



Full wwPDB X-ray Structure Validation Report ⓘ

May 2, 2022 – 06:16 PM JST

PDB ID : 7ER1
Title : Crystal structure of capsid P domain of norovirus GI.3 VA115 complexed with Gala1-3Galb1-4Glc
Authors : Chen, Y.
Deposited on : 2021-05-05
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.28.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

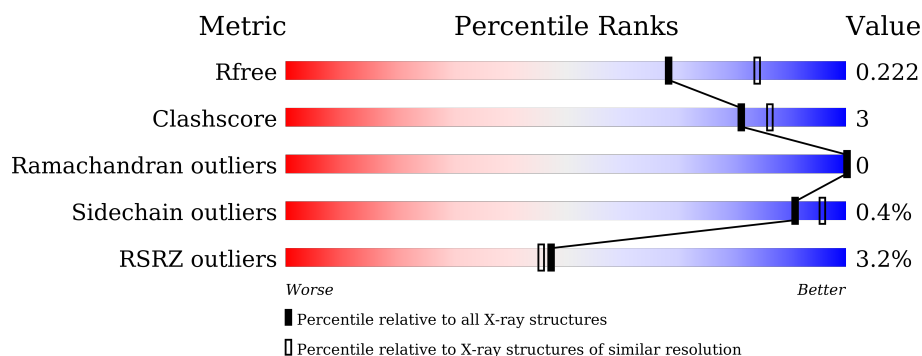
1 Overall quality at a glance

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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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	327	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 88%, grey 5%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 88% 5% 7% </div> </div>
1	B	327	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 1%, green 86%, grey 7%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 3% 86% 7% 7% </div> </div>
1	C	327	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 1%, green 89%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 89% • 8% </div> </div>
1	D	327	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 5%, orange 1%, yellow 1%, green 83%, grey 9%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 5% 83% 9% 8% </div> </div>
2	E	2	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 50%, yellow 50%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 50% 50% </div> </div>

2 Entry composition [i](#)

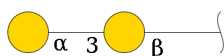
There are 3 unique types of molecules in this entry. The entry contains 9973 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 capsid P domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2311	1469	394	437	11			
1	B	303	Total	C	N	O	S	0	0	0
			2311	1469	394	437	11			
1	C	300	Total	C	N	O	S	0	0	0
			2290	1457	391	431	11			
1	D	300	Total	C	N	O	S	0	0	0
			2287	1454	391	431	11			

- Molecule 2 is an oligosaccharide called alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose.



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

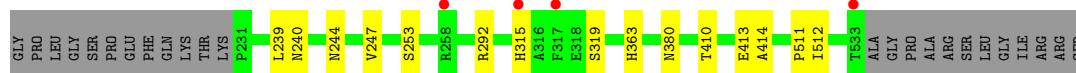
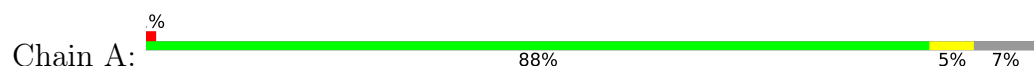
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	193	Total	O	0	0
			193	193		
3	B	171	Total	O	0	0
			171	171		
3	C	225	Total	O	0	0
			225	225		
3	D	162	Total	O	0	0
			162	162		

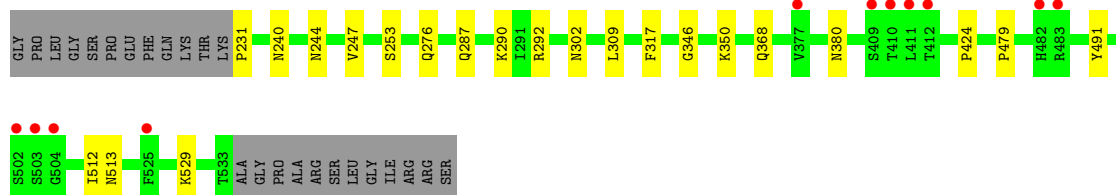
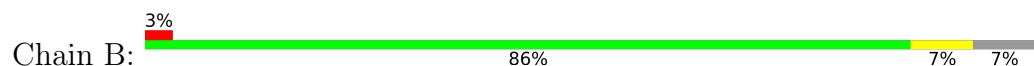
3 Residue-property plots [i](#)

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.

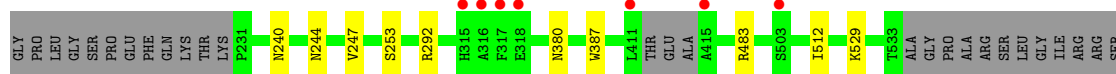
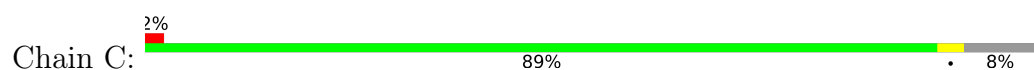
- Molecule 1: capsid P domain



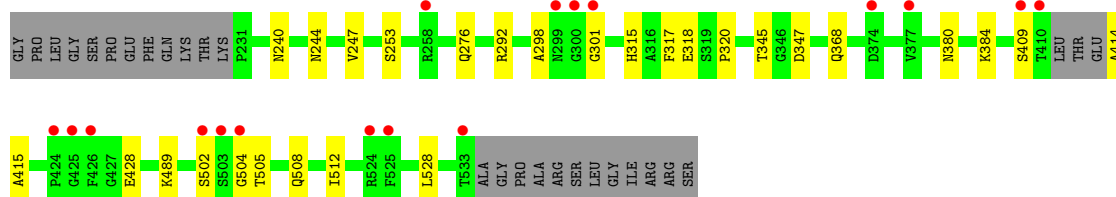
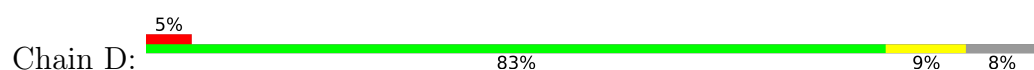
- Molecule 1: capsid P domain



- Molecule 1: capsid P domain



- Molecule 1: capsid P domain



- Molecule 2: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose

Chain E:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.29Å 59.64Å 91.42Å 102.28° 96.72° 109.77°	Depositor
Resolution (Å)	41.29 – 2.20 41.25 – 2.20	Depositor EDS
% Data completeness (in resolution range)	93.4 (41.29-2.20) 93.5 (41.25-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.81 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.178 , 0.220 0.184 , 0.222	Depositor DCC
R_{free} test set	2621 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.518	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9973	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.72% 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: GLA, GAL

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	0.64	0/2381	0.76	0/3255
1	B	0.64	0/2381	0.76	0/3255
1	C	0.62	0/2359	0.76	0/3223
1	D	0.65	0/2356	0.78	1/3219 (0.0%)
All	All	0.64	0/9477	0.76	1/12952 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	504	GLY	N-CA-C	5.80	127.60	113.10

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	2311	0	2218	10	0
1	B	2311	0	2218	15	0
1	C	2290	0	2199	7	0
1	D	2287	0	2193	18	0
2	E	23	0	21	0	0
3	A	193	0	0	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	171	0	0	2	0
3	C	225	0	0	2	0
3	D	162	0	0	2	0
All	All	9973	0	8849	46	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 3.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:384:LYS:HB3	3:D:746:HOH:O	1.40	1.18
1:A:315:HIS:HD2	3:A:757:HOH:O	1.32	1.12
1:C:483:ARG:HD2	1:D:318:GLU:HG3	1.75	0.66
1:A:292:ARG:HE	1:A:380:ASN:HD21	1.44	0.65
1:D:292:ARG:HE	1:D:380:ASN:HD21	1.45	0.65
1:B:292:ARG:HE	1:B:380:ASN:HD21	1.45	0.64
1:C:292:ARG:HE	1:C:380:ASN:HD21	1.46	0.64
1:D:320:PRO:HB3	1:D:415:ALA:HB1	1.82	0.61
1:A:319:SER:O	1:A:363:HIS:HD2	1.82	0.61
1:B:287:GLN:HG3	1:B:309:LEU:HD22	1.84	0.59
1:A:240:ASN:HB3	1:A:512:ILE:HG23	1.89	0.56
1:B:479:PRO:HG3	1:B:513:ASN:OD1	2.07	0.55
1:C:240:ASN:HB3	1:C:512:ILE:HG23	1.89	0.54
1:B:529:LYS:HE3	3:B:729:HOH:O	2.09	0.52
1:D:240:ASN:HB3	1:D:512:ILE:HG23	1.90	0.51
3:A:743:HOH:O	1:B:276:GLN:HG2	2.10	0.51
1:B:240:ASN:HB3	1:B:512:ILE:HG23	1.91	0.50
1:D:505:THR:HB	1:D:508:GLN:HB3	1.93	0.50
1:B:424:PRO:HG3	1:B:491:TYR:CZ	2.46	0.50
1:B:346:GLY:HA3	1:C:387:TRP:CH2	2.47	0.49
1:D:345:THR:HG22	1:D:347:ASP:H	1.78	0.48
1:D:384:LYS:CB	3:D:746:HOH:O	2.23	0.48
1:B:290:LYS:HB3	1:B:309:LEU:HD11	1.95	0.47
3:C:731:HOH:O	1:D:318:GLU:HG2	2.15	0.47
1:B:302:ASN:O	1:B:368:GLN:HG2	2.16	0.46
1:C:253:SER:HA	1:C:512:ILE:HD13	1.98	0.46
1:A:253:SER:HA	1:A:512:ILE:HD13	1.98	0.46
1:B:231:PRO:N	3:B:607:HOH:O	2.49	0.45
1:C:483:ARG:CD	1:D:318:GLU:HG3	2.46	0.45
1:B:479:PRO:HG3	1:B:513:ASN:CG	2.37	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:ASN:HB3	1:B:247:VAL:O	2.18	0.44
1:D:489:LYS:HG3	1:D:528:LEU:HD21	2.00	0.43
3:C:783:HOH:O	1:D:276:GLN:HG2	2.17	0.43
1:D:253:SER:HA	1:D:512:ILE:HD13	2.00	0.43
1:D:298:ALA:O	1:D:301:GLY:O	2.37	0.43
1:C:244:ASN:HB3	1:C:247:VAL:O	2.19	0.43
1:D:428:GLU:OE2	1:D:489:LYS:CE	2.67	0.42
1:A:511:PRO:HD3	1:B:317:PHE:CE1	2.54	0.42
1:D:244:ASN:HB3	1:D:247:VAL:O	2.19	0.42
1:B:253:SER:HA	1:B:512:ILE:HD13	2.02	0.41
1:A:410:THR:HG22	1:A:414:ALA:HB3	2.02	0.41
1:D:409:SER:OG	1:D:414:ALA:HA	2.20	0.41
1:A:244:ASN:HB3	1:A:247:VAL:O	2.20	0.41
1:A:413:GLU:OE1	3:A:601:HOH:O	2.21	0.40
1:D:315:HIS:HB3	1:D:317:PHE:CE2	2.57	0.40
1:A:239:LEU:HD23	1:A:239:LEU:HA	1.96	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	301/327 (92%)	294 (98%)	7 (2%)	0	100	100
1	B	301/327 (92%)	294 (98%)	7 (2%)	0	100	100
1	C	296/327 (90%)	289 (98%)	7 (2%)	0	100	100
1	D	296/327 (90%)	290 (98%)	6 (2%)	0	100	100
All	All	1194/1308 (91%)	1167 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	254/272 (93%)	254 (100%)	0	100	100
1	B	254/272 (93%)	253 (100%)	1 (0%)	91	96
1	C	252/272 (93%)	251 (100%)	1 (0%)	91	96
1	D	251/272 (92%)	249 (99%)	2 (1%)	81	90
All	All	1011/1088 (93%)	1007 (100%)	4 (0%)	91	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	350	LYS
1	C	529	LYS
1	D	368	GLN
1	D	502	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	363	HIS
1	A	378	ASN
1	A	380	ASN
1	B	315	HIS
1	B	380	ASN
1	C	363	HIS
1	C	380	ASN
1	C	416	GLN
1	C	527	GLN
1	D	368	GLN
1	D	380	ASN
1	D	475	HIS
1	D	508	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 ⓘ

2 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	GAL	E	1	2	12,12,12	0.54	0	17,17,17	0.64	0
2	GLA	E	2	2	11,11,12	0.38	0	15,15,17	1.40	1 (6%)

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

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	GLA	O5-C5-C6	4.29	113.93	107.20

There are no chirality outliers.

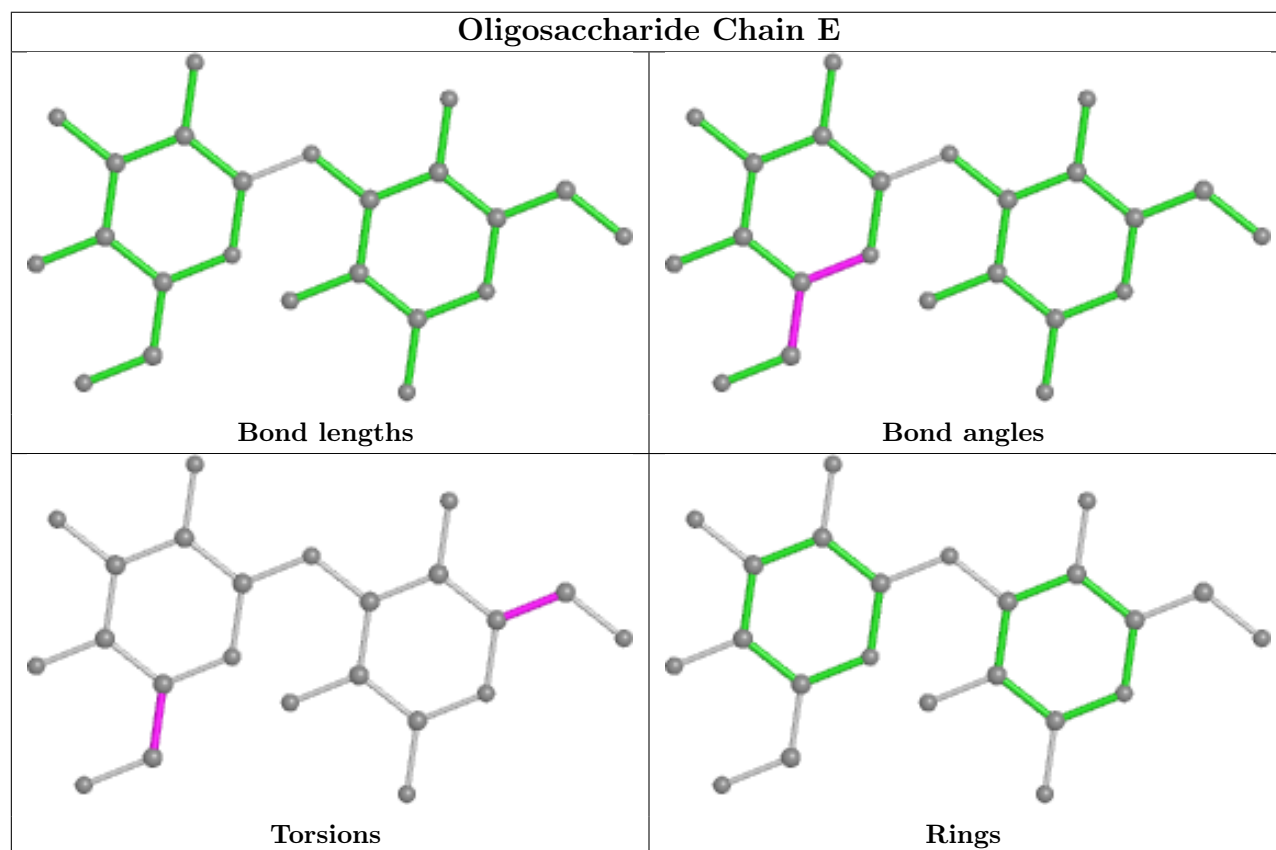
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	GLA	O5-C5-C6-O6
2	E	1	GAL	C4-C5-C6-O6
2	E	2	GLA	C4-C5-C6-O6
2	E	1	GAL	O5-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](#)

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 ⓘ

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	303/327 (92%)	-0.24	4 (1%) 77 75	13, 23, 47, 64	0
1	B	303/327 (92%)	-0.16	11 (3%) 42 41	12, 23, 50, 70	0
1	C	300/327 (91%)	-0.37	7 (2%) 60 58	12, 21, 43, 69	0
1	D	300/327 (91%)	0.10	17 (5%) 23 22	14, 28, 55, 84	0
All	All	1206/1308 (92%)	-0.17	39 (3%) 47 45	12, 24, 51, 84	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	503	SER	6.9
1	B	411	LEU	6.6
1	D	525	PHE	6.1
1	A	317	PHE	5.6
1	C	415	ALA	5.5
1	D	410	THR	5.1
1	B	525	PHE	4.7
1	D	426	PHE	4.7
1	D	299	ASN	4.6
1	C	317	PHE	4.2
1	D	503	SER	3.9
1	D	504	GLY	3.9
1	C	503	SER	3.8
1	D	533	THR	3.7
1	B	410	THR	3.3
1	C	411	LEU	3.2
1	D	301	GLY	3.1
1	B	502	SER	3.0
1	B	409	SER	2.9
1	D	258	ARG	2.9
1	B	482	HIS	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	412	THR	2.9
1	D	300	GLY	2.8
1	D	409	SER	2.8
1	B	504	GLY	2.7
1	A	258	ARG	2.7
1	D	374	ASP	2.6
1	D	424	PRO	2.6
1	D	502	SER	2.6
1	B	377	VAL	2.4
1	D	524	ARG	2.4
1	C	316	ALA	2.4
1	A	533	THR	2.3
1	D	425	GLY	2.3
1	A	315	HIS	2.3
1	D	377	VAL	2.2
1	B	483	ARG	2.1
1	C	315	HIS	2.1
1	C	318	GLU	2.1

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

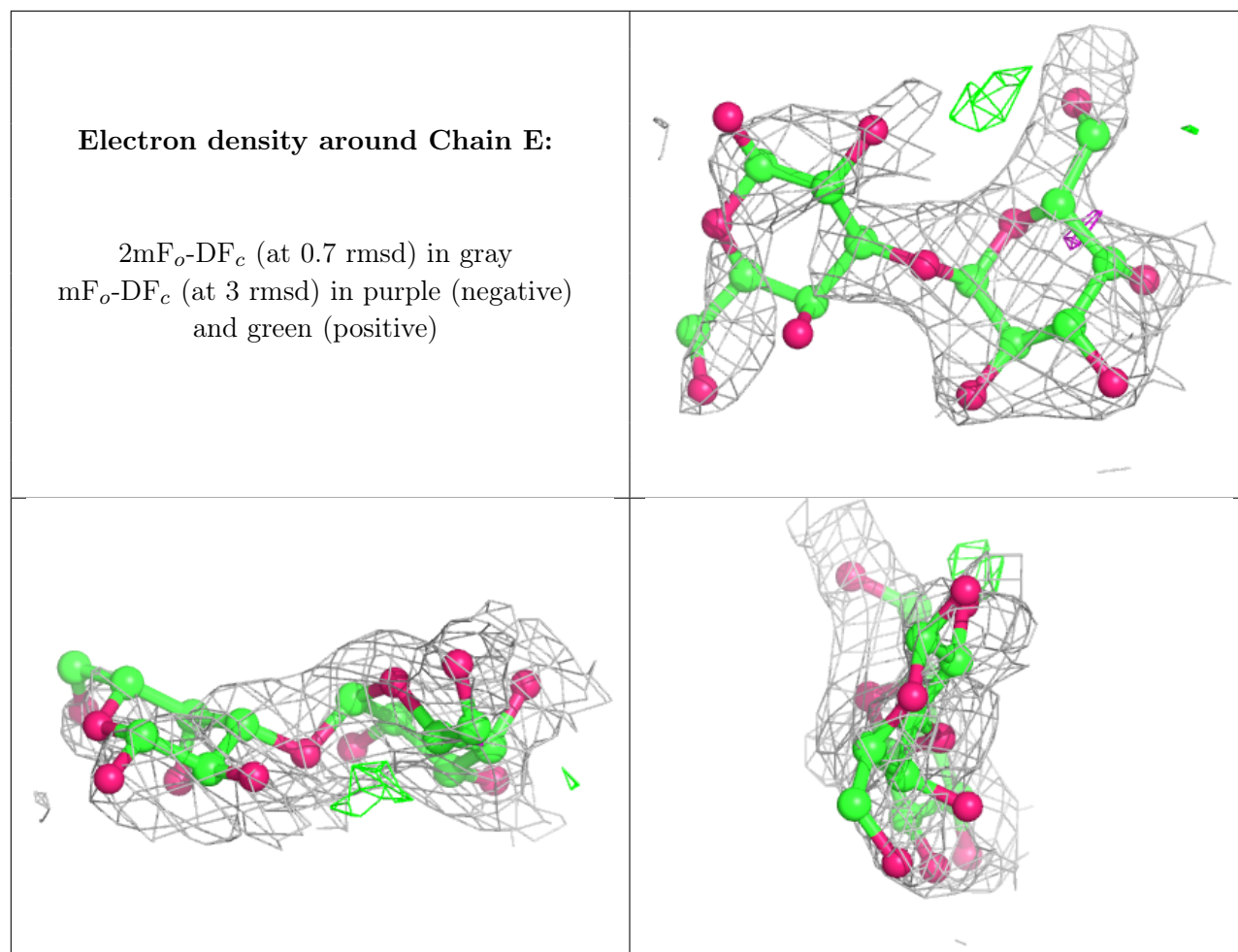
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [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(\AA^2)	Q<0.9
2	GAL	E	1	12/12	0.56	0.39	58,71,74,76	0
2	GLA	E	2	11/12	0.85	0.19	41,46,50,52	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.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.