



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:05 AM UTC

PDB ID : 4OJO / pdb_00004ojo
Title : Crystal Structure of Putative Tailspike Protein (TSP1, orf210) from Escherichia coli O157:H7 Bacteriophage CBA120 in Complex with Lactose
Authors : Chen, C.; Herzberg, O.
Deposited on : 2014-01-21
Resolution : 2.00 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

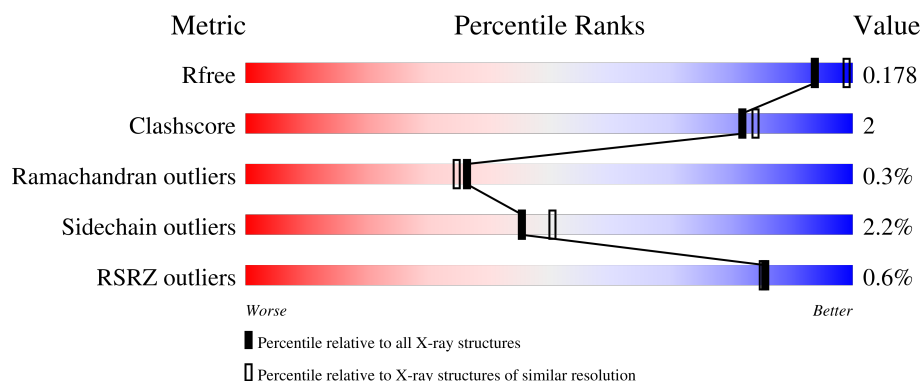
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	776	% 90% 7% ..
1	B	776	% 88% 9% ..
1	C	776	 91% 6% ..
2	D	2	 50% 50%
2	E	2	 50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19352 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 Tailspike protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	758	Total	C	N	O	S	1	0	0
			5675	3578	955	1123	19			
1	B	756	Total	C	N	O	S	0	0	0
			5653	3568	947	1119	19			
1	C	759	Total	C	N	O	S	1	0	0
			5679	3580	958	1122	19			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	771	HIS	-	expression tag	UNP G3M189
A	772	HIS	-	expression tag	UNP G3M189
A	773	HIS	-	expression tag	UNP G3M189
A	774	HIS	-	expression tag	UNP G3M189
A	775	HIS	-	expression tag	UNP G3M189
A	776	HIS	-	expression tag	UNP G3M189
B	771	HIS	-	expression tag	UNP G3M189
B	772	HIS	-	expression tag	UNP G3M189
B	773	HIS	-	expression tag	UNP G3M189
B	774	HIS	-	expression tag	UNP G3M189
B	775	HIS	-	expression tag	UNP G3M189
B	776	HIS	-	expression tag	UNP G3M189
C	771	HIS	-	expression tag	UNP G3M189
C	772	HIS	-	expression tag	UNP G3M189
C	773	HIS	-	expression tag	UNP G3M189
C	774	HIS	-	expression tag	UNP G3M189
C	775	HIS	-	expression tag	UNP G3M189
C	776	HIS	-	expression tag	UNP G3M189

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



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

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	1
			1	1		

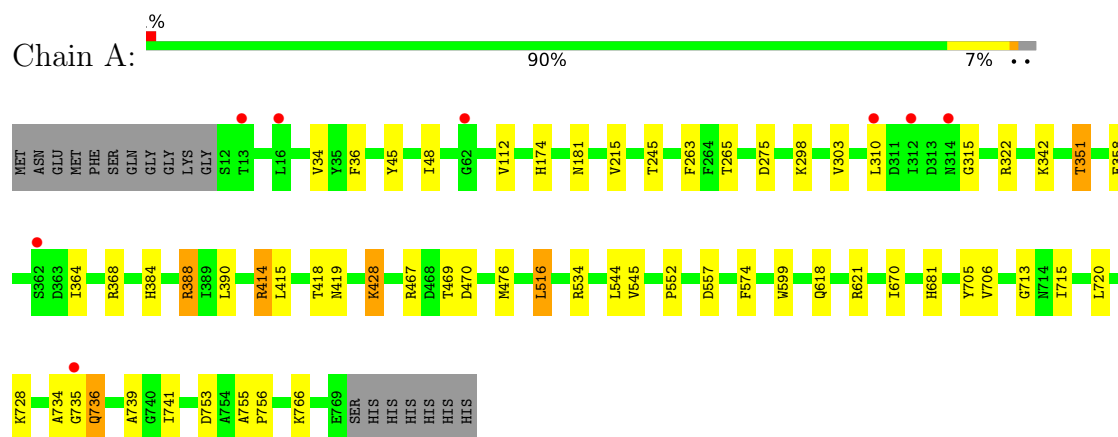
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	664	Total	O	0	0
			664	664		
4	B	820	Total	O	0	0
			820	820		
4	C	791	Total	O	0	0
			791	791		

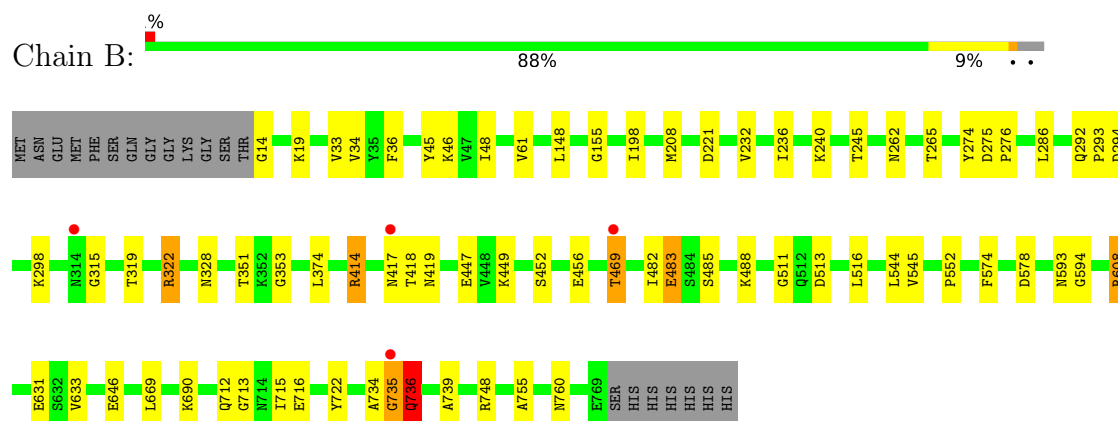
3 Residue-property plots

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.

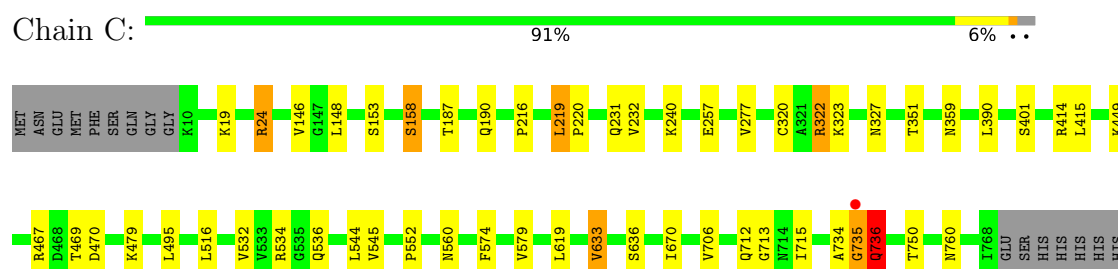
• Molecule 1: Tailspike protein



• Molecule 1: Tailspike protein



• Molecule 1: Tailspike protein



HIS

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

Chain D:  50% 50%

GLC1
GAL2

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

Chain E:  50% 50%

GLC1
GAL2

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

Chain F:  100%

GLC1
GAL2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	123.41Å 152.88Å 171.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.00 – 2.00 76.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.8 (76.00-2.00) 96.8 (76.00-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.177 , 0.214 0.179 , 0.178	Depositor DCC
R_{free} test set	11321 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19352	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 2.47% 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: GAL, ZN, 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	0.44	0/5779	0.96	13/7856 (0.2%)
1	B	0.47	0/5757	0.97	21/7828 (0.3%)
1	C	0.47	0/5783	0.97	19/7861 (0.2%)
All	All	0.46	0/17319	0.97	53/23545 (0.2%)

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	544	LEU	N-CA-C	7.75	119.51	111.14
1	B	198	ILE	CB-CA-C	-7.23	105.56	111.71
1	B	544	LEU	N-CA-C	7.21	118.92	111.14
1	C	545	VAL	N-CA-C	7.09	117.70	108.35
1	C	544	LEU	N-CA-C	6.76	118.45	111.14
1	A	315	GLY	N-CA-C	-6.74	106.40	115.36
1	C	401	SER	N-CA-C	6.73	118.84	109.15
1	C	414	ARG	N-CA-C	-6.48	100.89	110.48
1	B	545	VAL	N-CA-C	6.37	117.53	108.42
1	B	155	GLY	N-CA-C	6.15	119.78	112.33
1	B	414	ARG	N-CA-C	-6.15	101.37	110.48
1	B	736	GLN	N-CA-C	6.09	123.77	110.80
1	C	715	ILE	N-CA-C	6.04	117.46	108.46
1	C	734	ALA	N-CA-C	6.04	115.43	108.49
1	A	670	ILE	N-CA-C	5.96	116.75	107.28
1	B	469	THR	N-CA-C	5.93	117.42	111.07
1	C	670	ILE	N-CA-C	5.91	116.68	107.28
1	A	414	ARG	N-CA-C	-5.89	101.77	110.48
1	C	736	GLN	N-CA-C	5.88	123.33	110.80
1	C	320	CYS	N-CA-C	-5.83	103.44	110.44
1	B	734	ALA	N-CA-C	5.83	115.19	108.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	545	VAL	N-CA-C	5.74	116.62	108.42
1	B	315	GLY	N-CA-C	-5.71	107.76	115.36
1	A	706	VAL	N-CA-C	-5.62	105.05	110.72
1	C	713	GLY	N-CA-C	5.56	121.11	112.60
1	A	469	THR	N-CA-C	5.55	117.42	111.36
1	A	428	LYS	N-CA-C	5.52	113.18	108.22
1	C	277	VAL	N-CA-C	-5.51	105.47	110.82
1	C	469	THR	N-CA-C	5.48	116.94	110.97
1	A	599	TRP	N-CA-C	-5.41	105.46	111.36
1	B	755	ALA	CA-C-N	5.40	125.01	119.56
1	B	755	ALA	C-N-CA	5.40	125.01	119.56
1	C	219	LEU	CA-C-N	5.38	125.02	119.05
1	C	219	LEU	C-N-CA	5.38	125.02	119.05
1	B	482	ILE	N-CA-C	5.38	115.84	107.99
1	B	452	SER	CA-C-N	-5.38	114.44	120.14
1	B	452	SER	C-N-CA	-5.38	114.44	120.14
1	C	633	VAL	N-CA-C	5.33	117.06	108.85
1	A	303	VAL	N-CA-C	5.22	115.94	110.62
1	B	516	LEU	N-CA-C	5.22	118.80	112.23
1	C	516	LEU	N-CA-C	5.20	119.75	113.41
1	C	532	VAL	N-CA-C	5.17	116.02	108.58
1	B	221	ASP	N-CA-C	5.16	115.35	108.38
1	B	513	ASP	CA-C-N	5.16	124.88	119.82
1	B	513	ASP	C-N-CA	5.16	124.88	119.82
1	B	286	LEU	N-CA-C	-5.15	103.88	110.53
1	B	722	TYR	CB-CA-C	-5.14	110.66	116.63
1	B	713	GLY	N-CA-C	5.13	120.97	112.66
1	A	741	ILE	N-CA-C	5.12	116.02	108.45
1	C	706	VAL	N-CA-C	-5.11	105.44	111.00
1	A	713	GLY	N-CA-C	5.09	120.39	112.60
1	A	516	LEU	N-CA-C	5.04	118.58	112.23
1	C	495	LEU	N-CA-C	5.01	116.69	108.52

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	5675	0	5638	31	0
1	B	5653	0	5600	32	0
1	C	5679	0	5641	21	0
2	D	23	0	21	3	0
2	E	23	0	21	1	0
2	F	23	0	21	0	0
3	A	1	0	0	0	0
4	A	664	0	0	13	0
4	B	820	0	0	12	0
4	C	791	0	0	3	0
All	All	19352	0	16942	85	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 2.

All (85) 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:A:1530:HOH:O	2:D:1:GLC:C6	1.91	1.16
4:A:1530:HOH:O	2:D:1:GLC:H61	1.51	1.00
4:A:1530:HOH:O	2:D:1:GLC:O6	1.84	0.89
1:A:534:ARG:CZ	4:A:1558:HOH:O	2.20	0.88
1:A:681:HIS:HD2	1:A:705:TYR:H	1.26	0.83
1:B:414:ARG:NH2	1:B:418:THR:O	2.18	0.75
1:C:187:THR:HG22	1:C:190:GLN:HG3	1.73	0.70
1:C:216:PRO:HG2	1:C:219:LEU:HD21	1.75	0.68
1:B:449:LYS:NZ	4:B:1282:HOH:O	2.27	0.66
1:A:735:GLY:O	4:A:929:HOH:O	2.12	0.66
1:B:14:GLY:N	4:B:1688:HOH:O	2.30	0.65
1:B:322:ARG:NH1	4:B:1074:HOH:O	2.30	0.64
1:A:364:ILE:HG13	1:A:415:LEU:HB3	1.80	0.63
1:B:46:LYS:NZ	4:B:1629:HOH:O	2.33	0.62
1:A:414:ARG:NH2	1:A:418:THR:O	2.34	0.61
1:A:181:ASN:O	1:C:187:THR:HG21	2.00	0.61
1:C:24:ARG:NH2	4:C:1027:HOH:O	2.34	0.61
1:A:351:THR:HG22	1:A:384:HIS:HA	1.83	0.60
1:A:358:GLU:OE1	1:A:368:ARG:HD3	2.03	0.59
1:B:14:GLY:N	4:B:1280:HOH:O	2.35	0.59
1:B:417:ASN:HB3	1:B:488:LYS:HD3	1.85	0.58
1:B:593:ASN:ND2	4:B:1631:HOH:O	2.35	0.57
1:C:19:LYS:NZ	4:C:1357:HOH:O	2.38	0.57
1:A:388:ARG:NH2	4:A:1039:HOH:O	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:681:HIS:CD2	1:A:705:TYR:H	2.16	0.56
1:A:263:PHE:H	1:A:265:THR:HG23	1.70	0.56
1:A:467:ARG:HD2	1:A:470:ASP:OD1	2.05	0.55
1:B:578:ASP:CB	4:B:1702:HOH:O	2.54	0.55
1:C:736:GLN:HA	1:C:760:ASN:O	2.07	0.54
1:B:19:LYS:HE3	1:B:33:VAL:O	2.09	0.53
1:A:753:ASP:O	1:A:766:LYS:NZ	2.40	0.53
1:C:449:LYS:NZ	4:C:902:HOH:O	2.42	0.52
1:C:712:GLN:HG2	1:C:735:GLY:O	2.10	0.51
1:C:153:SER:OG	1:C:158:SER:HB3	2.12	0.50
1:C:467:ARG:HD2	1:C:470:ASP:OD1	2.12	0.49
1:B:712:GLN:HG2	1:B:735:GLY:O	2.12	0.49
1:B:328:ASN:HD22	1:B:353:GLY:HA3	1.78	0.49
1:B:690:LYS:NZ	1:B:716:GLU:OE2	2.44	0.48
1:B:736:GLN:HA	1:B:760:ASN:O	2.12	0.48
4:B:1614:HOH:O	2:E:1:GLC:O1	2.20	0.48
1:A:715:ILE:O	1:A:739:ALA:HA	2.13	0.48
1:A:476:MET:SD	1:C:479:LYS:HD3	2.54	0.47
1:B:417:ASN:ND2	1:B:485:SER:O	2.46	0.47
1:C:322:ARG:HG3	1:C:323:LYS:HG3	1.97	0.46
1:C:257:GLU:HA	1:C:327:ASN:O	2.14	0.46
1:A:298:LYS:HE2	4:A:1557:HOH:O	2.15	0.46
1:A:618:GLN:OE1	4:A:1530:HOH:O	2.20	0.46
1:B:262:ASN:HB2	1:B:265:THR:CG2	2.47	0.45
1:A:534:ARG:NH1	4:A:1558:HOH:O	2.41	0.45
1:A:756:PRO:HG3	1:A:766:LYS:HD2	1.98	0.45
1:B:298:LYS:NZ	4:B:1466:HOH:O	2.42	0.45
1:C:536:GLN:HA	1:C:560:ASN:HB3	1.99	0.45
1:A:621:ARG:HD2	1:A:621:ARG:N	2.32	0.44
1:B:265:THR:HG21	1:C:323:LYS:HD3	2.00	0.44
1:C:552:PRO:HB3	1:C:574:PHE:O	2.16	0.44
1:B:245:THR:HG22	1:B:275:ASP:O	2.17	0.44
4:A:1558:HOH:O	1:C:534:ARG:CZ	2.65	0.44
1:A:342:LYS:HB3	1:A:342:LYS:HE2	1.77	0.44
1:C:219:LEU:HA	1:C:220:PRO:HD3	1.84	0.44
1:A:728:LYS:NZ	1:A:755:ALA:O	2.44	0.43
1:B:36:PHE:HB2	1:B:48:ILE:HD11	2.00	0.43
1:C:579:VAL:HG23	1:C:619:LEU:HD22	2.01	0.43
1:B:208:MET:HE3	1:B:236:ILE:HD13	2.01	0.43
1:C:359:ASN:OD1	1:C:415:LEU:HD11	2.18	0.43
1:A:534:ARG:NH1	4:A:1517:HOH:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ASN:HB2	4:A:1499:HOH:O	2.19	0.42
1:C:24:ARG:HD3	1:C:24:ARG:HA	1.58	0.42
1:A:322:ARG:NH2	4:A:1269:HOH:O	2.37	0.42
1:B:715:ILE:O	1:B:739:ALA:HA	2.19	0.42
1:B:748:ARG:NH2	4:B:1640:HOH:O	2.52	0.42
1:A:36:PHE:HB2	1:A:48:ILE:HD11	2.00	0.42
1:A:34:VAL:HB	1:A:45:TYR:CD1	2.55	0.42
1:B:552:PRO:HB3	1:B:574:PHE:O	2.20	0.42
1:A:552:PRO:HB3	1:A:574:PHE:O	2.19	0.41
1:B:292:GLN:HB3	1:B:293:PRO:HD2	2.01	0.41
1:B:488:LYS:NZ	4:B:1496:HOH:O	2.52	0.41
1:B:456:GLU:HA	1:B:483:GLU:O	2.21	0.41
1:B:34:VAL:HB	1:B:45:TYR:CD1	2.55	0.41
1:B:274:TYR:CE2	1:B:276:PRO:HG3	2.56	0.41
1:B:594:GLY:C	1:B:608:ARG:HB3	2.46	0.41
1:A:34:VAL:HB	1:A:45:TYR:CG	2.56	0.41
1:A:245:THR:HG22	1:A:275:ASP:O	2.20	0.41
1:B:631:GLU:HG2	1:B:633:VAL:HG12	2.03	0.41
1:A:534:ARG:HG2	1:A:557:ASP:HB3	2.02	0.40
1:B:419:ASN:ND2	4:B:1381:HOH:O	2.55	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	756/776 (97%)	729 (96%)	25 (3%)	2 (0%)	36	35
1	B	754/776 (97%)	726 (96%)	25 (3%)	3 (0%)	30	27
1	C	757/776 (98%)	729 (96%)	26 (3%)	2 (0%)	36	35
All	All	2267/2328 (97%)	2184 (96%)	76 (3%)	7 (0%)	36	35

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	736	GLN
1	B	736	GLN
1	C	736	GLN
1	B	735	GLY
1	C	735	GLY
1	A	734	ALA
1	B	511	GLY

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	621/637 (98%)	610 (98%)	11 (2%)	51	58
1	B	615/637 (96%)	599 (97%)	16 (3%)	40	44
1	C	620/637 (97%)	606 (98%)	14 (2%)	44	49
All	All	1856/1911 (97%)	1815 (98%)	41 (2%)	45	50

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	VAL
1	A	174	HIS
1	A	215	VAL
1	A	310	LEU
1	A	351	THR
1	A	388	ARG
1	A	390	LEU
1	A	428	LYS
1	A	516	LEU
1	A	720	LEU
1	A	736	GLN
1	B	61	VAL
1	B	148	LEU
1	B	232	VAL

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Mol	Chain	Res	Type
1	B	240	LYS
1	B	294	ASP
1	B	319	THR
1	B	322	ARG
1	B	351	THR
1	B	374	LEU
1	B	447	GLU
1	B	469	THR
1	B	483	GLU
1	B	608	ARG
1	B	646	GLU
1	B	669	LEU
1	B	736	GLN
1	C	24	ARG
1	C	146	VAL
1	C	148	LEU
1	C	158	SER
1	C	231	GLN
1	C	232	VAL
1	C	240	LYS
1	C	322	ARG
1	C	351	THR
1	C	390	LEU
1	C	633	VAL
1	C	636	SER
1	C	736	GLN
1	C	750	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	174	HIS
1	A	176	GLN
1	A	262	ASN
1	A	280	ASN
1	A	327	ASN
1	A	424	GLN
1	A	451	ASN
1	A	681	HIS
1	A	692	ASN
1	B	292	GLN

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Mol	Chain	Res	Type
1	B	328	ASN
1	B	419	ASN
1	B	501	ASN
1	B	725	ASN
1	C	20	GLN
1	C	165	ASN
1	C	231	GLN
1	C	262	ASN
1	C	280	ASN
1	C	292	GLN
1	C	327	ASN
1	C	402	ASN
1	C	481	HIS
1	C	725	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 ⓘ

6 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	D	1	2	12,12,12	0.53	0	17,17,17	0.41	0
2	GAL	D	2	2	11,11,12	0.59	0	15,15,17	0.67	0
2	GLC	E	1	2	12,12,12	0.47	0	17,17,17	0.62	0
2	GAL	E	2	2	11,11,12	0.55	0	15,15,17	0.58	0
2	GLC	F	1	2	12,12,12	0.53	0	17,17,17	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GAL	F	2	2	11,11,12	0.56	0	15,15,17	0.62	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	D	1	2	-	2/2/22/22	0/1/1/1
2	GAL	D	2	2	-	0/2/19/22	0/1/1/1
2	GLC	E	1	2	-	0/2/22/22	0/1/1/1
2	GAL	E	2	2	-	2/2/19/22	0/1/1/1
2	GLC	F	1	2	-	1/2/22/22	0/1/1/1
2	GAL	F	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

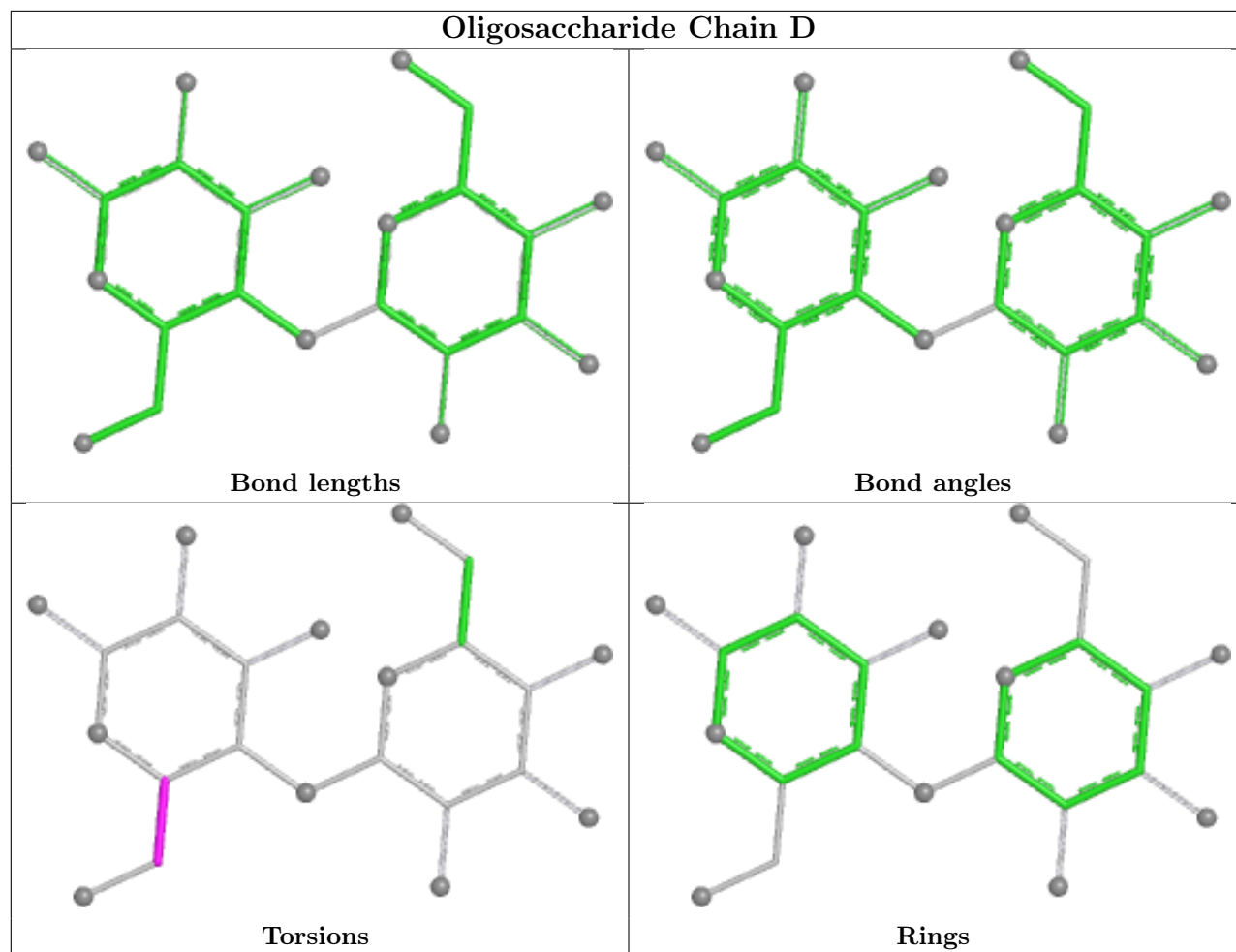
Mol	Chain	Res	Type	Atoms
2	D	1	GLC	O5-C5-C6-O6
2	D	1	GLC	C4-C5-C6-O6
2	F	1	GLC	O5-C5-C6-O6
2	E	2	GAL	C4-C5-C6-O6
2	E	2	GAL	O5-C5-C6-O6

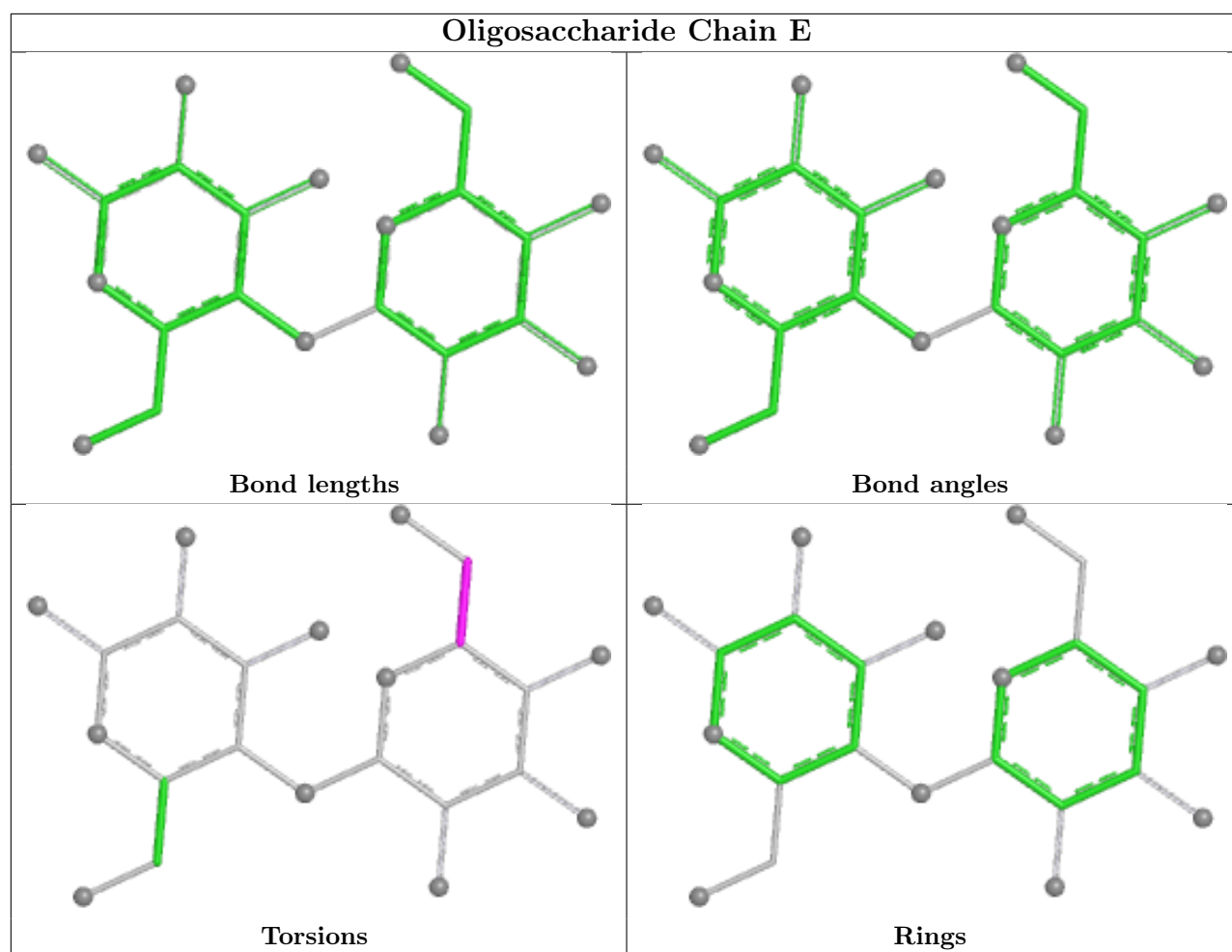
There are no ring outliers.

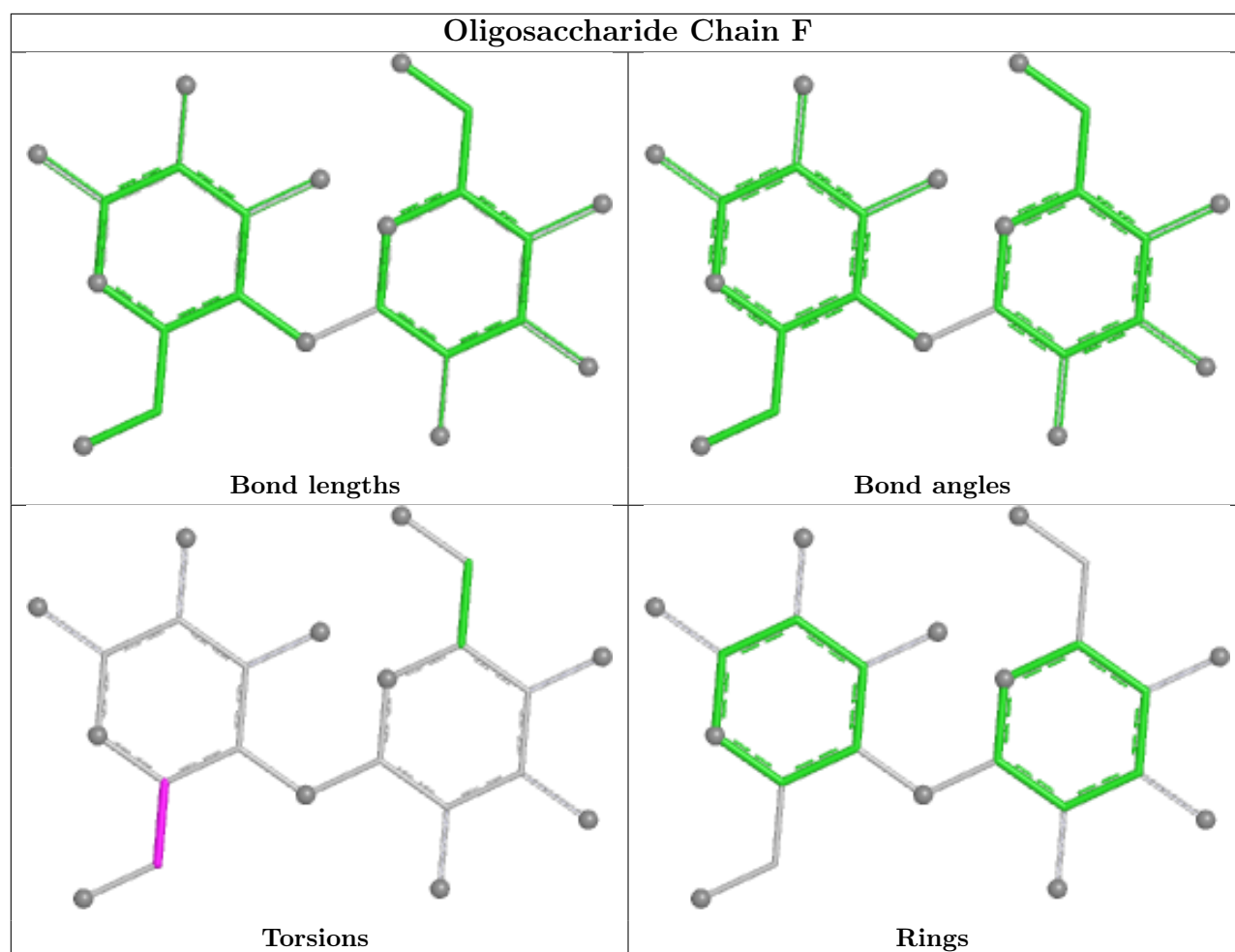
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	GLC	1	0
2	D	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.







5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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	758/776 (97%)	-0.21	8 (1%) 78 77	20, 29, 43, 63	1 (0%)
1	B	756/776 (97%)	-0.41	4 (0%) 87 87	16, 25, 39, 56	0
1	C	759/776 (97%)	-0.41	1 (0%) 92 91	18, 25, 40, 56	0
All	All	2273/2328 (97%)	-0.35	13 (0%) 85 85	16, 27, 41, 63	1 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	735	GLY	8.2
1	B	735	GLY	6.6
1	C	735	GLY	6.5
1	B	417	ASN	2.9
1	B	469	THR	2.5
1	A	310	LEU	2.5
1	A	13	THR	2.3
1	A	314	ASN	2.3
1	B	314	ASN	2.2
1	A	362	SER	2.1
1	A	62	GLY	2.1
1	A	312	ILE	2.1
1	A	16	LEU	2.1

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

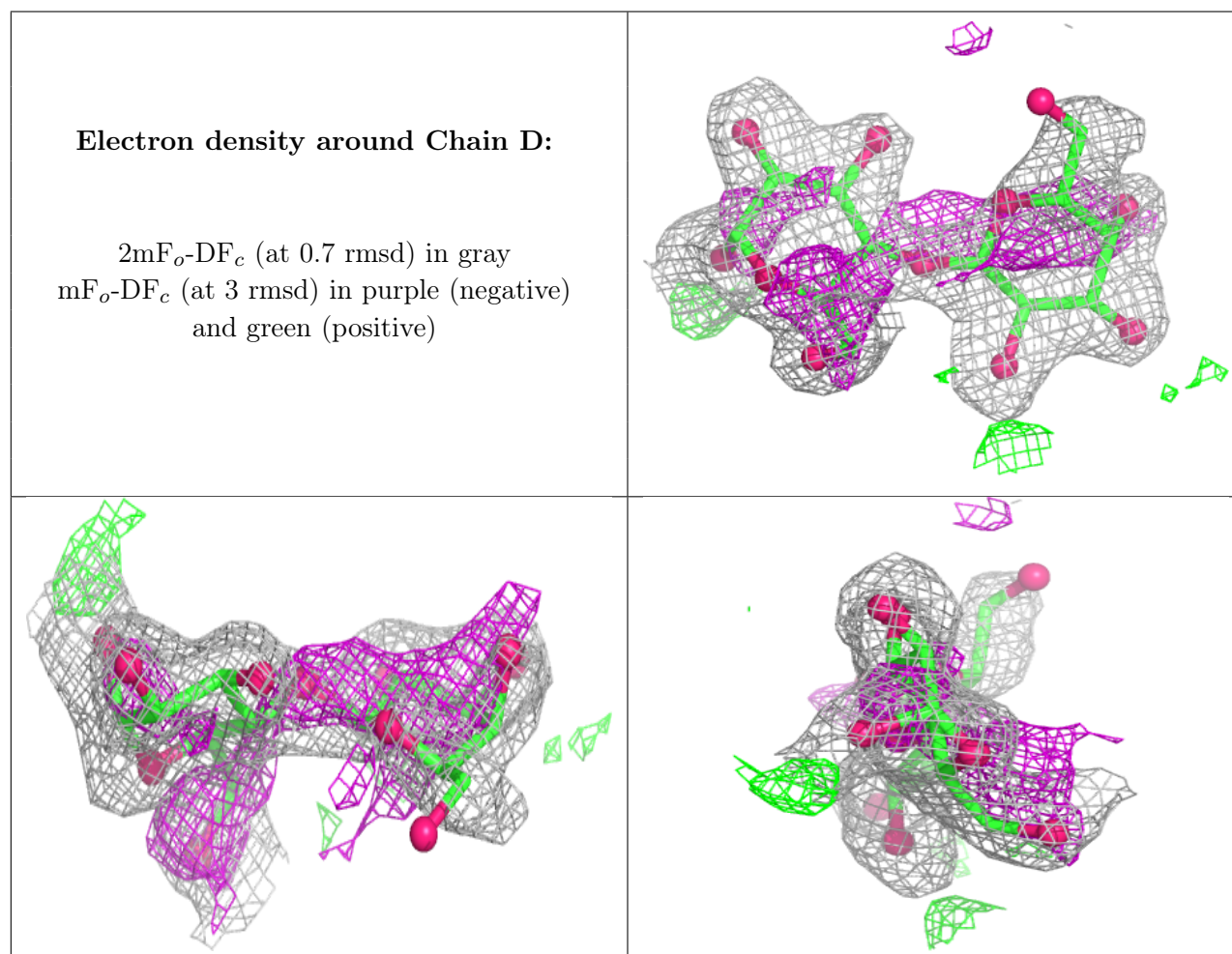
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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.

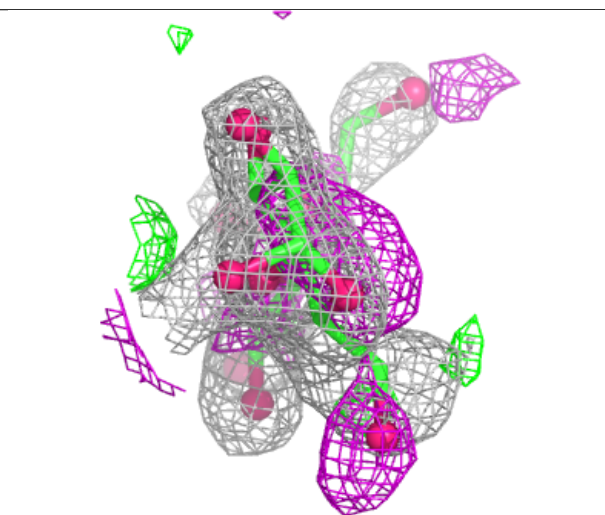
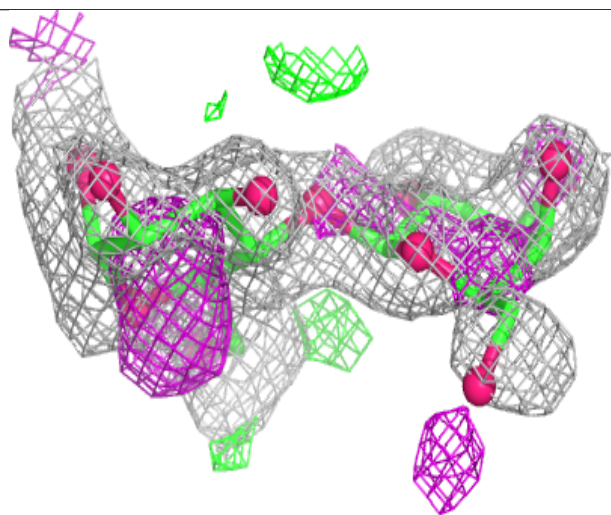
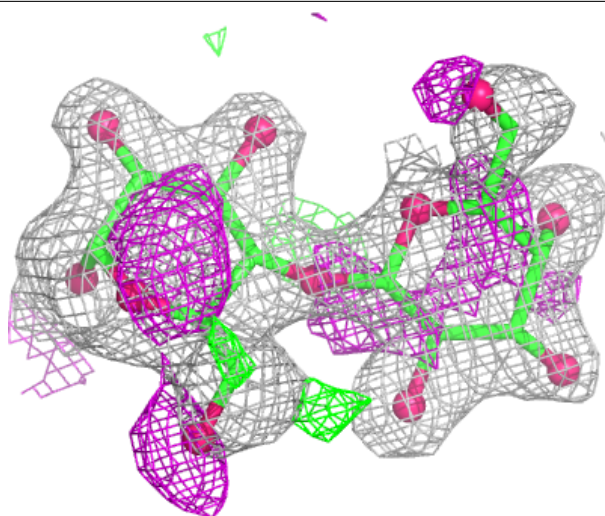
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GAL	D	2	11/12	0.72	0.16	43,53,60,63	0
2	GLC	E	1	12/12	0.76	0.14	40,44,50,52	0
2	GLC	F	1	12/12	0.77	0.14	40,46,51,51	0
2	GLC	D	1	12/12	0.80	0.13	40,48,52,53	0
2	GAL	E	2	11/12	0.81	0.14	44,52,57,59	0
2	GAL	F	2	11/12	0.81	0.13	41,51,55,56	0

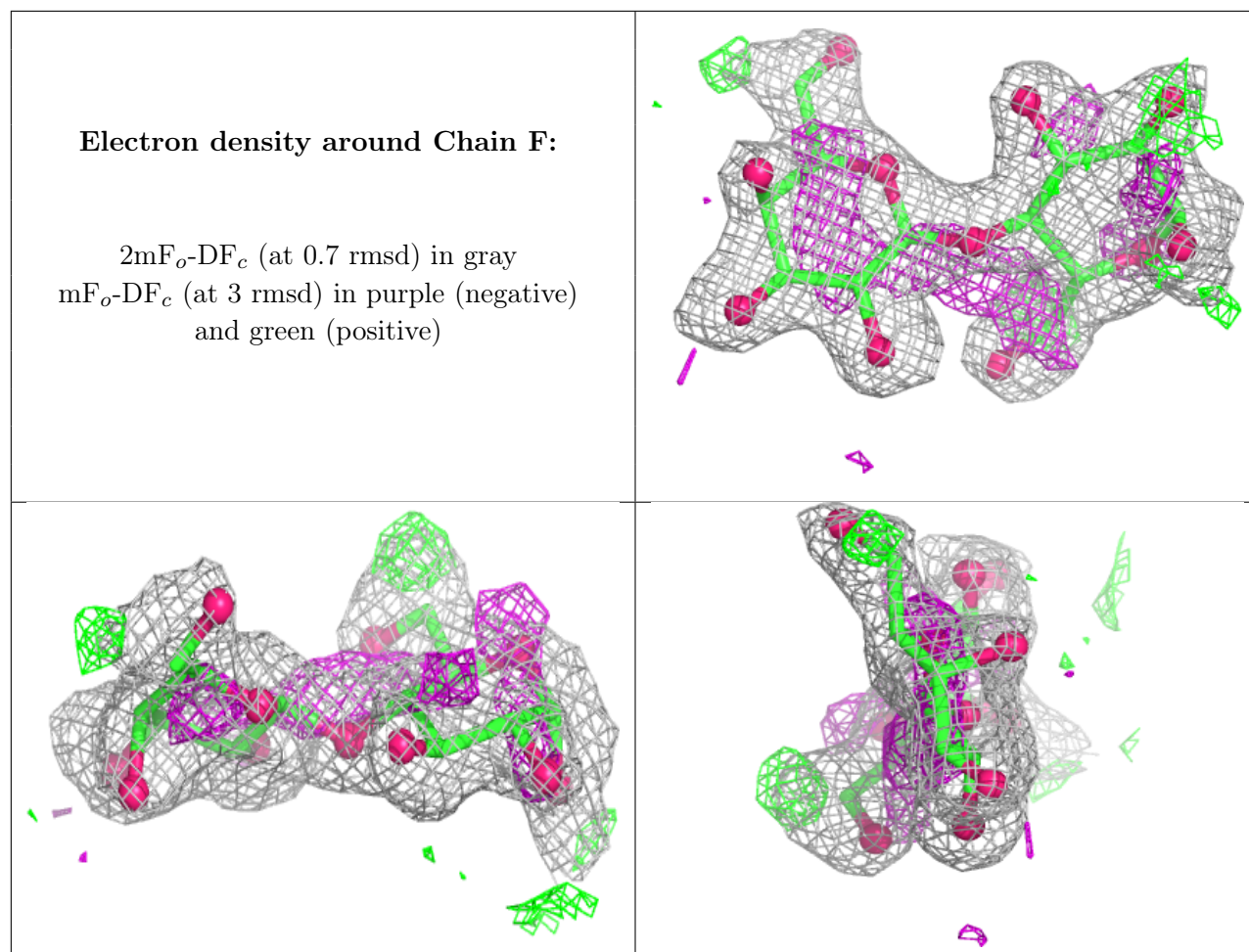
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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)





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
3	ZN	A	802[A]	1/1	0.98	0.06	45,45,45,45	1

6.5 Other polymers [i](#)

There are no such residues in this entry.