:B:105:CYS:SG	2.54	0.47
1:B:379:ILE:HG13	1:B:388:LYS:HA	1.97	0.47
1:A:306:PHE:CZ	1:A:335:ILE:HG23	2.50	0.47
1:A:56:LEU:HD13	1:A:129:ILE:HD11	1.95	0.47
1:B:310:LYS:HB3	1:B:323:ARG:HB3	1.96	0.46
1:A:99:ARG:HB3	1:A:105:CYS:SG	2.56	0.46
1:A:165:THR:HG22	1:A:167:GLN:H	1.80	0.46
1:B:310:LYS:CB	1:B:323:ARG:HB3	2.46	0.46
1:B:377:TYR:HB3	1:B:379:ILE:CD1	2.45	0.46
1:A:198:LEU:HD11	1:A:270:ILE:HD11	1.97	0.46
1:B:345:ARG:HD3	1:B:345:ARG:HA	1.70	0.46
1:A:47:LYS:HG2	1:A:138:THR:HB	1.98	0.46
1:A:149:HIS:CE1	2:C:3:FUC:H63	2.51	0.46
1:B:20:TRP:CD1	1:B:286:ARG:HH12	2.31	0.46
1:B:132:PRO:HG3	1:B:193:PHE:HB2	1.96	0.46
1:A:1:MET:HE3	1:A:150:ALA:HB3	1.98	0.45
1:B:47:LYS:HG2	1:B:138:THR:HB	1.99	0.45
1:A:24:VAL:HG13	1:A:284:LYS:HG2	1.99	0.45
4:E:2:NAG:H4	4:E:3:BMA:O2	2.17	0.45
1:B:191:LEU:HD22	1:B:196:MET:HE3	1.99	0.44
1:B:205:ALA:HB2	1:B:272:MET:HE2	1.99	0.44
1:A:71:GLU:HB2	1:A:82:LEU:HD21	1.99	0.44
1:B:195:GLU:HB3	1:B:196:MET:HE2	2.00	0.43
1:B:380:VAL:HG13	1:B:387:LEU:HB2	2.00	0.43
1:A:19:SER:O	1:A:288:ARG:HA	2.18	0.43
1:B:41:LEU:HD11	1:B:292:LEU:HD11	2.00	0.43
1:B:65:LEU:HD11	1:B:238:VAL:HG13	2.00	0.43
1:A:53:PRO:HB2	1:A:128:LYS:HB3	2.01	0.43
1:A:323:ARG:HA	1:A:365:VAL:O	2.19	0.42
4:E:1:NAG:H61	4:E:2:NAG:N2	2.35	0.42
1:A:221:LEU:HD21	1:A:230:ASN:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ALA:HB3	1:A:38:LYS:HB2	2.02	0.42
1:A:380:VAL:HG13	1:A:387:LEU:HB2	2.01	0.42
2:C:1:NAG:H61	2:C:2:NAG:N2	2.35	0.41
1:A:65:LEU:HD11	1:A:238:VAL:HG13	2.02	0.41
4:E:1:NAG:H61	4:E:2:NAG:HN2	1.85	0.41
2:C:1:NAG:H61	2:C:2:NAG:HN2	1.86	0.41
1:B:343:GLU:O	1:B:344:LYS:HB2	2.21	0.41
1:B:91:ILE:HD13	1:B:234:LYS:HB2	2.03	0.40
1:B:323:ARG:HA	1:B:365:VAL:O	2.21	0.40
1:B:336:PRO:HD2	1:B:381:GLY:HA2	2.03	0.40
1:B:1:MET:HE1	1:B:366:ASN:HB2	2.02	0.40
1:B:91:ILE:O	1:B:116:CYS:HA	2.21	0.40
1:A:132:PRO:HG3	1:A:193:PHE:HB2	2.03	0.40
1:A:336:PRO:HD2	1:A:381:GLY:HA2	2.02	0.40
1:B:195:GLU:HG2	1:B:209:HIS:HE1	1.79	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	385/422 (91%)	353 (92%)	29 (8%)	3 (1%)	16	44
1	B	386/422 (92%)	357 (92%)	23 (6%)	6 (2%)	7	28
All	All	771/844 (91%)	710 (92%)	52 (7%)	9 (1%)	10	34

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	345	ARG
1	A	176	THR
1	B	146	GLY

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Mol	Chain	Res	Type
1	B	344	LYS
1	A	148	GLU
1	A	150	ALA
1	B	176	THR
1	B	148	GLU
1	B	84	GLU

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	339/366 (93%)	302 (89%)	37 (11%)	6	23
1	B	339/366 (93%)	300 (88%)	39 (12%)	5	21
All	All	678/732 (93%)	602 (89%)	76 (11%)	6	22

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	GLU
1	A	61	ILE
1	A	64	LYS
1	A	76	THR
1	A	84	GLU
1	A	88	LYS
1	A	95	SER
1	A	120	THR
1	A	125	MET
1	A	128	LYS
1	A	130	VAL
1	A	135	LEU
1	A	141	ILE
1	A	162	ILE
1	A	164	ILE
1	A	176	THR
1	A	182	THR

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Mol	Chain	Res	Type
1	A	184	GLU
1	A	194	ASN
1	A	201	MET
1	A	206	TRP
1	A	207	LEU
1	A	208	VAL
1	A	209	HIS
1	A	229	SER
1	A	241	LYS
1	A	252	VAL
1	A	253	LEU
1	A	272	MET
1	A	298	SER
1	A	308	ILE
1	A	320	ILE
1	A	338	GLU
1	A	343	GLU
1	A	351	LEU
1	A	382	VAL
1	A	390	ASN
1	B	49	GLU
1	B	52	GLN
1	B	61	ILE
1	B	64	LYS
1	B	76	THR
1	B	84	GLU
1	B	95	SER
1	B	120	THR
1	B	128	LYS
1	B	134	ASN
1	B	141	ILE
1	B	164	ILE
1	B	165	THR
1	B	180	THR
1	B	184	GLU
1	B	191	LEU
1	B	207	LEU
1	B	226	THR
1	B	247	LYS
1	B	252	VAL
1	B	253	LEU
1	B	270	ILE

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Mol	Chain	Res	Type
1	B	271	GLN
1	B	280	THR
1	B	287	LEU
1	B	307	LYS
1	B	308	ILE
1	B	320	ILE
1	B	338	GLU
1	B	339	ILE
1	B	341	ASP
1	B	345	ARG
1	B	346	HIS
1	B	351	LEU
1	B	376	SER
1	B	377	TYR
1	B	379	ILE
1	B	390	ASN
1	B	392	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	ASN
1	A	149	HIS
1	A	167	GLN
1	A	194	ASN
1	A	200	GLN
1	A	227	GLN
1	A	244	HIS
1	A	317	HIS
1	B	8	ASN
1	B	194	ASN
1	B	230	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

13 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	2,1	14,14,15	0.41	0	17,19,21	0.83	0
2	NAG	C	2	2	14,14,15	0.25	0	17,19,21	0.74	1 (5%)
2	FUC	C	3	2	10,10,11	0.45	0	14,14,16	1.25	2 (14%)
3	NAG	D	1	3,1	14,14,15	0.28	0	17,19,21	1.10	1 (5%)
3	NAG	D	2	3	14,14,15	0.34	0	17,19,21	1.58	2 (11%)
4	NAG	E	1	4,1	14,14,15	0.43	0	17,19,21	0.71	0
4	NAG	E	2	4	14,14,15	0.29	0	17,19,21	1.00	2 (11%)
4	BMA	E	3	4	11,11,12	0.44	0	15,15,17	1.24	1 (6%)
4	BMA	E	4	4	11,11,12	0.50	0	15,15,17	0.93	1 (6%)
4	BMA	E	5	4	11,11,12	0.48	0	15,15,17	1.80	1 (6%)
4	FUC	E	6	4	10,10,11	0.52	0	14,14,16	1.30	1 (7%)
3	NAG	F	1	3,1	14,14,15	0.28	0	17,19,21	0.72	1 (5%)
3	NAG	F	2	3	14,14,15	0.36	0	17,19,21	1.63	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	FUC	C	3	2	-	-	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
4	NAG	E	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	BMA	E	3	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	E	4	4	-	1/2/19/22	0/1/1/1
4	BMA	E	5	4	-	0/2/19/22	1/1/1/1
4	FUC	E	6	4	-	-	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	5	BMA	C1-O5-C5	6.47	120.86	112.19
3	D	2	NAG	C1-O5-C5	5.44	119.47	112.19
3	F	2	NAG	C1-O5-C5	5.39	119.41	112.19
3	D	1	NAG	C1-O5-C5	4.13	117.72	112.19
3	F	2	NAG	O5-C1-C2	3.67	116.97	111.29
4	E	6	FUC	C1-O5-C5	3.63	121.53	112.97
4	E	3	BMA	O3-C3-C2	3.58	117.35	110.05
2	C	3	FUC	C1-O5-C5	3.48	121.18	112.97
3	D	2	NAG	O5-C1-C2	3.31	116.42	111.29
4	E	2	NAG	O5-C1-C2	-2.62	107.23	111.29
4	E	2	NAG	C1-O5-C5	2.27	115.23	112.19
4	E	4	BMA	C1-C2-C3	2.20	112.85	109.64
2	C	3	FUC	C1-C2-C3	2.20	112.85	109.64
2	C	2	NAG	O5-C1-C2	-2.18	107.92	111.29
3	F	1	NAG	C1-O5-C5	2.07	114.95	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	NAG	O5-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
4	E	1	NAG	C4-C5-C6-O6
4	E	4	BMA	O5-C5-C6-O6
2	C	1	NAG	C1-C2-N2-C7

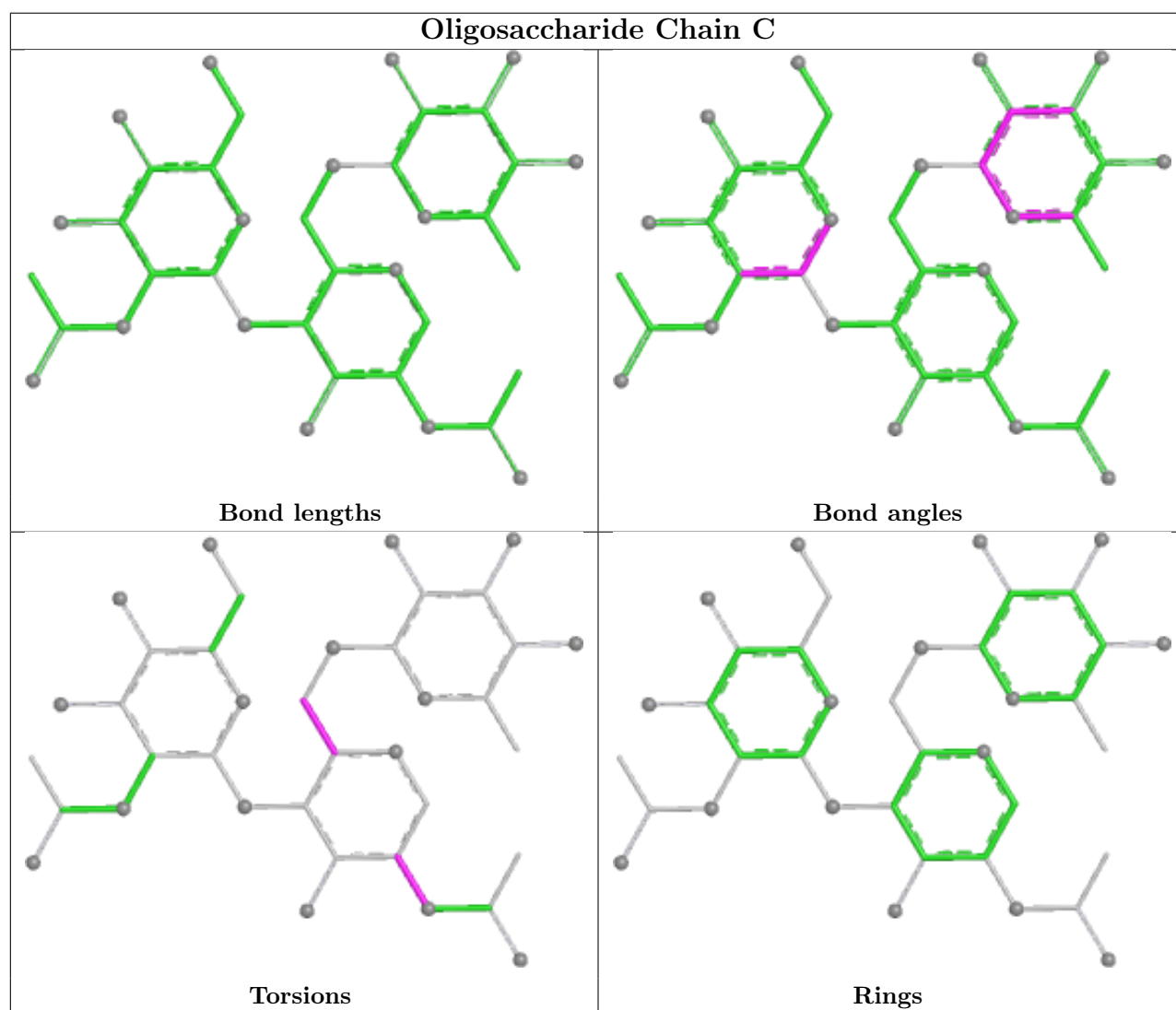
All (1) ring outliers are listed below:

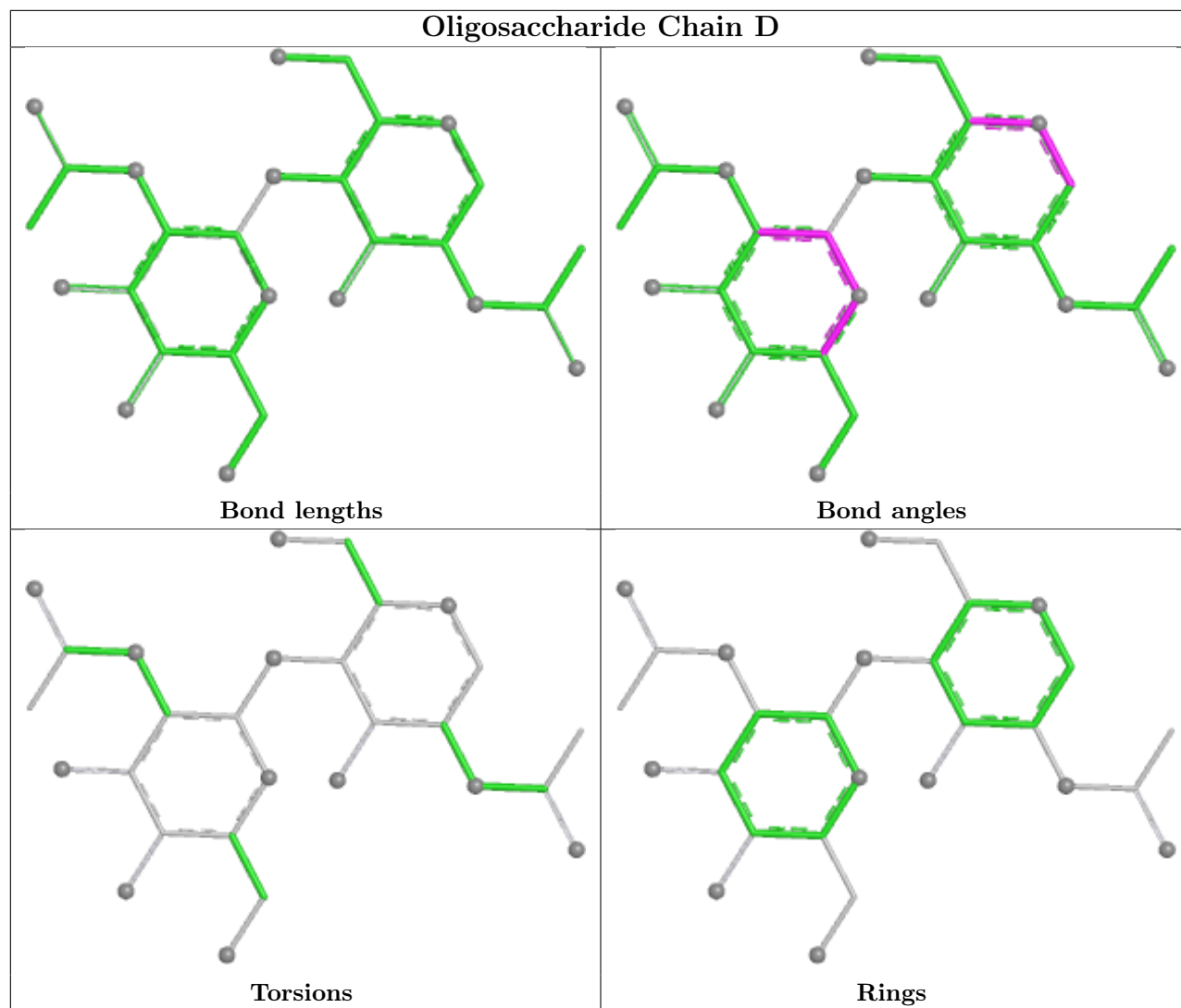
Mol	Chain	Res	Type	Atoms
4	E	5	BMA	C1-C2-C3-C4-C5-O5

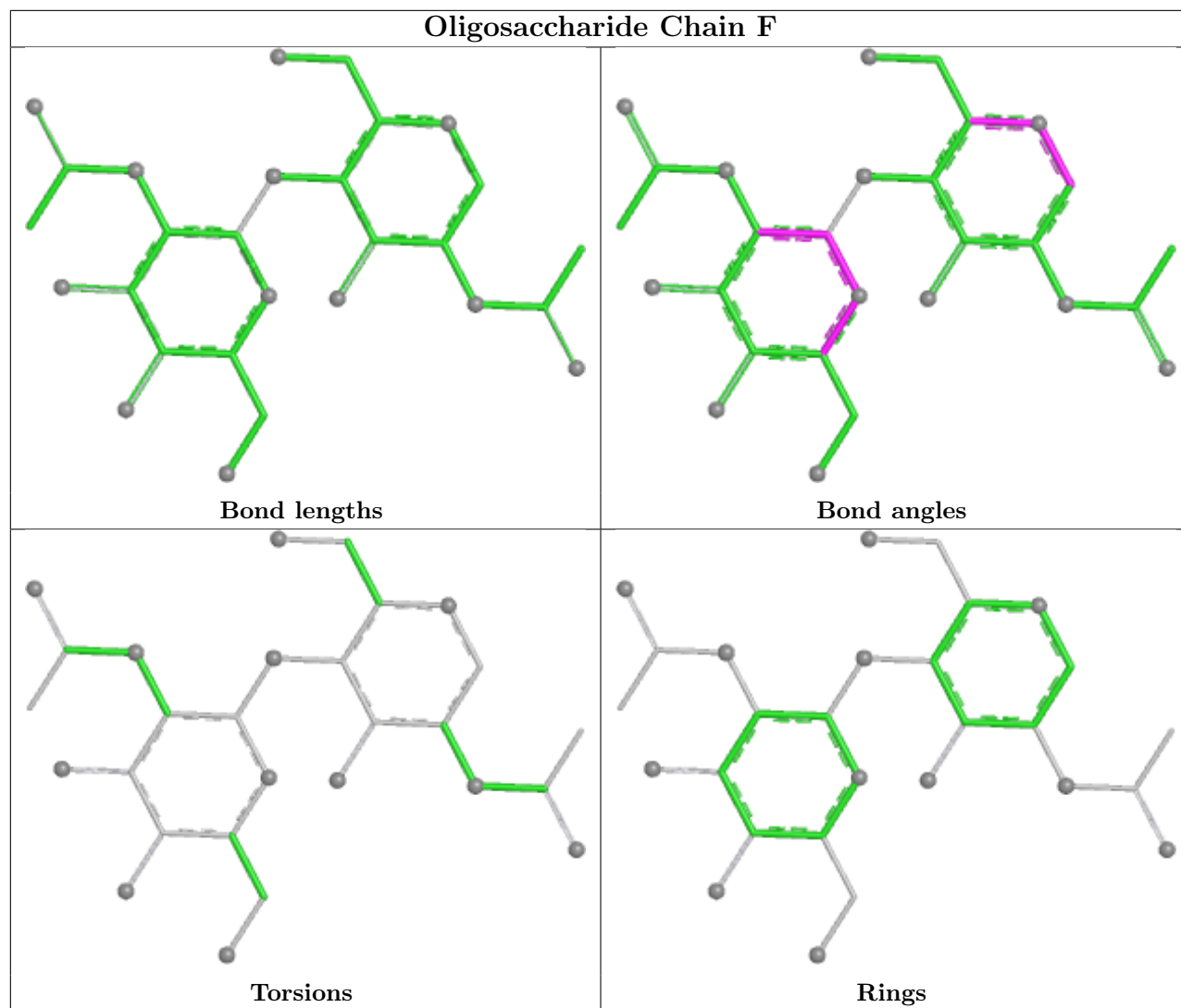
7 monomers are involved in 11 short contacts:

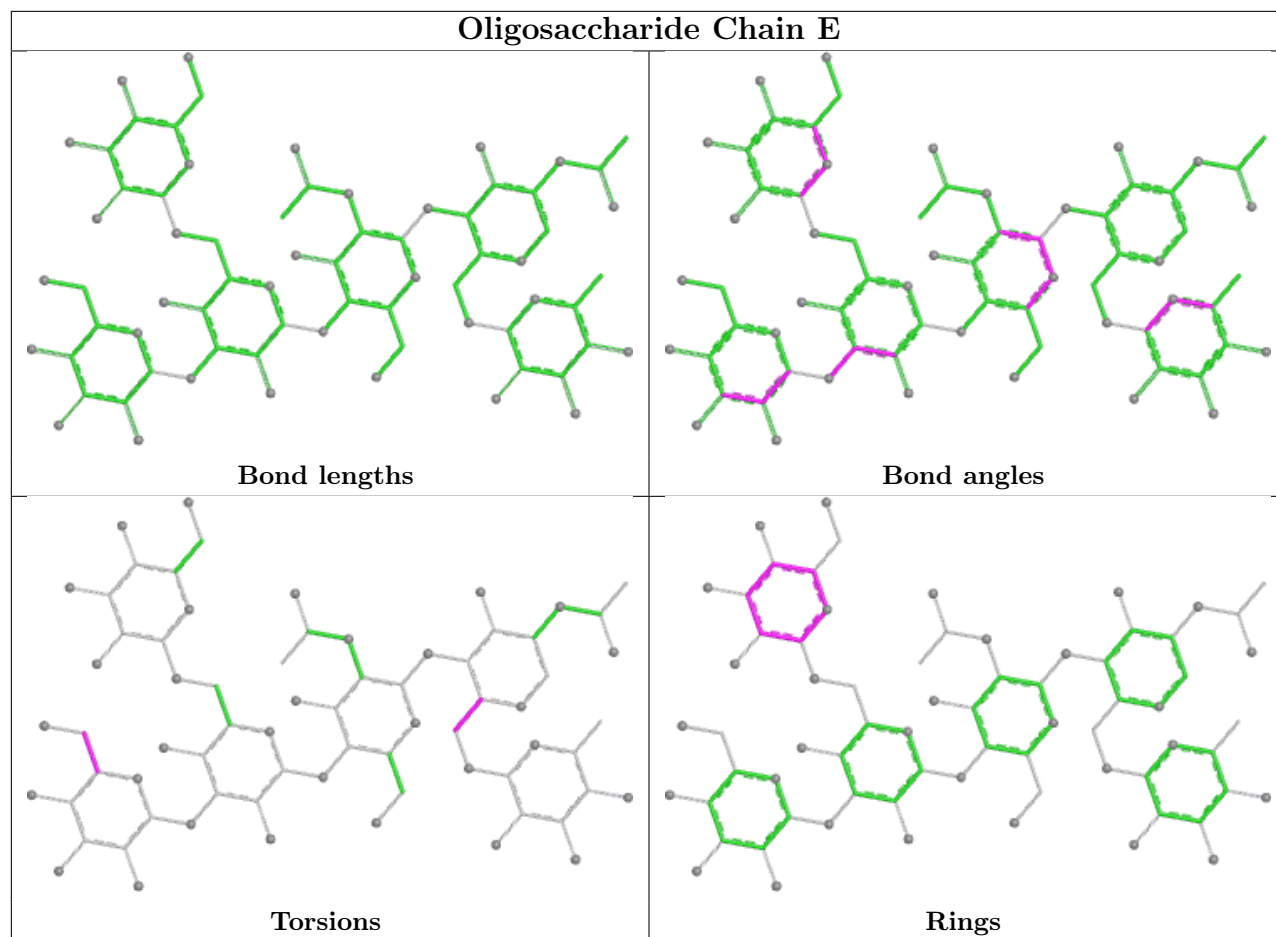
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3	FUC	2	0
2	C	1	NAG	3	0
4	E	1	NAG	3	0
4	E	2	NAG	5	0
4	E	6	FUC	1	0
2	C	2	NAG	3	0
4	E	3	BMA	2	0

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









5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	391/422 (92%)	-0.27	1 (0%) 90 80	46, 78, 125, 147	0
1	B	390/422 (92%)	-0.20	0 100 100	40, 86, 118, 134	0
All	All	781/844 (92%)	-0.24	1 (0%) 92 86	40, 82, 121, 147	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	135	LEU	2.4

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.

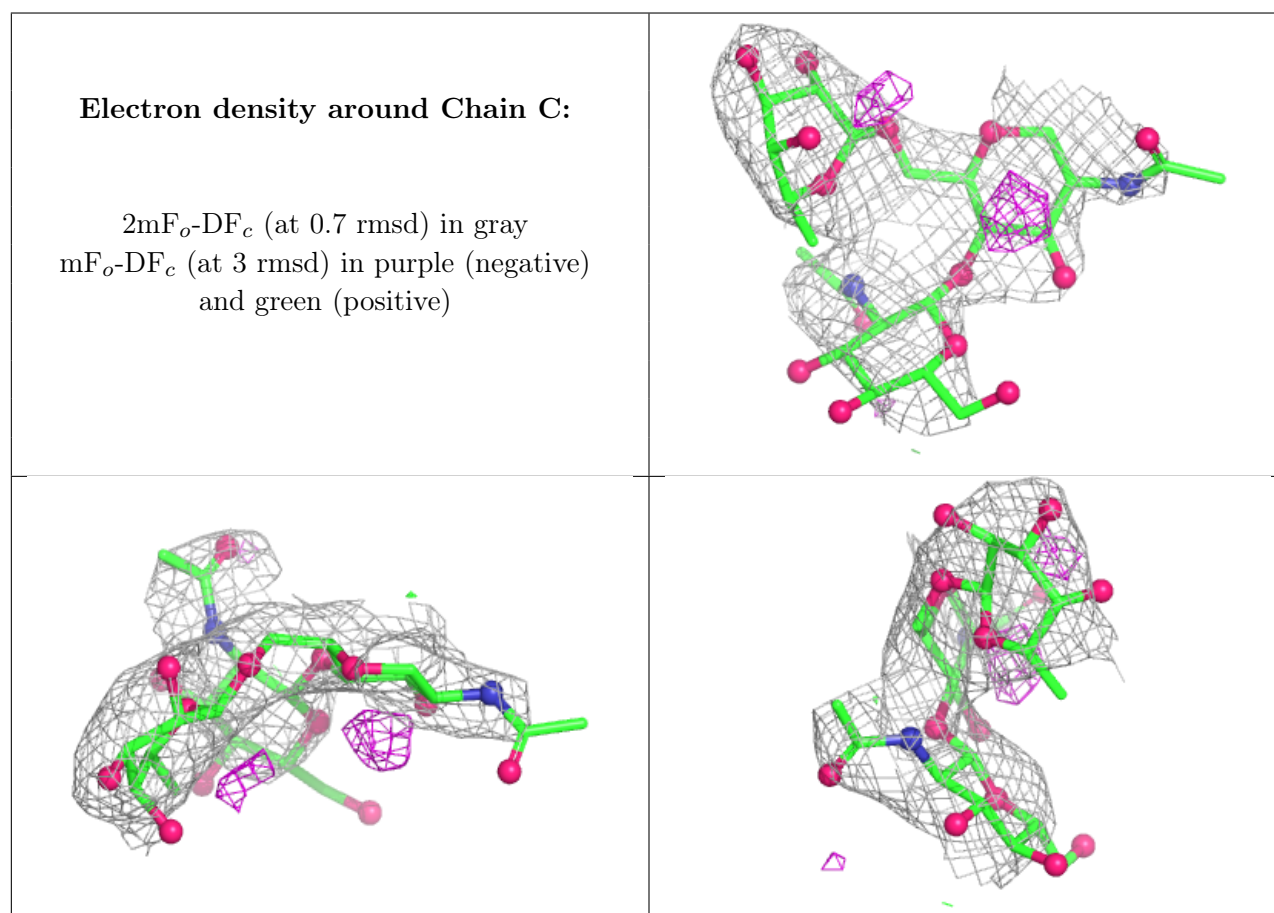
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	C	2	14/15	0.40	0.13	145,152,156,156	0
3	NAG	D	2	14/15	0.48	0.12	138,146,147,148	0
3	NAG	F	2	14/15	0.52	0.10	121,123,126,127	0
2	FUC	C	3	10/11	0.67	0.10	123,125,126,127	0
4	BMA	E	3	11/12	0.67	0.13	92,94,101,102	0
3	NAG	D	1	14/15	0.72	0.10	113,119,126,132	0
4	BMA	E	4	11/12	0.73	0.12	95,100,104,108	0
3	NAG	F	1	14/15	0.76	0.09	100,106,113,115	0

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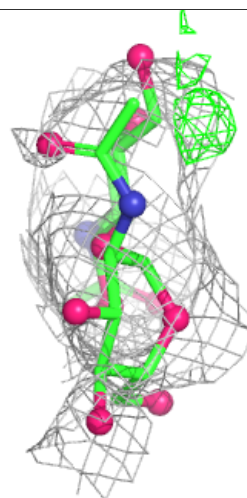
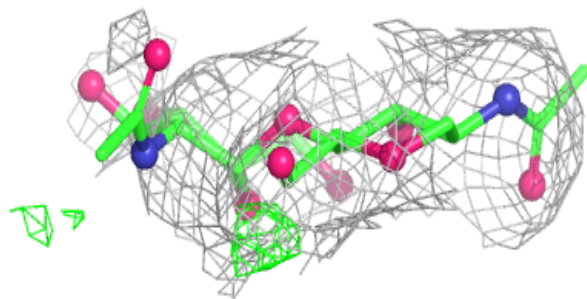
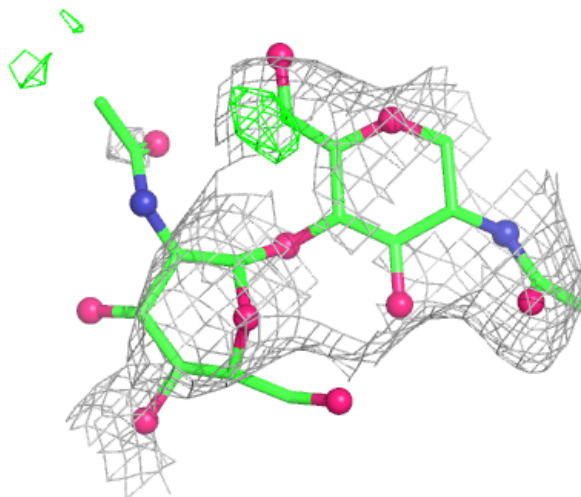
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	C	1	14/15	0.76	0.15	129,136,140,145	0
4	NAG	E	2	14/15	0.84	0.10	83,86,88,89	0
4	BMA	E	5	11/12	0.84	0.07	92,93,96,98	0
4	FUC	E	6	10/11	0.85	0.09	61,69,72,73	0
4	NAG	E	1	14/15	0.92	0.09	75,81,88,90	0

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.



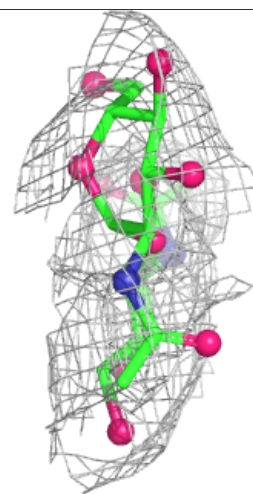
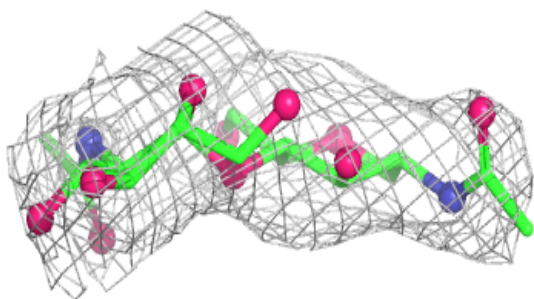
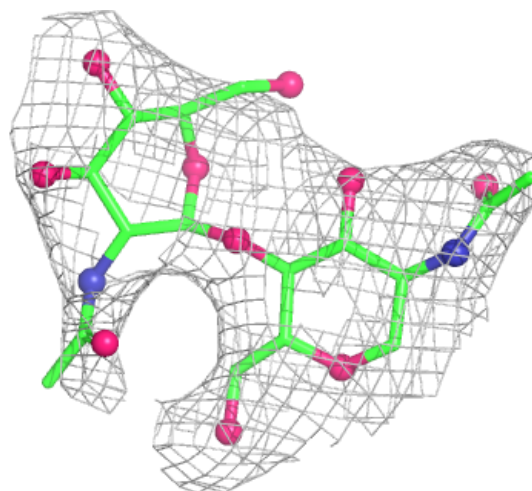
Electron density around Chain D:

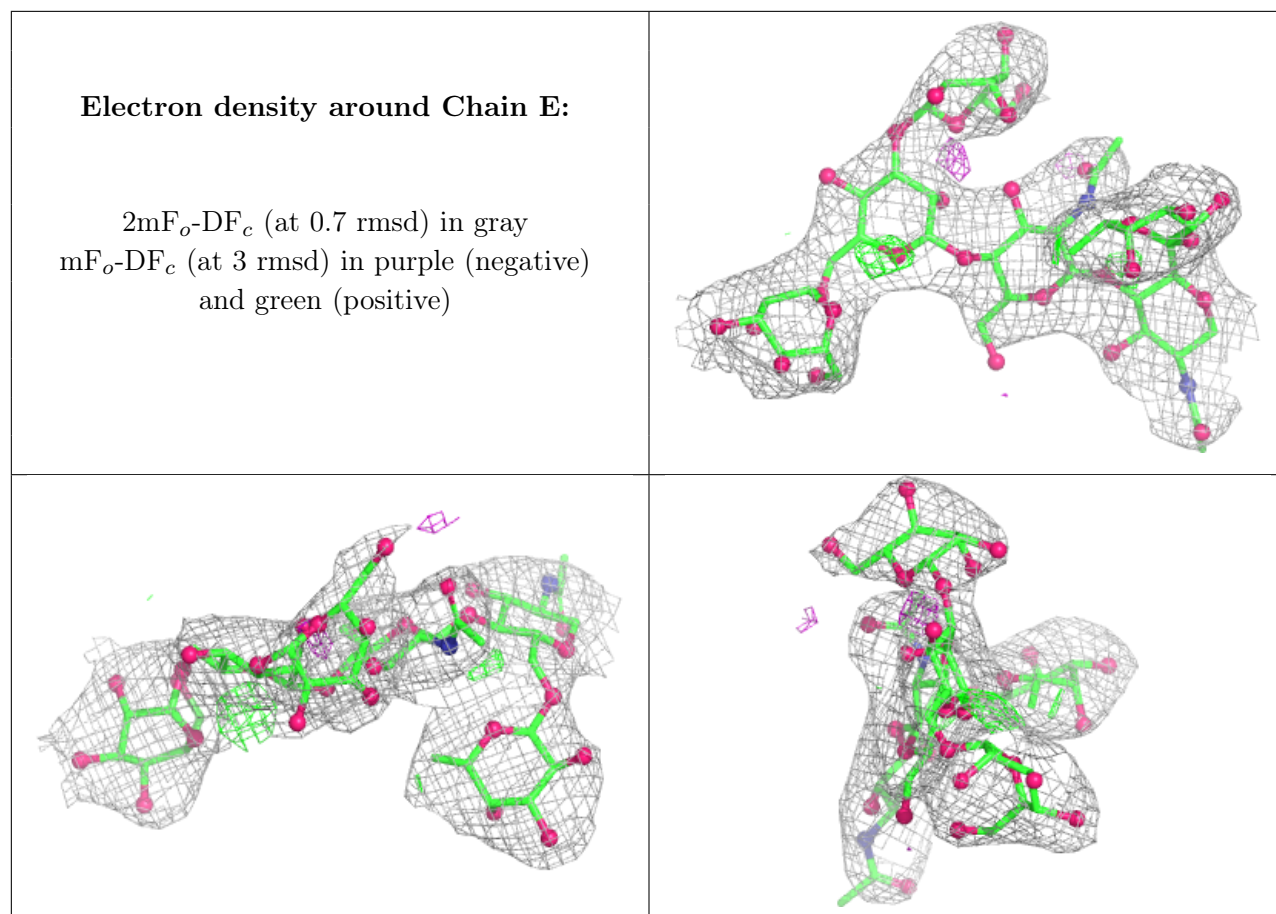
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.