WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Nov 19, 2023 – 06:35 PM JST

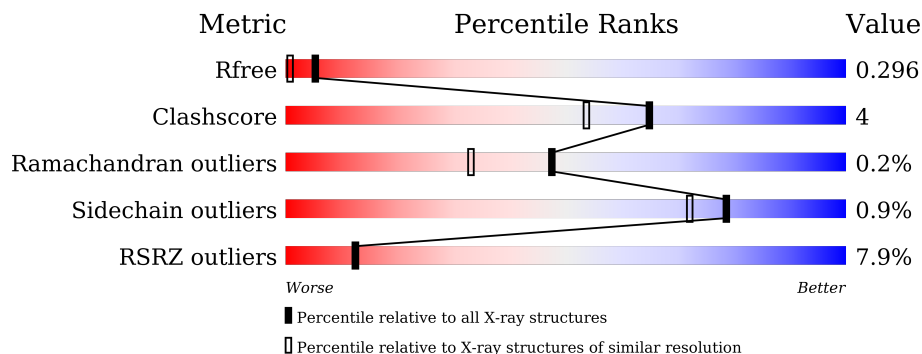|		
PDB ID	:	6LZT
Title	:	N409A mutant of chitin-specific solute binding protein from Vibrio harveyi co-crystalized with chitobiose
Authors	:	Kitaoku, Y.; Ubonbal, P.; Tran, L.T.; Robinson, R.C.; Suginta, W.
Deposited on	:	2020-02-19
Resolution	:	1.85 Å(reported)

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
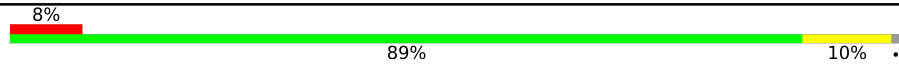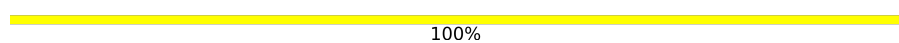*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	Percentile Ranks	Value
Rfree		0.296
Clashscore		4
Ramachandran outliers		0.2%
Sidechain outliers		0.9%
RSRZ outliers		7.9%

Worse ← → *Better*

▌ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 <=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	8% / 89% / 10% ·
2	B	2	100%

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 4455 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	530	4289	2750	713	815	11	0	6	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	409	ALA	ASN	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-a cetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	29	16	2	11	0	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	135	Total 135	O 135	0	0

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: Peptide ABC transporter, periplasmic peptide-binding protein
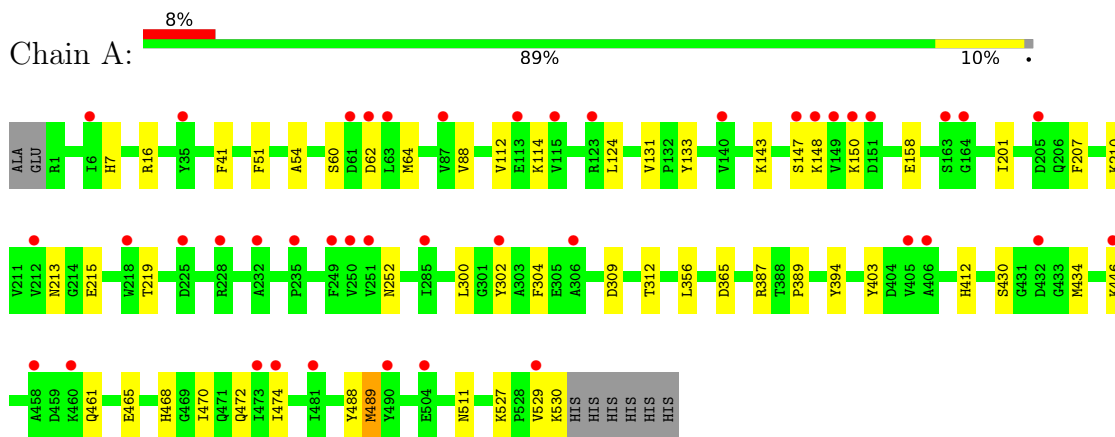
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose
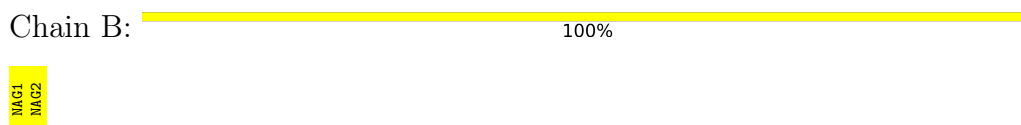
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	59.47Å 56.44Å 80.88Å 90.00° 100.98° 90.00°	Depositor
Resolution (Å)	23.65 – 1.85 23.65 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.6 (23.65-1.85) 98.6 (23.65-1.85)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 1.85Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.235 , 0.296 0.237 , 0.296	Depositor DCC
R_{free} test set	2236 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	28.8	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 53.2	EDS
L-test for twinning[2]	$< |L| > = 0.46, < L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4455	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.22% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CA, MG, 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	0.41	0/4417	0.55	0/6012

There are no bond length outliers.

There are no bond angle outliers.

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	4289	0	4095	35	0
2	B	29	0	27	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	135	0	0	1	0
All	All	4455	0	4122	35	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 4.

All (35) 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:88:VAL:HG21	1:A:114:LYS:HB2	1.79	0.64
1:A:461:GLN:O	1:A:465:GLU:HG2	2.05	0.57
1:A:124:LEU:HD11	1:A:131:VAL:HG11	1.88	0.55
1:A:529:VAL:HG22	1:A:530[B]:LYS:HD3	1.87	0.55
1:A:529:VAL:HG22	1:A:530[A]:LYS:H	1.72	0.54
1:A:60:SER:HB2	1:A:62:ASP:OD1	2.08	0.52
1:A:389:PRO:HG2	1:A:394:TYR:HB2	1.91	0.51
1:A:7:HIS:HB3	1:A:219:THR:HG22	1.93	0.49
1:A:300:LEU:HD11	1:A:304:PHE:O	2.13	0.49
1:A:529:VAL:HG22	1:A:530[B]:LYS:H	1.78	0.49
1:A:62:ASP:O	1:A:64:MET:HG2	2.14	0.48
1:A:16:ARG:HG2	1:A:158:GLU:HB3	1.95	0.48
1:A:213:ASN:OD1	5:A:701:HOH:O	2.20	0.48
1:A:312:THR:OG1	1:A:472:GLN:HG2	2.14	0.48
1:A:7:HIS:CE1	1:A:201:ILE:HB	2.49	0.47
1:A:489:MET:H	1:A:489:MET:HG3	1.43	0.47
1:A:430:SER:O	1:A:434:MET:HG3	2.14	0.47
1:A:207:PHE:HE1	1:A:219:THR:HG21	1.80	0.46
1:A:530[B]:LYS:HE2	1:A:530[B]:LYS:HB2	1.70	0.46
1:A:412:HIS:HB3	1:A:488:TYR:OH	2.16	0.46
1:A:470:ILE:O	1:A:474[A]:ILE:HG12	2.16	0.45
1:A:210[A]:LYS:NZ	1:A:215:GLU:OE2	2.41	0.44
1:A:365:ASP:OD1	1:A:365:ASP:N	2.51	0.44
1:A:60:SER:HB2	1:A:62:ASP:CG	2.39	0.43
1:A:252:ASN:HB2	1:A:403:TYR:CZ	2.53	0.43
1:A:309:ASP:HB2	1:A:468:HIS:CG	2.53	0.42
1:A:446:LYS:H	1:A:446:LYS:HG2	1.70	0.42
1:A:530[B]:LYS:HD3	1:A:530[B]:LYS:H	1.85	0.42
1:A:51:PHE:HB3	1:A:54:ALA:O	2.20	0.42
1:A:41:PHE:CE1	1:A:133:TYR:HA	2.55	0.42
1:A:150:LYS:HA	1:A:150:LYS:HD2	1.57	0.42
1:A:488:TYR:HB3	1:A:511:ASN:HD21	1.85	0.41
1:A:356:LEU:HD13	1:A:387:ARG:CZ	2.51	0.41
1:A:143:LYS:HB3	1:A:143:LYS:HE2	1.75	0.40
1:A:88:VAL:HA	1:A:112:VAL:HG21	2.04	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	533/538 (99%)	508 (95%)	24 (4%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	302	TYR

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	460/461 (100%)	456 (99%)	4 (1%)	78	72

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

Mol	Chain	Res	Type
1	A	147	SER
1	A	148	LYS
1	A	489	MET
1	A	527	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	NAG	B	1	2	15,15,15	0.58	0	21,21,21	1.24	3 (14%)
2	NAG	B	2	2	14,14,15	0.42	0	17,19,21	0.88	1 (5%)

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	B	1	2	-	0/6/26/26	0/1/1/1
2	NAG	B	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(^{o})	Ideal(^{o})
2	B	1	NAG	C1-O5-C5	-2.67	108.63	113.66
2	B	1	NAG	O1-C1-C2	2.58	114.58	109.22
2	B	2	NAG	O3-C3-C4	-2.19	105.28	110.35
2	B	1	NAG	C1-C2-C3	-2.14	107.63	110.54

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.

Oligosaccharide Chain B

Bond lengths

Bond angles

Torsions

Rings
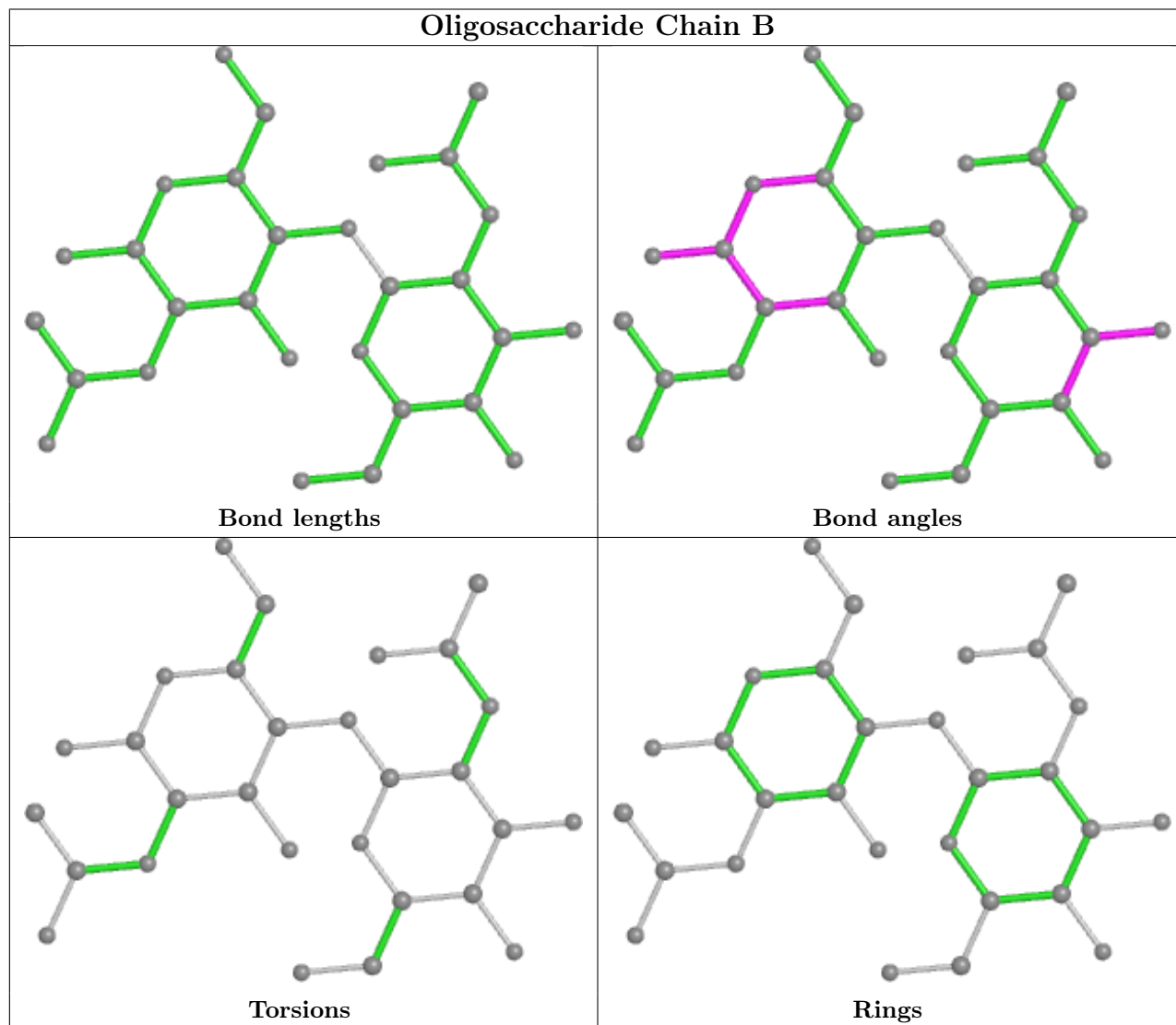
5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are 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 ⓘ

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	530/538 (98%)	0.65	42 (7%)	12	12	20, 35, 55, 76	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	232	ALA	5.2
1	A	529	VAL	5.1
1	A	149	VAL	5.0
1	A	302	TYR	4.8
1	A	147	SER	3.7
1	A	150	LYS	3.7
1	A	458	ALA	3.6
1	A	61	ASP	3.4
1	A	62	ASP	3.3
1	A	123	ARG	3.3
1	A	251	VAL	3.1
1	A	115	VAL	3.0
1	A	205	ASP	2.9
1	A	481	ILE	2.9
1	A	250	VAL	2.8
1	A	63	LEU	2.8
1	A	151	ASP	2.7
1	A	306	ALA	2.7
1	A	460	LYS	2.7
1	A	113	GLU	2.7
1	A	218	TRP	2.5
1	A	148	LYS	2.5
1	A	504	GLU	2.5
1	A	249	PHE	2.4
1	A	212	VAL	2.4
1	A	87	VAL	2.4
1	A	228[A]	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	235	PRO	2.3
1	A	225	ASP	2.2
1	A	490	TYR	2.2
1	A	405	VAL	2.2
1	A	140	VAL	2.2
1	A	432	ASP	2.2
1	A	285	ILE	2.1
1	A	163	SER	2.1
1	A	473	ILE	2.1
1	A	35	TYR	2.1
1	A	446	LYS	2.1
1	A	474[A]	ILE	2.1
1	A	6	ILE	2.0
1	A	164	GLY	2.0
1	A	406	ALA	2.0

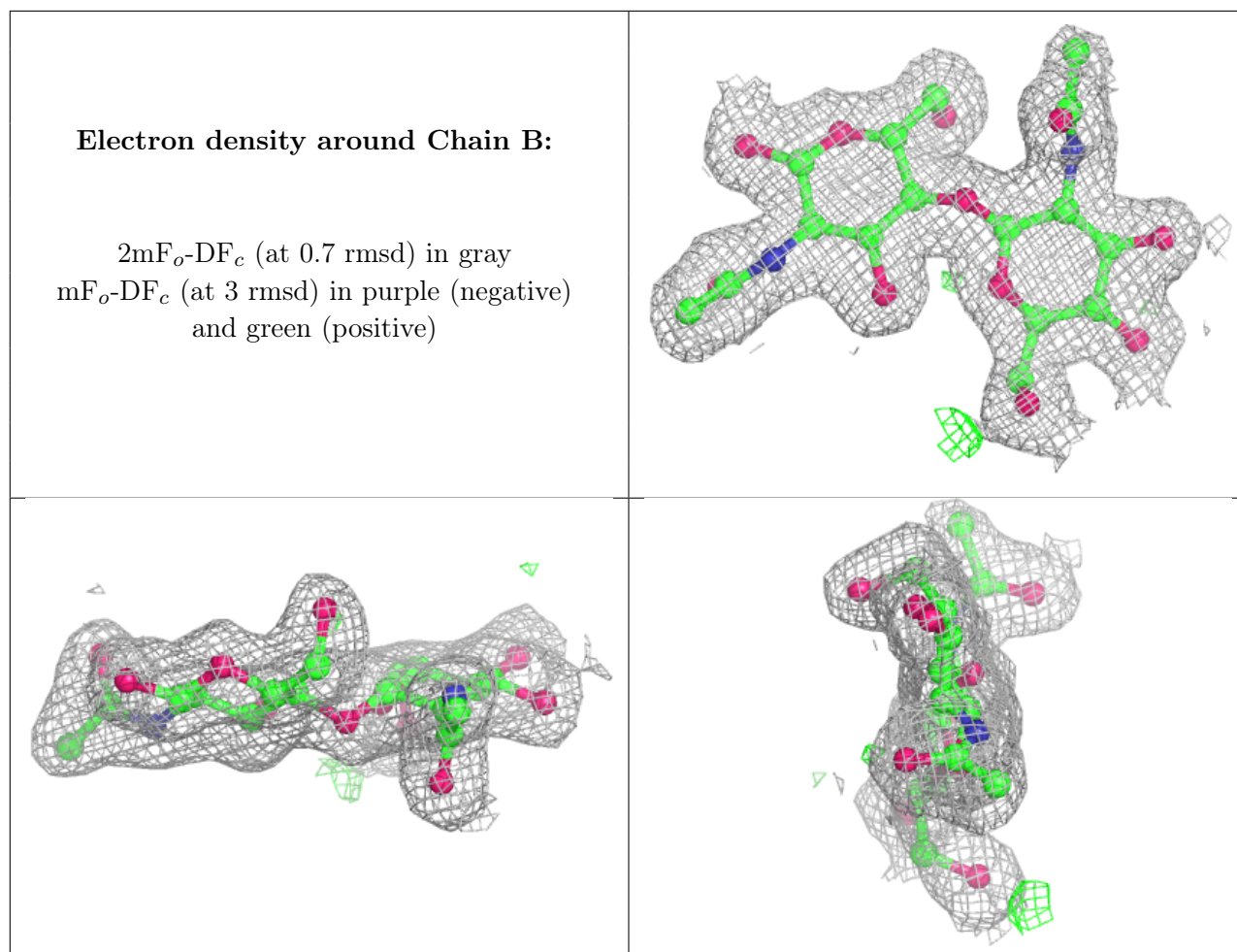## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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	NAG	B	1	15/15	0.92	0.11	21,25,29,30	0
2	NAG	B	2	14/15	0.95	0.10	17,24,27,28	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 B:

$2mF_o$-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(Å^2)	Q<0.9
3	MG	A	602	1/1	0.89	0.09	22,22,22,22	0
4	CA	A	603	1/1	0.98	0.05	31,31,31,31	0

6.5 Other polymers (i)

There are no such residues in this entry.