



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:49 PM UTC

PDB ID : 4KYT / pdb_00004kyt
Title : The structure of superinhibitory phospholamban bound to the calcium pump SERCA1a
Authors : Hurley, T.D.; Akin, B.L.; Jones, L.R.
Deposited on : 2013-05-29
Resolution : 2.83 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

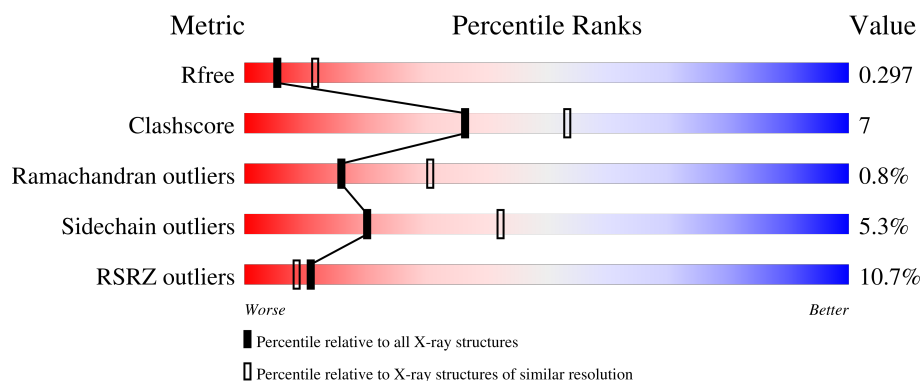
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.83 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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	994	9% 79% 17% ..
2	B	52	15% 52% 44% .
2	C	52	17% 25% 71% .
3	D	2	100%
3	E	2	100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7908 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 SERCA1a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	975	Total	C	N	O	S	0	0	0
			7520	4786	1262	1415	57			

- Molecule 2 is a protein called Cardiac phospholamban.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	29	Total	C	N	O	S	0	0	0
			223	148	37	34	4			
2	C	15	Total	C	N	O	S	0	0	0
			118	80	18	18	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	27	ALA	ASN	engineered mutation	UNP P61012
B	30	CYS	ASN	engineered mutation	UNP P61012
B	37	ALA	LEU	engineered mutation	UNP P61012
B	49	GLY	VAL	engineered mutation	UNP P61012
C	27	ALA	ASN	engineered mutation	UNP P61012
C	30	CYS	ASN	engineered mutation	UNP P61012
C	37	ALA	LEU	engineered mutation	UNP P61012
C	49	GLY	VAL	engineered mutation	UNP P61012

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



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

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

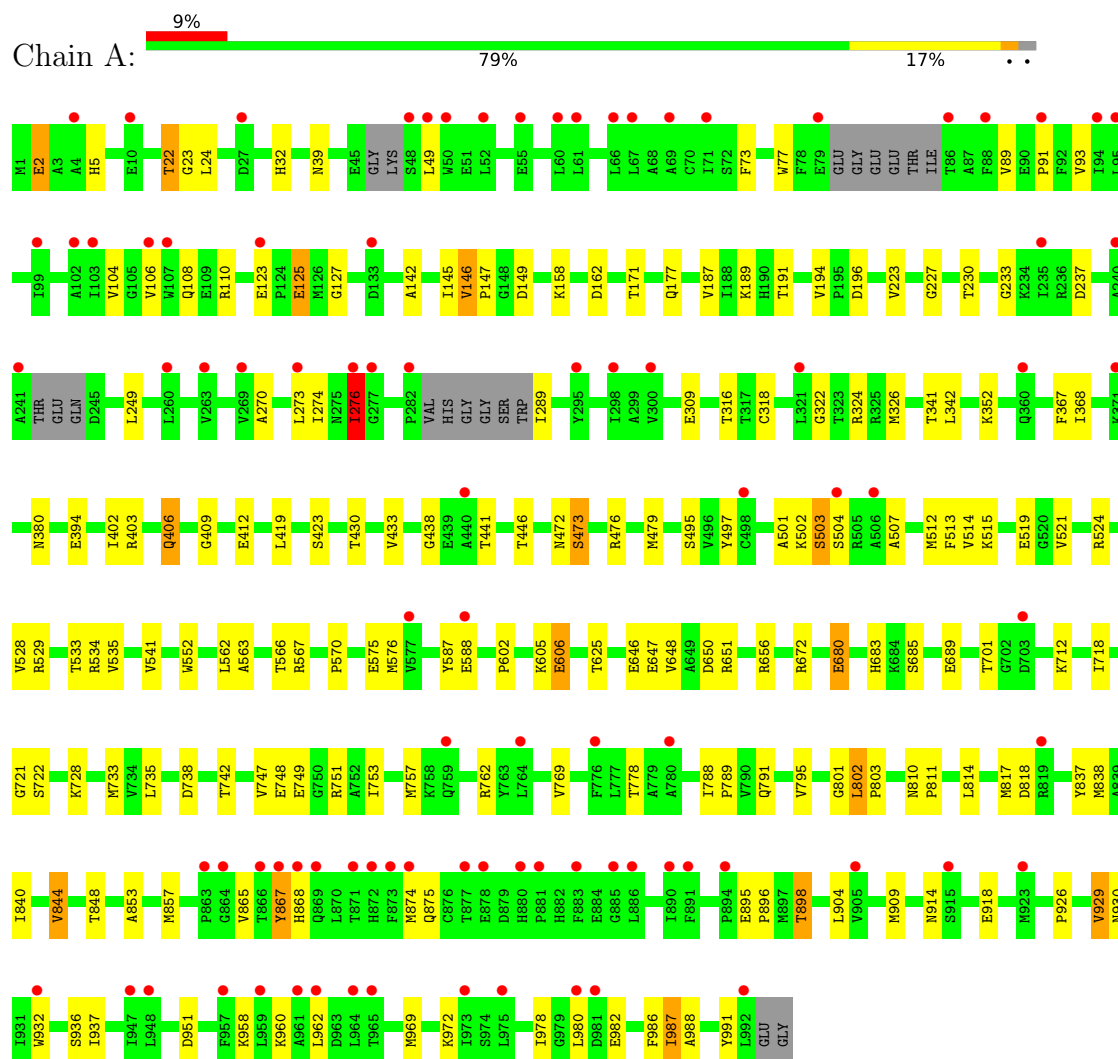
- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		

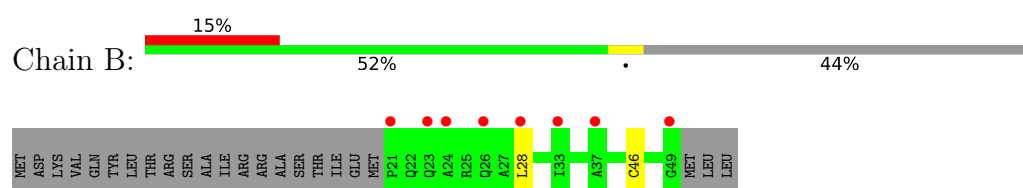
3 Residue-property plots

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.

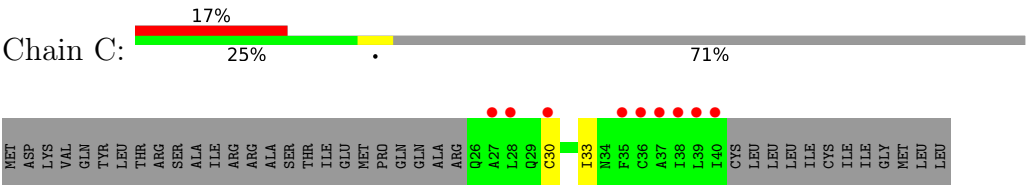
• Molecule 1: SERCA1a



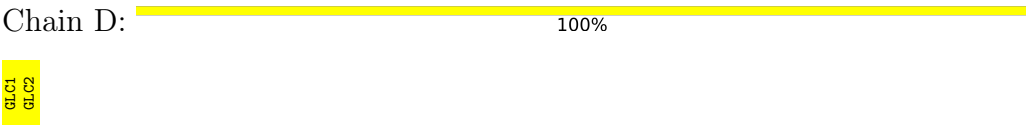
• Molecule 2: Cardiac phospholamban



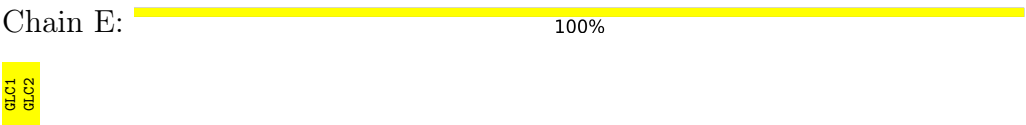
● Molecule 2: Cardiac phospholamban



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.59Å 93.09Å 316.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.83 50.00 – 2.83	Depositor EDS
% Data completeness (in resolution range)	96.7 (50.00-2.83) 96.7 (50.00-2.83)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.239 , 0.284 (Not available) , 0.297	Depositor DCC
R_{free} test set	2167 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	75.4	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7908	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.57	0/7654	0.88	7/10376 (0.1%)
2	B	0.43	0/225	0.75	0/303
2	C	0.54	0/119	0.64	0/160
All	All	0.57	0/7998	0.87	7/10839 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	194	VAL	CA-C-N	6.10	126.28	119.32
1	A	194	VAL	C-N-CA	6.10	126.28	119.32
1	A	2	GLU	N-CA-C	5.89	117.38	111.07
1	A	814	LEU	N-CA-C	5.45	117.02	111.14
1	A	575	GLU	N-CA-C	-5.22	106.86	114.12
1	A	960	LYS	N-CA-C	5.20	117.03	110.33
1	A	602	PRO	O-C-N	5.15	123.57	121.15

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7520	0	7623	114	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	223	0	246	1	0
2	C	118	0	125	1	0
3	D	23	0	21	0	0
3	E	23	0	21	0	0
4	A	1	0	0	0	0
All	All	7908	0	8036	115	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 (115) 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:748:GLU:HA	1:A:817:MET:HE3	1.31	1.11
1:A:788:ILE:HG13	1:A:789:PRO:HD2	1.53	0.91
1:A:751:ARG:HD2	1:A:817:MET:HE2	1.54	0.88
1:A:419:LEU:HD11	1:A:479:MET:SD	2.31	0.71
1:A:895:GLU:H	1:A:896:PRO:HD2	1.56	0.70
1:A:810:ASN:HB3	1:A:930:ASN:HD22	1.58	0.68
1:A:747:VAL:HG12	1:A:817:MET:HE1	1.75	0.68
1:A:810:ASN:HB2	1:A:811:PRO:HD2	1.77	0.67
1:A:909:MET:HE2	1:A:937:ILE:HA	1.78	0.66
1:A:24:LEU:HD12	1:A:149:ASP:HB3	1.79	0.64
1:A:521:VAL:CG2	1:A:563:ALA:HB3	2.28	0.64
1:A:749:GLU:O	1:A:753:ILE:HG12	1.97	0.64
1:A:811:PRO:HG3	1:A:929:VAL:HG13	1.80	0.64
1:A:521:VAL:HG21	1:A:563:ALA:HB3	1.81	0.63
1:A:751:ARG:HD2	1:A:817:MET:CE	2.27	0.63
1:A:32:HIS:CB	1:A:146:VAL:HG11	2.30	0.62
1:A:32:HIS:HB3	1:A:146:VAL:HG11	1.83	0.60
1:A:22:THR:HG22	1:A:23:GLY:O	2.02	0.59
1:A:177:GLN:HE22	1:A:189:LYS:NZ	2.00	0.59
1:A:769:VAL:HG21	1:A:838:MET:HE1	1.85	0.59
1:A:32:HIS:HB3	1:A:146:VAL:CG1	2.31	0.59
1:A:748:GLU:HA	1:A:817:MET:CE	2.20	0.59
1:A:762:ARG:HH21	1:A:918:GLU:HA	1.68	0.59
1:A:322:GLY:HA3	1:A:753:ILE:HD12	1.85	0.58
1:A:524:ARG:HD2	1:A:588:GLU:O	2.03	0.58
1:A:791:GLN:NE2	1:A:958:LYS:HG2	2.19	0.58
1:A:895:GLU:N	1:A:896:PRO:HD2	2.18	0.58
1:A:322:GLY:HA3	1:A:753:ILE:CD1	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:LEU:CD1	1:A:479:MET:SD	2.92	0.57
1:A:987:ILE:O	1:A:987:ILE:HG22	2.05	0.57
1:A:874:MET:HG3	1:A:875:GLN:HG3	1.86	0.56
1:A:368:ILE:HD13	1:A:409:GLY:HA3	1.88	0.56
1:A:104:VAL:HG11	1:A:801:GLY:HA2	1.86	0.56
1:A:227:GLY:O	1:A:230:THR:HG22	2.06	0.56
1:A:273:LEU:O	1:A:276:ILE:HG23	2.06	0.55
1:A:49:LEU:HG	1:A:110:ARG:HH12	1.72	0.55
1:A:978:ILE:O	1:A:982:GLU:HG2	2.05	0.55
1:A:501:ALA:O	1:A:503:SER:N	2.39	0.55
1:A:501:ALA:C	1:A:503:SER:H	2.14	0.55
1:A:748:GLU:CA	1:A:817:MET:HE3	2.21	0.55
1:A:352:LYS:HD3	1:A:625:THR:CG2	2.37	0.54
1:A:125:GLU:OE1	1:A:158:LYS:HE3	2.07	0.54
1:A:865:VAL:HG12	1:A:867:TYR:H	1.72	0.54
1:A:926:PRO:HD2	1:A:929:VAL:HG23	1.88	0.54
1:A:762:ARG:HG3	1:A:837:TYR:HE2	1.72	0.53
1:A:352:LYS:HD3	1:A:625:THR:HG21	1.91	0.53
1:A:650:ASP:O	1:A:672:ARG:NH1	2.42	0.53
1:A:898:THR:HG23	1:A:958:LYS:HB2	1.90	0.52
1:A:473:SER:HA	1:A:476:ARG:HB2	1.90	0.52
1:A:513:PHE:HD1	1:A:566:THR:HG22	1.75	0.51
1:A:352:LYS:CB	1:A:625:THR:HG22	2.40	0.51
1:A:909:MET:HE3	1:A:937:ILE:HG12	1.92	0.51
1:A:651:ARG:HG2	1:A:651:ARG:HH11	1.76	0.51
1:A:230:THR:HG23	1:A:233:GLY:H	1.76	0.50
1:A:177:GLN:HE22	1:A:189:LYS:HZ1	1.59	0.50
1:A:986:PHE:C	1:A:988:ALA:H	2.19	0.50
1:A:73:PHE:HB2	1:A:91:PRO:HG3	1.93	0.50
1:A:147:PRO:HA	1:A:223:VAL:HG12	1.93	0.49
1:A:762:ARG:HG3	1:A:837:TYR:CE2	2.47	0.49
1:A:24:LEU:CD1	1:A:149:ASP:HB3	2.42	0.49
1:A:352:LYS:HB3	1:A:625:THR:HG22	1.95	0.49
1:A:528:VAL:HG11	1:A:541:VAL:HG11	1.95	0.49
1:A:795:VAL:HG21	1:A:904:LEU:HD23	1.95	0.48
1:A:5:HIS:HE1	1:A:196:ASP:O	1.95	0.48
1:A:753:ILE:O	1:A:757:MET:HG2	2.13	0.48
1:A:762:ARG:NH2	1:A:918:GLU:HA	2.27	0.48
1:A:810:ASN:HB3	1:A:930:ASN:ND2	2.25	0.48
1:A:969:MET:HA	1:A:972:LYS:HG2	1.95	0.48
1:A:721:GLY:O	1:A:728:LYS:NZ	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:932:TRP:CZ3	2:B:28:LEU:HG	2.49	0.47
1:A:32:HIS:HB2	1:A:146:VAL:HG11	1.96	0.46
1:A:802:LEU:HB2	1:A:803:PRO:CD	2.45	0.46
1:A:680:GLU:HB2	1:A:683:HIS:CE1	2.51	0.46
1:A:840:ILE:HD13	1:A:980:LEU:HD23	1.98	0.46
1:A:909:MET:CE	1:A:937:ILE:HA	2.44	0.46
1:A:162:ASP:CG	1:A:230:THR:OG1	2.59	0.46
1:A:495:SER:HB3	1:A:514:VAL:HG22	1.96	0.46
1:A:735:LEU:HD22	1:A:742:THR:HB	1.98	0.45
1:A:497:TYR:HD1	1:A:512:MET:HE2	1.81	0.45
1:A:895:GLU:N	1:A:896:PRO:CD	2.80	0.45
1:A:367:PHE:HD2	1:A:552:TRP:CH2	2.34	0.45
1:A:802:LEU:HB3	1:A:936:SER:HB2	1.99	0.45
1:A:895:GLU:H	1:A:896:PRO:CD	2.27	0.45
1:A:39:ASN:HB3	1:A:142:ALA:O	2.17	0.45
1:A:722:SER:OG	1:A:738:ASP:OD2	2.31	0.44
1:A:762:ARG:NH1	1:A:914:ASN:O	2.48	0.44
1:A:802:LEU:HB2	1:A:803:PRO:HD3	2.00	0.44
1:A:533:THR:HG22	1:A:534:ARG:N	2.32	0.44
1:A:791:GLN:HE22	1:A:958:LYS:HG2	1.81	0.44
1:A:840:ILE:O	1:A:844:VAL:HG12	2.18	0.44
1:A:501:ALA:C	1:A:503:SER:N	2.76	0.43
1:A:423:SER:OG	1:A:438:GLY:HA3	2.18	0.43
1:A:646:GLU:HG2	1:A:647:GLU:O	2.19	0.42
1:A:512:MET:HE3	1:A:570:PRO:HB2	2.02	0.42
1:A:270:ALA:O	1:A:274:ILE:HG12	2.20	0.42
1:A:342:LEU:CD2	1:A:733:MET:HE1	2.49	0.42
1:A:412:GLU:CD	1:A:529:ARG:HE	2.27	0.42
1:A:795:VAL:HG21	1:A:904:LEU:CD2	2.49	0.42
1:A:853:ALA:O	1:A:857:MET:HG2	2.19	0.42
1:A:512:MET:HB2	1:A:567:ARG:HB3	2.01	0.42
1:A:127:GLY:HA3	1:A:145:ILE:HD11	2.03	0.41
1:A:515:LYS:HD2	1:A:562:LEU:HD13	2.02	0.41
1:A:576:MET:HE3	1:A:587:TYR:CG	2.55	0.41
1:A:701:THR:HA	1:A:718:ILE:O	2.20	0.41
1:A:403:ARG:O	1:A:406:GLN:HG2	2.21	0.41
1:A:605:LYS:HG2	1:A:606:GLU:OE1	2.21	0.41
1:A:788:ILE:CG1	1:A:789:PRO:HD2	2.38	0.41
2:C:30:CYS:O	2:C:33:ILE:HG22	2.21	0.41
1:A:519:GLU:CD	1:A:519:GLU:H	2.29	0.41
1:A:533:THR:HG22	1:A:534:ARG:H	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:848:THR:HG21	1:A:904:LEU:HD13	2.03	0.40
1:A:177:GLN:NE2	1:A:189:LYS:NZ	2.68	0.40
1:A:326:MET:CE	1:A:342:LEU:HD23	2.51	0.40
1:A:89:VAL:O	1:A:93:VAL:HG23	2.20	0.40
1:A:446:THR:HG23	1:A:472:ASN:ND2	2.37	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	965/994 (97%)	904 (94%)	53 (6%)	8 (1%)	16	31
2	B	27/52 (52%)	25 (93%)	2 (7%)	0	100	100
2	C	13/52 (25%)	13 (100%)	0	0	100	100
All	All	1005/1098 (92%)	942 (94%)	55 (6%)	8 (1%)	16	31

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	867	TYR
1	A	502	LYS
1	A	507	ALA
1	A	504	SER
1	A	802	LEU
1	A	987	ILE
1	A	503	SER
1	A	276	ILE

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	824/840 (98%)	779 (94%)	45 (6%)	19	40
2	B	25/46 (54%)	24 (96%)	1 (4%)	28	53
2	C	13/46 (28%)	13 (100%)	0	100	100
All	All	862/932 (92%)	816 (95%)	46 (5%)	20	42

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

Mol	Chain	Res	Type
1	A	2	GLU
1	A	22	THR
1	A	77	TRP
1	A	106	VAL
1	A	108	GLN
1	A	123	GLU
1	A	125	GLU
1	A	146	VAL
1	A	171	THR
1	A	187	VAL
1	A	191	THR
1	A	237	ASP
1	A	249	LEU
1	A	276	ILE
1	A	289	ILE
1	A	309	GLU
1	A	316	THR
1	A	318	CYS
1	A	324	ARG
1	A	341	THR
1	A	380	ASN
1	A	394	GLU
1	A	402	ILE
1	A	406	GLN
1	A	430	THR
1	A	433	VAL

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Mol	Chain	Res	Type
1	A	441	THR
1	A	473	SER
1	A	535	VAL
1	A	606	GLU
1	A	648	VAL
1	A	656	ARG
1	A	680	GLU
1	A	685	SER
1	A	689	GLU
1	A	712	LYS
1	A	778	THR
1	A	818	ASP
1	A	844	VAL
1	A	868	HIS
1	A	898	THR
1	A	929	VAL
1	A	951	ASP
1	A	962	LEU
1	A	991	TYR
2	B	46	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	108	GLN
1	A	177	GLN
1	A	201	ASN
1	A	251	GLN
1	A	330	ASN
1	A	380	ASN
1	A	406	GLN
1	A	759	GLN
1	A	768	ASN
1	A	868	HIS
1	A	920	GLN

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 ⓘ

4 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
3	GLC	D	1	3	12,12,12	0.81	0	17,17,17	1.66	4 (23%)
3	GLC	D	2	3	11,11,12	0.28	0	15,15,17	1.74	1 (6%)
3	GLC	E	1	3	12,12,12	0.65	0	17,17,17	1.40	2 (11%)
3	GLC	E	2	3	11,11,12	0.43	0	15,15,17	1.01	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLC	D	1	3	-	0/2/22/22	0/1/1/1
3	GLC	D	2	3	-	2/2/19/22	0/1/1/1
3	GLC	E	1	3	-	0/2/22/22	0/1/1/1
3	GLC	E	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	GLC	C1-O5-C5	5.99	120.21	112.19
3	E	1	GLC	C1-O5-C5	3.43	120.28	113.65
3	D	1	GLC	C1-C2-C3	3.38	117.25	110.36
3	D	1	GLC	O5-C1-C2	3.00	115.58	110.30
3	E	2	GLC	C1-O5-C5	2.53	115.58	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1	GLC	O5-C5-C4	-2.48	105.23	109.70
3	E	1	GLC	C3-C4-C5	-2.27	106.12	110.23
3	D	1	GLC	O1-C1-C2	2.08	115.01	108.98

There are no chirality outliers.

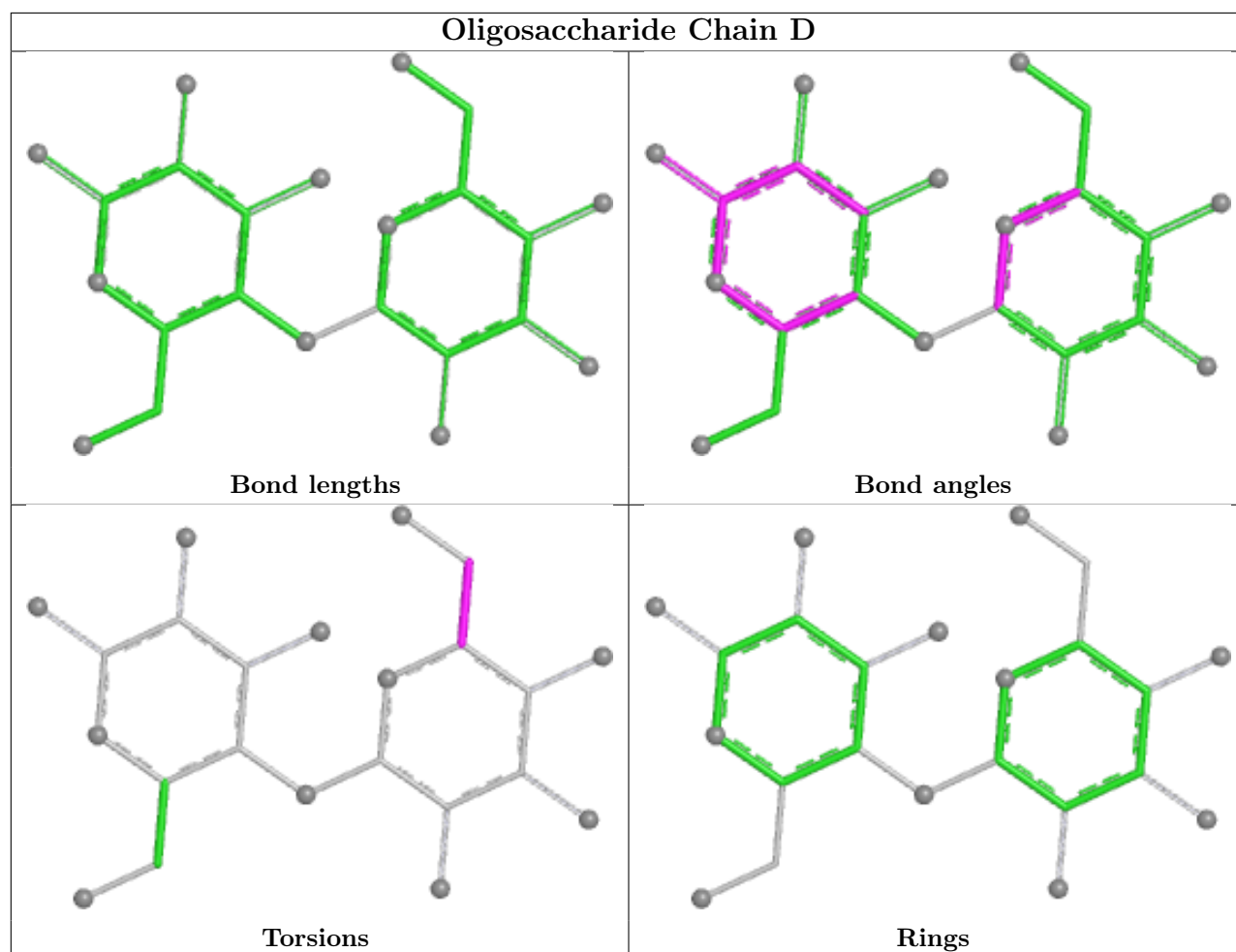
All (2) torsion outliers are listed below:

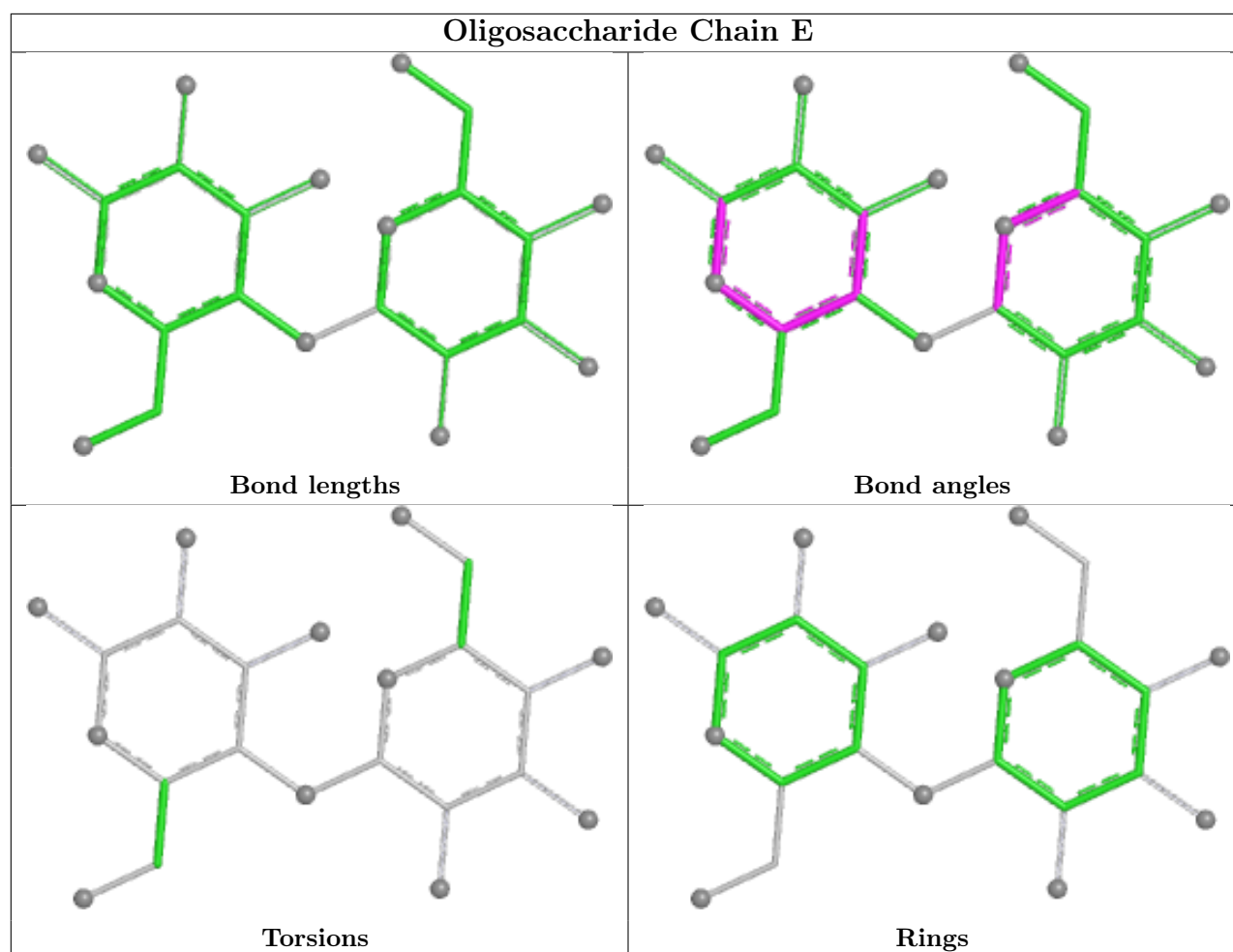
Mol	Chain	Res	Type	Atoms
3	D	2	GLC	O5-C5-C6-O6
3	D	2	GLC	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





5.6 Ligand geometry [i](#)

Of 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	975/994 (98%)	0.60	92 (9%)	14 11	44, 77, 153, 208	0
2	B	29/52 (55%)	1.74	8 (27%)	1 1	115, 128, 177, 199	0
2	C	15/52 (28%)	2.43	9 (60%)	0 0	111, 176, 205, 208	0
All	All	1019/1098 (92%)	0.66	109 (10%)	11 8	44, 80, 161, 208	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	49	GLY	6.3
1	A	49	LEU	5.1
1	A	885	GLY	4.7
1	A	881	PRO	4.7
1	A	868	HIS	4.5
1	A	975	LEU	4.5
2	B	28	LEU	4.4
1	A	981	ASP	4.4
1	A	962	LEU	4.3
1	A	890	ILE	4.2
1	A	88	PHE	4.1
2	C	27	ALA	4.0
1	A	871	THR	4.0
2	B	26	GLN	3.8
1	A	103	ILE	3.7
1	A	886	LEU	3.7
1	A	321	LEU	3.7
2	C	30	CYS	3.6
2	C	40	ILE	3.6
1	A	992	LEU	3.6
1	A	877	THR	3.6
1	A	94	ILE	3.5
1	A	276	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	24	ALA	3.4
1	A	869	GLN	3.3
2	C	38	ILE	3.2
1	A	277	GLY	3.2
1	A	703	ASP	3.1
1	A	872	HIS	3.1
1	A	759	GLN	3.1
1	A	282	PRO	3.1
1	A	107	TRP	3.0
1	A	961	ALA	3.0
1	A	298	ILE	3.0
1	A	506	ALA	3.0
1	A	295	TYR	3.0
1	A	102	ALA	3.0
2	C	37	ALA	3.0
1	A	957	PHE	3.0
1	A	947	ILE	2.9
1	A	273	LEU	2.9
1	A	948	LEU	2.9
1	A	964	LEU	2.9
1	A	48	SER	2.9
1	A	263	VAL	2.9
1	A	241	ALA	2.9
1	A	965	THR	2.9
2	B	21	PRO	2.9
1	A	883	PHE	2.9
1	A	61	LEU	2.8
1	A	95	LEU	2.8
1	A	235	ILE	2.8
1	A	819	ARG	2.7
1	A	780	ALA	2.7
1	A	980	LEU	2.7
1	A	878	GLU	2.7
1	A	588	GLU	2.7
1	A	106	VAL	2.7
1	A	440	ALA	2.6
2	B	37	ALA	2.6
1	A	55	GLU	2.6
2	C	39	LEU	2.6
2	C	36	CYS	2.6
1	A	880	HIS	2.5
1	A	67	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	269	VAL	2.5
1	A	891	PHE	2.5
2	C	35	PHE	2.5
1	A	52	LEU	2.5
1	A	66	LEU	2.5
1	A	123	GLU	2.5
1	A	360	GLN	2.5
1	A	371	LYS	2.5
1	A	300	VAL	2.4
1	A	577	VAL	2.4
1	A	60	LEU	2.4
1	A	27	ASP	2.3
1	A	79	GLU	2.3
1	A	504	SER	2.3
1	A	99	ILE	2.3
1	A	894	PRO	2.3
1	A	864	GLY	2.3
1	A	4	ALA	2.3
2	B	23	GLN	2.3
2	B	33	ILE	2.3
1	A	91	PRO	2.3
1	A	764	LEU	2.3
1	A	915	SER	2.3
1	A	866	THR	2.3
1	A	776	PHE	2.3
1	A	873	PHE	2.3
1	A	923	MET	2.3
1	A	973	ILE	2.3
1	A	86	THR	2.2
1	A	932	TRP	2.2
1	A	863	PRO	2.2
1	A	905	VAL	2.2
1	A	260	LEU	2.2
1	A	50	TRP	2.2
1	A	133	ASP	2.2
1	A	959	LEU	2.1
2	C	28	LEU	2.1
1	A	69	ALA	2.1
1	A	498	CYS	2.1
1	A	874	MET	2.1
1	A	240	ALA	2.1
1	A	71	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	867	TYR	2.0
1	A	10	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

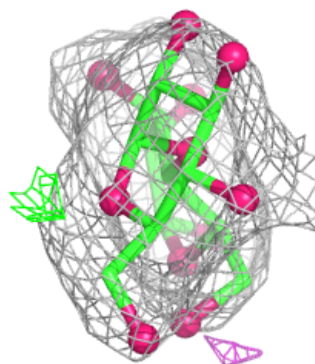
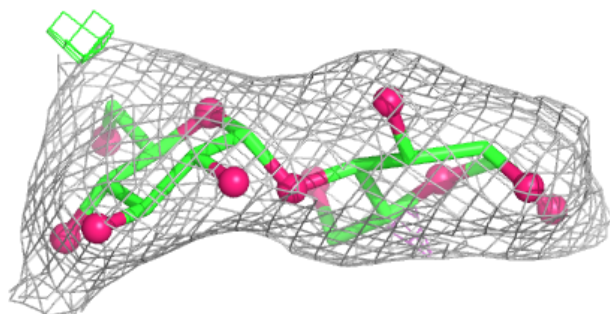
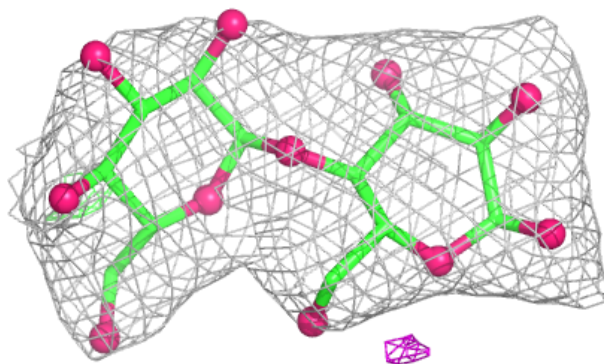
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

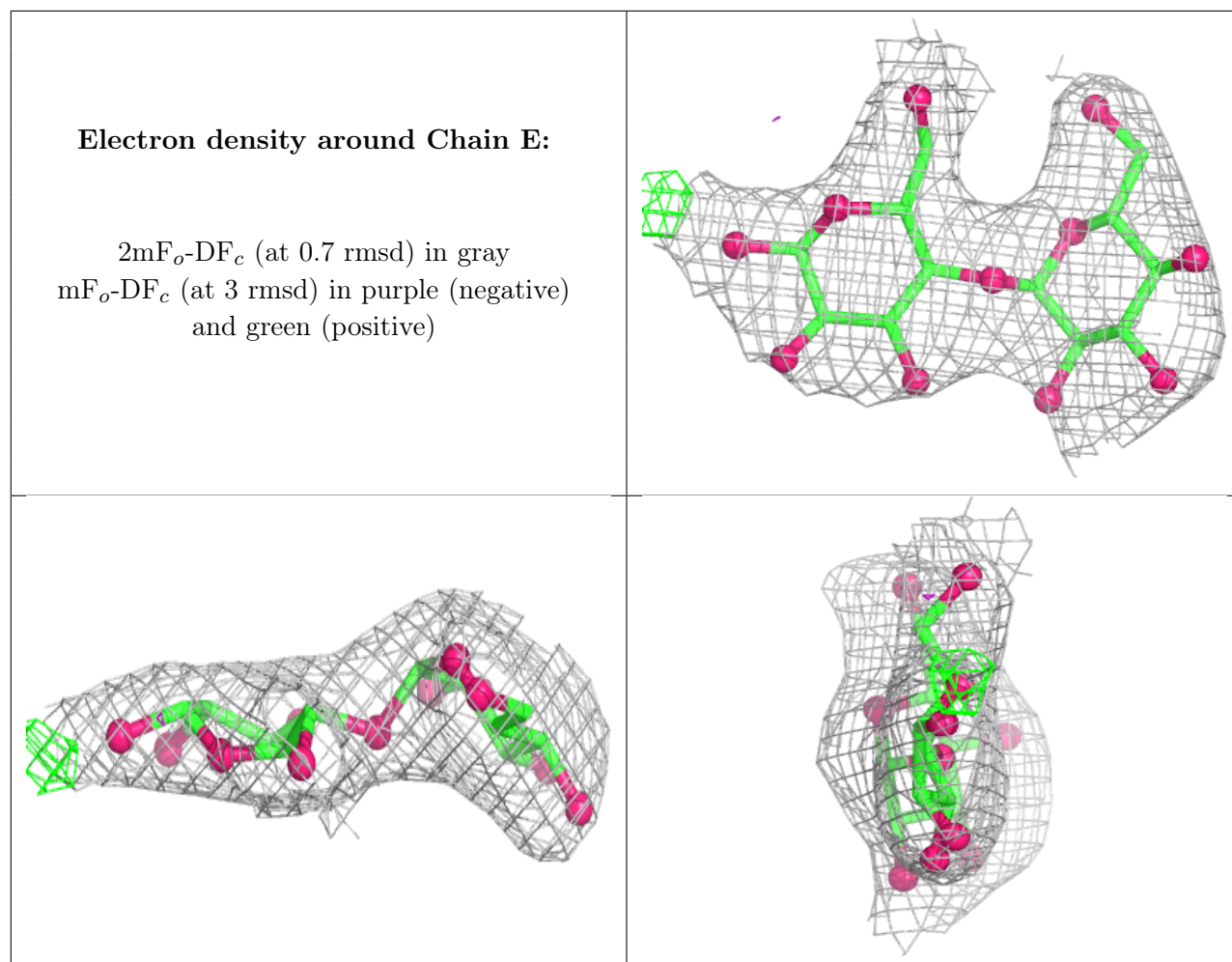
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GLC	D	2	11/12	0.87	0.10	76,79,80,80	0
3	GLC	E	2	11/12	0.87	0.09	89,90,91,91	0
3	GLC	E	1	12/12	0.90	0.09	90,90,90,90	0
3	GLC	D	1	12/12	0.92	0.07	81,82,82,83	0

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)





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	K	A	1003	1/1	0.95	0.09	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.