Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2022 – 03:52 pm GMT

PDB ID	:	6SJV
Title	:	Structure of HPV18 E6 oncoprotein in complex with mutant E6AP LxxLL motif
Authors	:	Suarez, I.P.; Cousido-Siah, A.; Bonhoure, A.; Kostmann, C.; Mitschler, A.; Podjarny, A.; Trave, G.
Deposited on	:	2019-08-14
Resolution	:	2.03 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:

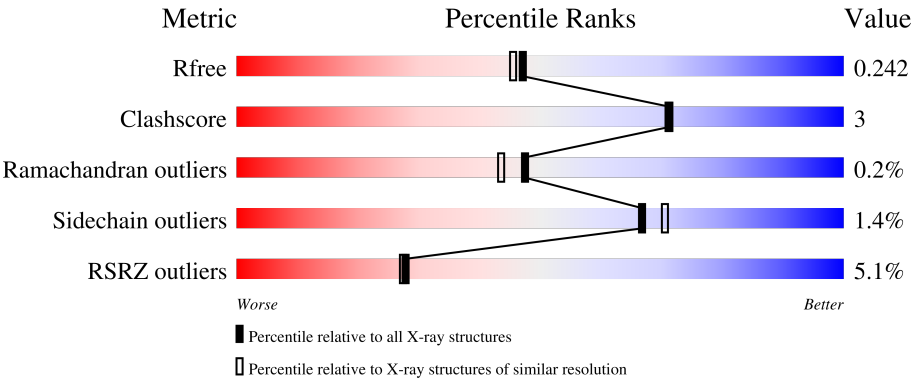
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.03 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 <=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	543	5%, 88%, 9%, .
2	B	2	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4307 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 Maltodextrin-binding protein,Protein E6,Ubiquitin-protein ligase E3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	529	4161	2657	703	783	18	0	1	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A376KDN7
A	83	ALA	ASP	conflict	UNP A0A376KDN7
A	84	ALA	LYS	engineered mutation	UNP A0A376KDN7
A	240	ALA	LYS	engineered mutation	UNP A0A376KDN7
A	363	ALA	LYS	engineered mutation	UNP A0A376KDN7
A	364	ALA	ASP	engineered mutation	UNP A0A376KDN7
A	368	ASN	-	linker	UNP A0A376KDN7
A	369	ALA	-	linker	UNP A0A376KDN7
A	370	ALA	-	linker	UNP A0A376KDN7
A	371	ALA	-	linker	UNP A0A376KDN7
A	1049	ARG	PHE	engineered mutation	UNP P06463
A	2375	GLY	-	linker	UNP P06463
A	2376	SER	-	linker	UNP P06463
A	2377	ALA	-	linker	UNP P06463
A	2378	ALA	-	linker	UNP P06463
A	2379	ALA	-	linker	UNP P06463
A	2386	PHE	LEU	engineered mutation	UNP Q05086
A	2393	ARG	GLU	engineered mutation	UNP Q05086

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

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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Zn 2 2	0	0

- Molecule 4 is water.

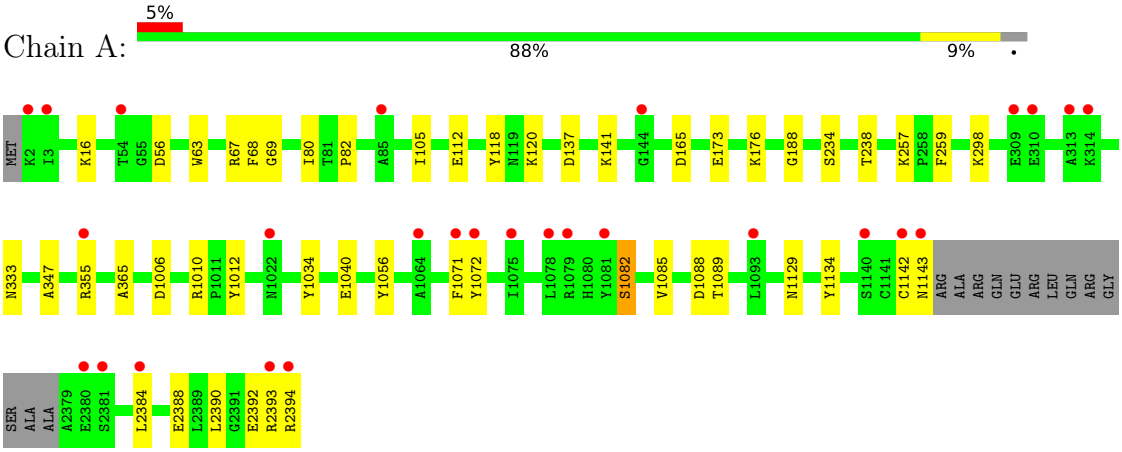
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	121	Total O 121 121	0	0

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.

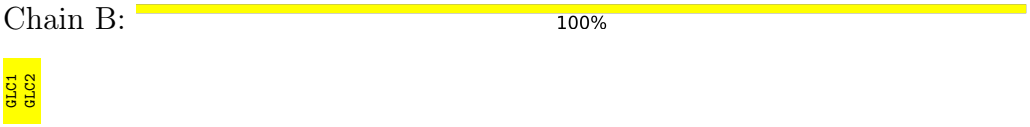
• Molecule 1: Maltodextrin-binding protein,Protein E6,Ubiquitin-protein ligase E3A

Chain A:



• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	106.83Å 106.83Å 100.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.79 – 2.03 19.79 – 2.03	Depositor EDS
% Data completeness (in resolution range)	98.8 (19.79-2.03) 98.8 (19.79-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.26 (at 2.02Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.203 , 0.242 0.203 , 0.242	Depositor DCC
R_{free} test set	1985 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å^2)	36.7	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4307	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: 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	0.39	0/4261	0.54	0/5778

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	4161	0	4104	29	0
2	B	23	0	21	0	0
3	A	2	0	0	0	0
4	A	121	0	0	2	0
All	All	4307	0	4125	29	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 (29) 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:80:ILE:HG22	1:A:82:PRO:HD3	1.54	0.89
1:A:1010:ARG:HD3	1:A:1056:TYR:CE1	2.38	0.58
1:A:1129:ASN:HB2	1:A:1134:TYR:CE1	2.40	0.56
1:A:2390:LEU:HB2	1:A:2392:GLU:HG3	1.89	0.53
1:A:1071:PHE:HD1	1:A:1072:TYR:CD1	2.27	0.52
1:A:1006:ASP:O	1:A:1010:ARG:HG2	2.10	0.51
1:A:2388:GLU:OE2	1:A:2394:ARG:HG2	2.11	0.51
1:A:1010:ARG:HD3	1:A:1056:TYR:CD1	2.45	0.51
1:A:63:TRP:CD1	1:A:67:ARG:HG3	2.48	0.49
1:A:1010:ARG:HD2	1:A:1012:TYR:OH	2.13	0.49
1:A:1034:TYR:CD1	1:A:1072:TYR:HE2	2.31	0.48
1:A:137:ASP:O	1:A:141:LYS:HG2	2.14	0.47
1:A:1034:TYR:CG	1:A:1072:TYR:HE2	2.32	0.47
1:A:1040:GLU:HG3	4:A:2603:HOH:O	2.13	0.47
1:A:16:LYS:HE3	1:A:112:GLU:OE1	2.14	0.47
1:A:1071:PHE:HD1	1:A:1072:TYR:HD1	1.62	0.47
1:A:1085:VAL:HB	1:A:1089:THR:HB	1.97	0.46
1:A:234:SER:O	1:A:238:THR:HG23	2.16	0.46
1:A:1082:SER:HB3	1:A:1129:ASN:HB3	1.99	0.44
1:A:234:SER:OG	1:A:298:LYS:HD3	2.17	0.44
1:A:69:GLY:HA3	1:A:333:ASN:O	2.17	0.44
1:A:173:GLU:O	1:A:176:LYS:HE3	2.17	0.44
1:A:165:ASP:O	1:A:188:GLY:HA3	2.17	0.43
1:A:347:ALA:HB2	1:A:365:ALA:HB2	2.00	0.43
1:A:2392:GLU:O	1:A:2393:ARG:HB2	2.20	0.42
1:A:118:TYR:CE2	1:A:120:LYS:HG2	2.55	0.42
1:A:257:LYS:HD2	4:A:2572:HOH:O	2.20	0.41
1:A:68:PHE:HB3	1:A:105:ILE:HD13	2.02	0.41
1:A:2384:LEU:HD21	1:A:2394:ARG:C	2.41	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	526/543 (97%)	517 (98%)	8 (2%)	1 (0%)	47 43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1082	SER

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	436/445 (98%)	430 (99%)	6 (1%)	67 70

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	ASP
1	A	259	PHE
1	A	355	ARG
1	A	1088	ASP
1	A	1142	CYS
1	A	1143	ASN

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

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	GLC	B	1	2	12,12,12	0.68	0	17,17,17	1.45	2 (11%)
2	GLC	B	2	2	11,11,12	0.79	0	15,15,17	1.31	2 (13%)

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	B	1	2	-	0/2/22/22	0/1/1/1
2	GLC	B	2	2	-	0/2/19/22	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	2	GLC	C1-O5-C5	4.10	117.75	112.19
2	B	1	GLC	O5-C1-C2	3.88	117.20	110.28
2	B	1	GLC	C1-O5-C5	2.47	118.33	113.66
2	B	2	GLC	C6-C5-C4	-2.14	107.98	113.00

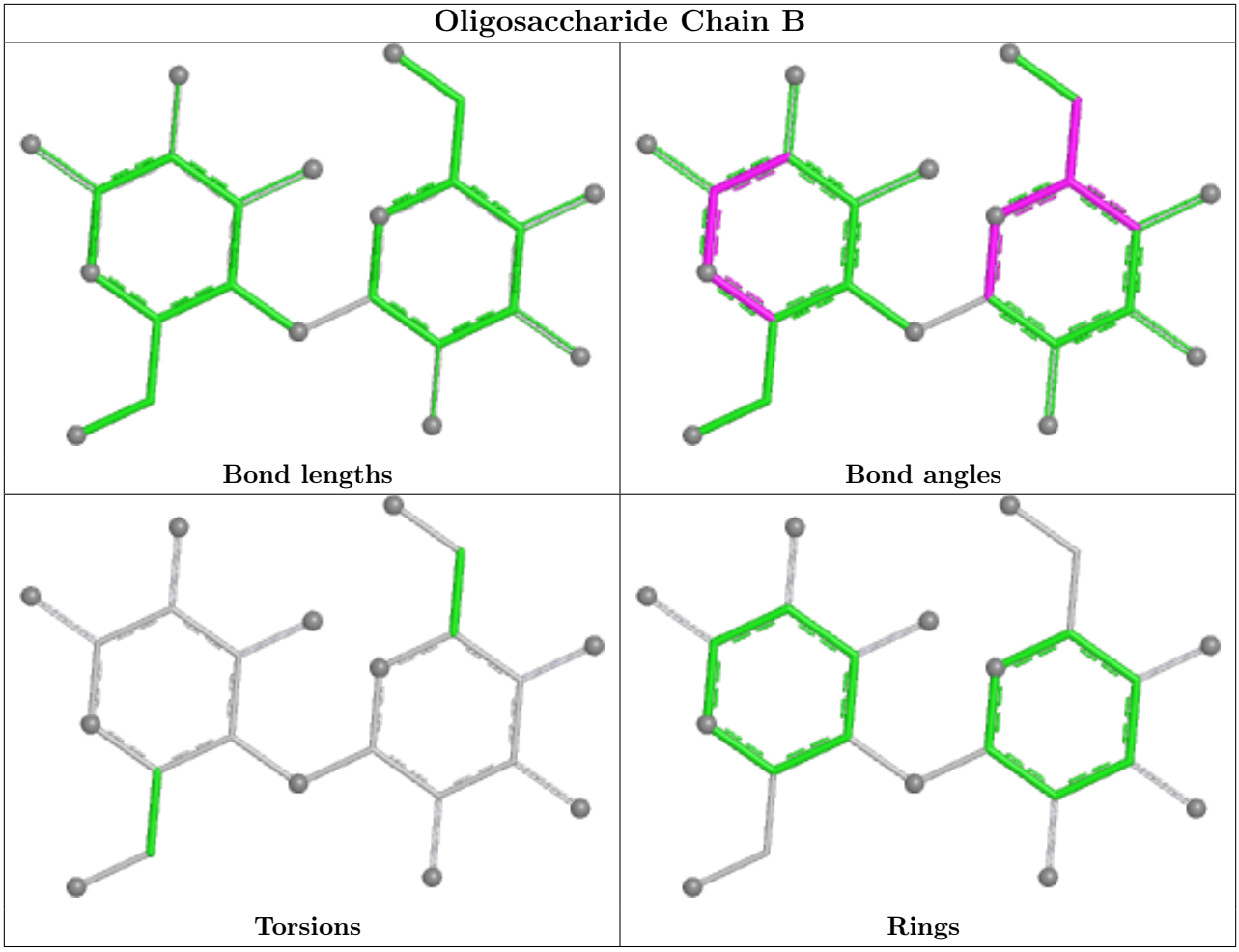
There are no chirality outliers.

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

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 (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, 95^{th} 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	529/543 (97%)	0.07	27 (5%) 28 27	24, 41, 62, 88	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2394	ARG	6.7
1	A	2380	GLU	4.8
1	A	313	ALA	4.6
1	A	2381	SER	4.0
1	A	1081	TYR	3.6
1	A	3	ILE	3.6
1	A	1142	CYS	3.5
1	A	2384	LEU	3.0
1	A	1071	PHE	2.9
1	A	1022	ASN	2.9
1	A	310	GLU	2.9
1	A	2	LYS	2.8
1	A	1079	ARG	2.7
1	A	1143	ASN	2.7
1	A	54	THR	2.6
1	A	1064	ALA	2.6
1	A	355	ARG	2.5
1	A	1072	TYR	2.5
1	A	1093	LEU	2.4
1	A	85	ALA	2.3
1	A	309	GLU	2.3
1	A	2393	ARG	2.3
1	A	1078	LEU	2.2
1	A	1075	ILE	2.2
1	A	314	LYS	2.2
1	A	1140	SER	2.1
1	A	144	GLY	2.1

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

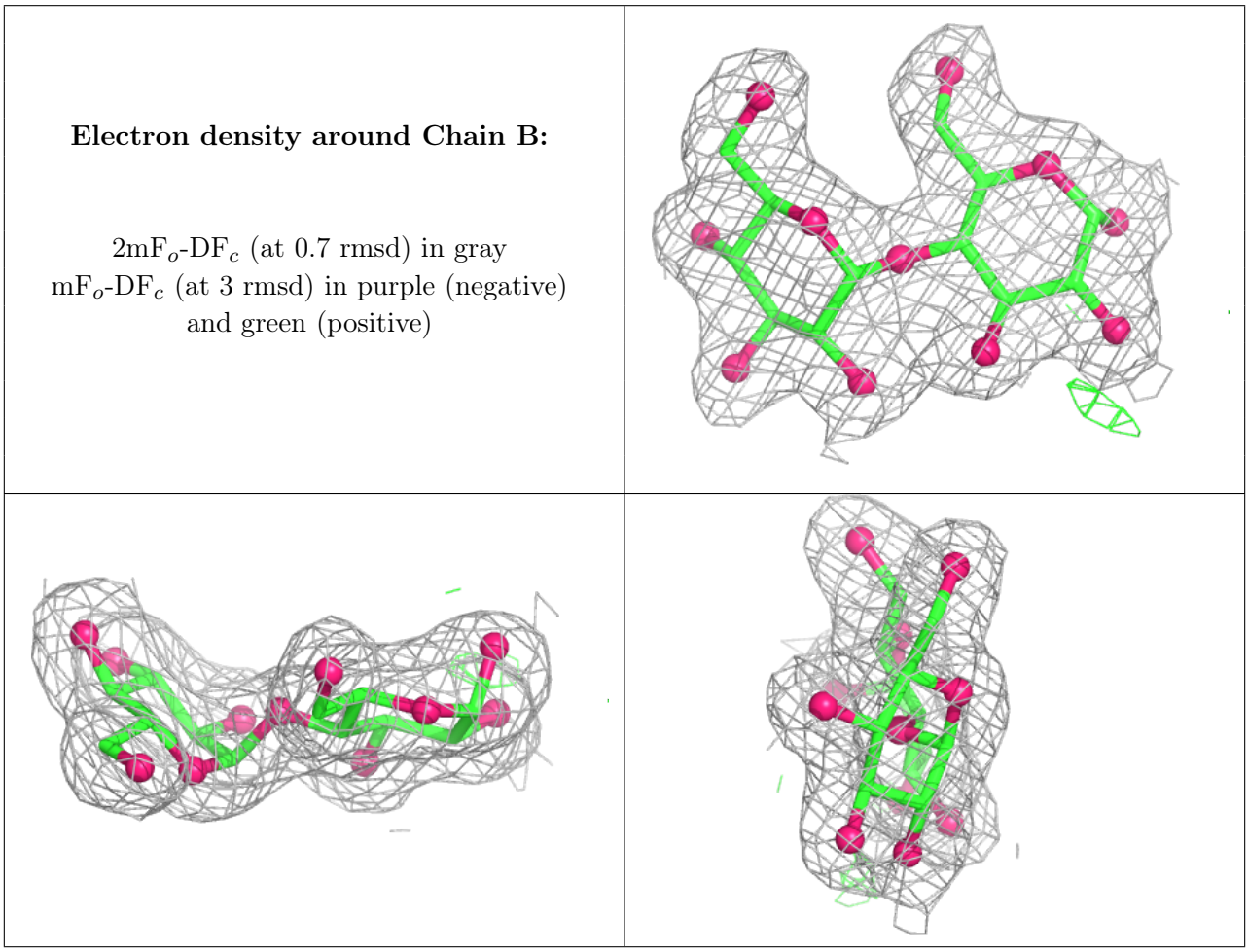
There are no non-standard protein/DNA/RNA residues in this entry.

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, 95^{th} 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	GLC	B	1	12/12	0.95	0.09	25,31,35,36	0
2	GLC	B	2	11/12	0.98	0.08	25,26,29,30	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

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, 95^{th} 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	ZN	A	2402	1/1	0.96	0.06	52,52,52,52	0
3	ZN	A	2401	1/1	0.98	0.05	45,45,45,45	0

6.5 Other polymers

There are no such residues in this entry.