



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:20 PM UTC

PDB ID : 6LZW / pdb_00006lzw
Title : W513A mutant of chitin-specific solute binding protein from *Vibrio harveyi* co-crystallized with chitobiose.
Authors : Kitaoku, Y.; Ubonbal, P.; Tran, L.T.; Robinson, R.C.; Suginta, W.
Deposited on : 2020-02-19
Resolution : 1.90 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

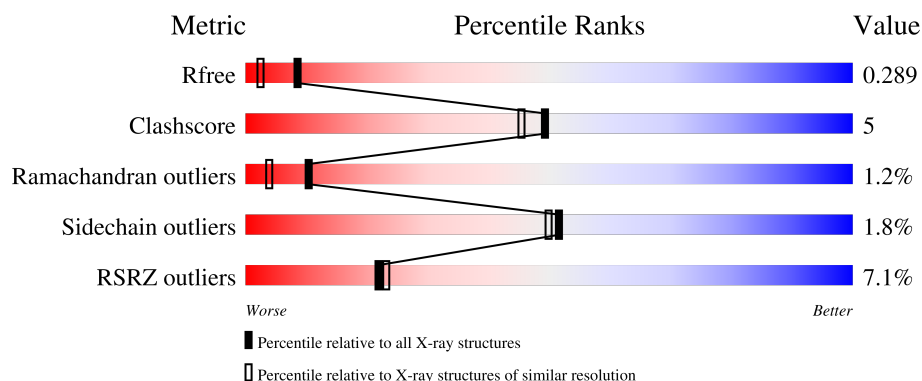
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	538	7% 83% 13% ..
2	G	2	50% 50%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4330 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.

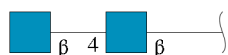
- Molecule 1 is a protein called Peptide ABC transporter, periplasmic peptide-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	524	4161	2659	696	795	11	0	3	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	513	ALA	TRP	engineered mutation	UNP D0XC84
A	531	HIS	-	expression tag	UNP D0XC84
A	532	HIS	-	expression tag	UNP D0XC84
A	533	HIS	-	expression tag	UNP D0XC84
A	534	HIS	-	expression tag	UNP D0XC84
A	535	HIS	-	expression tag	UNP D0XC84
A	536	HIS	-	expression tag	UNP D0XC84

- Molecule 2 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
			Total	C	N	O			
2	G	2	29	16	2	11	0	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	133	Total	O	0	0
			133	133		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.68Å 57.11Å 81.52Å 90.00° 101.70° 90.00°	Depositor
Resolution (Å)	26.89 – 1.90 26.89 – 1.90	Depositor EDS
% Data completeness (in resolution range)	87.6 (26.89-1.90) 88.6 (26.89-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.23	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.227 , 0.290 (Not available) , 0.289	Depositor DCC
R_{free} test set	1993 reflections (4.44%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.676	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4330	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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: CL, MG, NAG, CA, EDO

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	0.52	0/4279	0.90	11/5836 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	415	ASP	CA-C-N	-7.91	112.76	120.83
1	A	415	ASP	C-N-CA	-7.91	112.76	120.83
1	A	198	VAL	N-CA-C	7.53	115.66	107.60
1	A	19	ASN	CA-C-N	6.83	126.79	119.28
1	A	19	ASN	C-N-CA	6.83	126.79	119.28
1	A	131	VAL	CA-C-N	-6.78	112.00	119.19
1	A	131	VAL	C-N-CA	-6.78	112.00	119.19
1	A	66	VAL	N-CA-C	6.19	118.30	108.89
1	A	164	GLY	CA-C-N	5.58	125.25	119.05
1	A	164	GLY	C-N-CA	5.58	125.25	119.05
1	A	115	VAL	N-CA-C	5.05	119.84	109.34

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	4161	0	3890	44	0
2	G	29	0	27	0	0
3	A	4	0	6	0	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	133	0	0	2	0
All	All	4330	0	3923	44	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 5.

All (44) 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:114:LYS:O	1:A:116:ASN:N	2.14	0.78
1:A:145:VAL:HG21	1:A:161:VAL:HG21	1.72	0.71
1:A:116:ASN:HB3	1:A:119:GLN:HB2	1.71	0.71
1:A:66:VAL:HG23	1:A:122:PHE:HB2	1.72	0.70
1:A:9:LYS:HD2	1:A:28:HIS:CE1	2.34	0.63
1:A:59[B]:MET:HG2	1:A:66:VAL:HG12	1.80	0.61
1:A:254:LYS:HE2	1:A:441:PHE:HB3	1.84	0.60
1:A:40:VAL:HG13	1:A:517:PRO:HB2	1.85	0.59
1:A:104:GLY:O	1:A:105:ILE:HB	2.04	0.58
1:A:142:PRO:HG3	1:A:161:VAL:HB	1.90	0.54
1:A:10:GLU:HG3	7:A:783:HOH:O	2.08	0.54
1:A:65:SER:HA	1:A:124:LEU:HD22	1.88	0.54
1:A:102:GLN:OE1	1:A:106:ASN:HB2	2.09	0.53
1:A:267:VAL:HG22	1:A:270:ARG:NH2	2.24	0.53
1:A:267:VAL:HG22	1:A:270:ARG:HH22	1.74	0.52
1:A:102:GLN:HE22	1:A:106:ASN:HB2	1.75	0.51
1:A:296:PHE:O	1:A:482:PRO:HG2	2.13	0.49
1:A:107:SER:O	1:A:107:SER:OG	2.27	0.48
1:A:105:ILE:HG23	1:A:107:SER:H	1.79	0.47
1:A:267:VAL:HG23	7:A:806:HOH:O	2.14	0.47
1:A:115:VAL:HG11	1:A:121:LYS:HE3	1.97	0.47
1:A:117:ASP:OD1	1:A:117:ASP:N	2.43	0.46
1:A:271:ARG:HD3	1:A:319:TYR:CD1	2.50	0.46
1:A:125:SER:OG	1:A:126:GLU:N	2.49	0.46
1:A:260:LYS:HE2	1:A:354:GLU:O	2.16	0.45
1:A:110:THR:O	1:A:123:ARG:HB2	2.17	0.45
1:A:434:MET:HA	1:A:434:MET:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:PRO:HB2	1:A:437:PHE:CD2	2.51	0.44
1:A:234:SER:HB3	1:A:237:HIS:CG	2.53	0.43
1:A:72:LYS:HE2	1:A:118:TYR:CD2	2.53	0.43
1:A:102:GLN:NE2	1:A:106:ASN:HB2	2.33	0.43
1:A:234:SER:HB3	1:A:237:HIS:CD2	2.54	0.43
1:A:266:ASN:OD1	1:A:268[A]:ASP:HB2	2.19	0.43
1:A:59[B]:MET:HE2	1:A:59[B]:MET:HB3	1.94	0.43
1:A:182:ASN:HB3	1:A:185:TYR:HB2	1.99	0.43
1:A:91:PHE:CZ	1:A:135:ILE:HG23	2.54	0.42
1:A:82:PHE:CZ	1:A:140:VAL:HG11	2.54	0.42
1:A:207:PHE:CE2	1:A:221:SER:HB2	2.55	0.41
1:A:396:GLN:NE2	1:A:400:GLU:OE2	2.53	0.41
1:A:309:ASP:HB2	1:A:468:HIS:CG	2.56	0.41
1:A:59[B]:MET:HE3	1:A:66:VAL:HG13	2.03	0.41
1:A:141:VAL:HB	1:A:146:TRP:CD1	2.56	0.41
1:A:166:PHE:HB3	1:A:179:GLN:HG2	2.03	0.41
1:A:372:LEU:HD23	1:A:372:LEU:HA	1.96	0.41

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	521/538 (97%)	489 (94%)	26 (5%)	6 (1%)	10 4

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	115	VAL
1	A	148	LYS
1	A	149	VAL
1	A	105	ILE

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Mol	Chain	Res	Type
1	A	153	SER
1	A	150	LYS

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	437/461 (95%)	429 (98%)	8 (2%)	51 50

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLU
1	A	25	THR
1	A	39	VAL
1	A	67	THR
1	A	105	ILE
1	A	115	VAL
1	A	126	GLU
1	A	226	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	106	ASN
1	A	213	ASN
1	A	320	ASN
1	A	367	ASN
1	A	468	HIS
1	A	478	GLN

5.3.3 RNA [i](#)

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	NAG	G	1	2	15,15,15	0.64	0	21,21,21	1.33	4 (19%)
2	NAG	G	2	2	14,14,15	0.37	0	17,19,21	0.80	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	NAG	G	1	2	-	0/6/26/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	NAG	C1-C2-C3	-3.62	105.61	110.54
2	G	1	NAG	O5-C1-C2	-2.48	107.03	109.52
2	G	1	NAG	C1-O5-C5	-2.31	109.18	113.65
2	G	1	NAG	C3-C2-N2	2.02	114.34	110.62

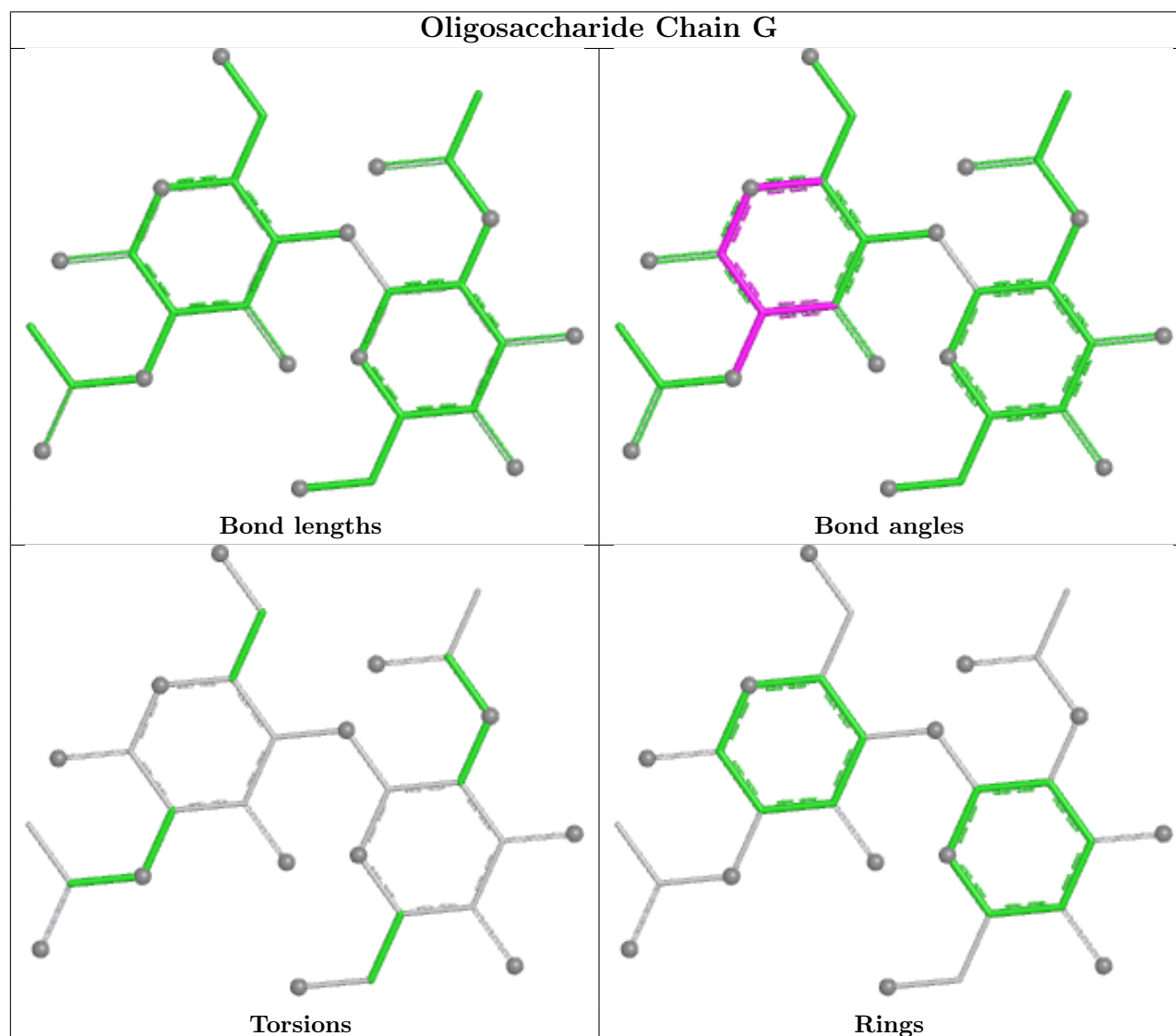
There are no chirality outliers.

There are no torsion outliers.

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 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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	EDO	A	601	-	3,3,3	0.11	0	2,2,2	0.27	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
3	EDO	A	601	-	-	0/1/1/1	-

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 [i](#)

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	524/538 (97%)	0.58	37 (7%) 22 23	10, 31, 61, 72	3 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	105	ILE	4.5
1	A	64	MET	3.7
1	A	88	VAL	3.5
1	A	145	VAL	3.4
1	A	93	LEU	3.4
1	A	84	ALA	3.1
1	A	109	VAL	2.9
1	A	161	VAL	2.9
1	A	94	VAL	2.8
1	A	104	GLY	2.8
1	A	112	VAL	2.8
1	A	76	TRP	2.6
1	A	149	VAL	2.6
1	A	98	PRO	2.5
1	A	188	ALA	2.5
1	A	111	GLY	2.5
1	A	66	VAL	2.4
1	A	529	VAL	2.4
1	A	103	SER	2.4
1	A	87	VAL	2.4
1	A	21	PHE	2.4
1	A	110	THR	2.4
1	A	127	ALA	2.3
1	A	82	PHE	2.3
1	A	92	ASN	2.3
1	A	20	PRO	2.2
1	A	431	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	89	TYR	2.2
1	A	122	PHE	2.2
1	A	453	SER	2.1
1	A	152	PRO	2.1
1	A	22	LEU	2.1
1	A	65	SER	2.1
1	A	520	LEU	2.1
1	A	11	PHE	2.0
1	A	70	ILE	2.0
1	A	141	VAL	2.0

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

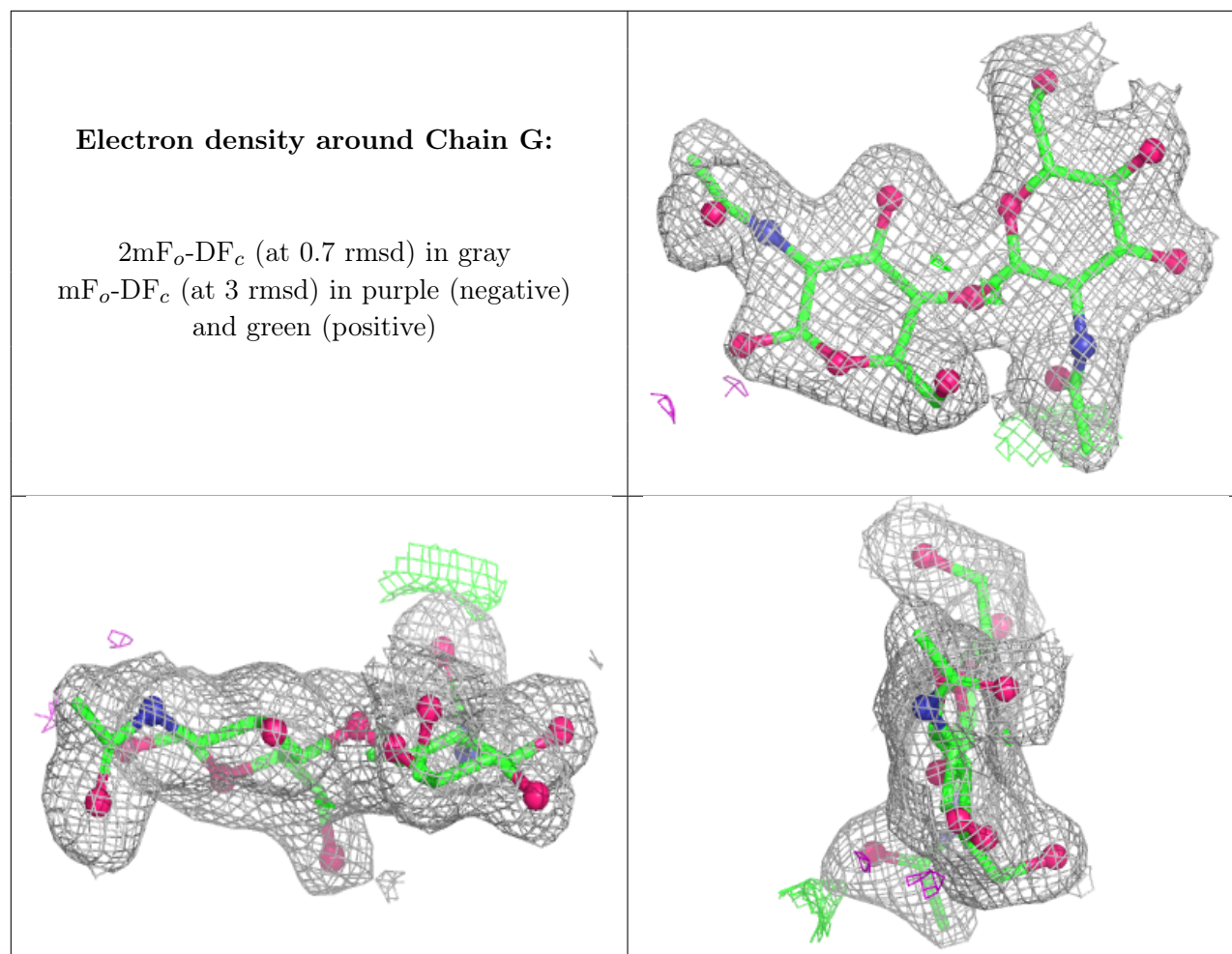
There are no non-standard protein/DNA/RNA residues in this entry.

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
2	NAG	G	1	15/15	-	-	18,24,32,38	0
2	NAG	G	2	14/15	-	-	19,23,28,30	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](#)

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
3	EDO	A	601	4/4	0.91	0.09	24,25,26,33	0
6	MG	A	604	1/1	0.94	0.13	25,25,25,25	0
5	CL	A	603	1/1	0.98	0.05	24,24,24,24	0
4	CA	A	602	1/1	0.98	0.02	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.