



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 04:34 PM UTC

PDB ID : 6SIV / pdb_00006siv
Title : Structure of HPV16 E6 oncoprotein in complex with mutant IRF3 LxxLL motif
Authors : Suarez, I.P.; Cousido-Siah, A.; Bonhoure, A.; Mitschler, A.; Podjarny, A.; Trave, G.
Deposited on : 2019-08-12
Resolution : 1.75 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

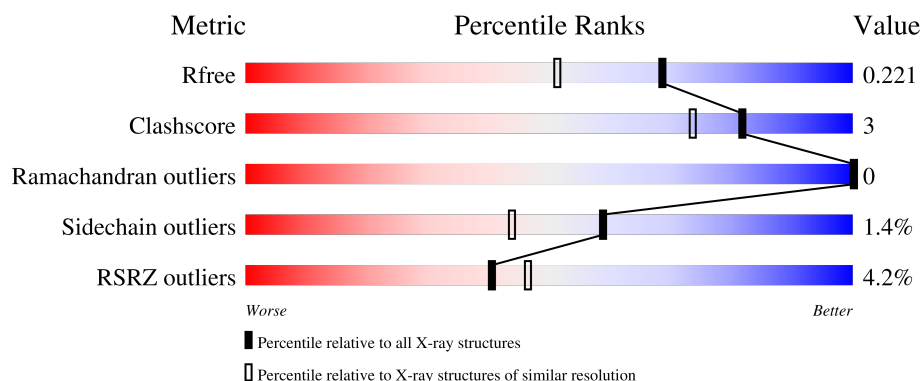
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	383	94% 6%
2	B	153	12% 79% 8% 11%
3	C	5	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4614 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 Maltose/maltodextrin-binding periplasmic protein, Interferon regulatory factor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	2	0
			2967	1907	481	572	7			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	ALA	conflict	UNP P0AEX9
A	83	ALA	ASP	conflict	UNP P0AEX9
A	84	ALA	LYS	engineered mutation	UNP P0AEX9
A	240	ALA	LYS	engineered mutation	UNP P0AEX9
A	360	ALA	GLU	engineered mutation	UNP P0AEX9
A	363	ALA	-	linker	UNP P0AEX9
A	364	ALA	-	linker	UNP P0AEX9
A	365	ALA	-	linker	UNP P0AEX9
A	366	GLN	-	linker	UNP P0AEX9
A	367	THR	-	linker	UNP P0AEX9
A	368	ASN	-	linker	UNP P0AEX9
A	369	ALA	-	linker	UNP P0AEX9
A	370	ALA	-	linker	UNP P0AEX9
A	371	ALA	-	linker	UNP P0AEX9
A	2146	GLU	ASN	engineered mutation	UNP Q14653
A	2147	GLU	MET	engineered mutation	UNP Q14653
A	2148	ARG	VAL	engineered mutation	UNP Q14653

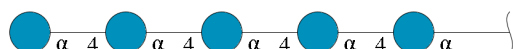
- Molecule 2 is a protein called Protein E6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	136	Total	C	N	O	S	0	0	0
			1144	717	213	203	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	999	GLY	THR	conflict	UNP P03126
B	1047	ARG	PHE	engineered mutation	UNP P03126
B	1080	SER	CYS	engineered mutation	UNP P03126
B	1097	SER	CYS	engineered mutation	UNP P03126
B	1111	SER	CYS	engineered mutation	UNP P03126
B	1140	SER	CYS	engineered mutation	UNP P03126

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	C	5	Total	C	O	0	0	0
			56	30	26			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Zn	0	0
			2	2		

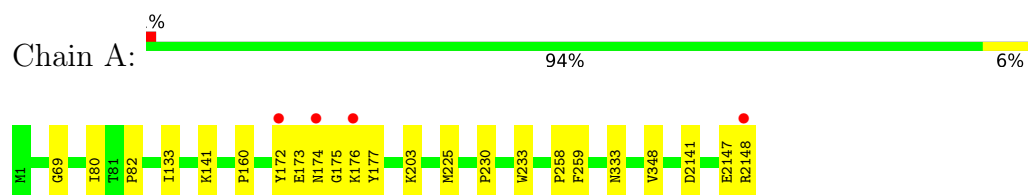
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	371	Total	O	0	10
			381	381		
5	B	64	Total	O	0	0
			64	64		

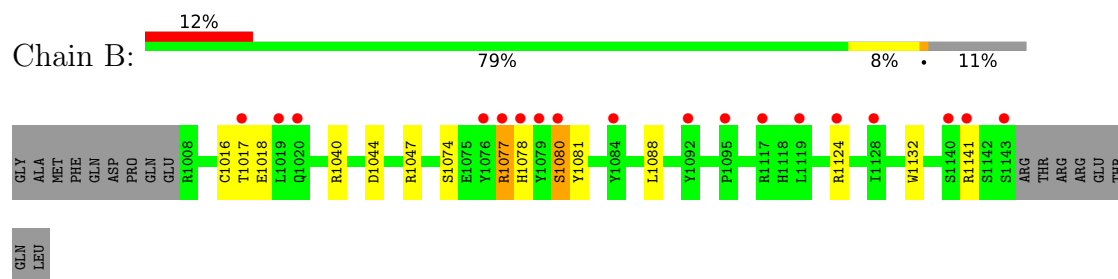
3 Residue-property plots [i](#)

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: Maltose/maltodextrin-binding periplasmic protein, Interferon regulatory factor 3



- Molecule 2: Protein E6



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	97.03Å 132.47Å 42.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.52 – 1.75 48.52 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.0 (48.52-1.75) 97.6 (48.52-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.16rc1_3531	Depositor
R, R_{free}	0.182 , 0.220 0.184 , 0.221	Depositor DCC
R_{free} test set	2751 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.8	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	0.96	EDS
Total number of atoms	4614	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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: 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	0.30	0/3036	0.48	0/4125
2	B	0.22	0/1168	0.42	0/1570
All	All	0.28	0/4204	0.46	0/5695

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 [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	2967	0	2929	12	0
2	B	1144	0	1141	9	0
3	C	56	0	48	0	0
4	B	2	0	0	0	0
5	A	381	0	0	1	0
5	B	64	0	0	2	0
All	All	4614	0	4118	21	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 (21) 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	1.60	0.81
2:B:1141:ARG:NH1	5:B:1302:HOH:O	2.26	0.69
2:B:1044:ASP:OD1	2:B:1047:ARG:NH2	2.27	0.67
2:B:1077:ARG:HA	2:B:1077:ARG:HE	1.66	0.61
1:A:69:GLY:HA3	1:A:333:ASN:O	2.10	0.52
1:A:173:GLU:OE1	1:A:174:ASN:ND2	2.43	0.51
1:A:133:ILE:HD12	1:A:225:MET:HE1	1.95	0.47
2:B:1088:LEU:HD21	2:B:1132:TRP:CE2	2.49	0.47
1:A:172:TYR:CZ	1:A:175:GLY:HA2	2.51	0.46
1:A:172:TYR:OH	1:A:175:GLY:HA2	2.17	0.45
2:B:1016:CYS:C	2:B:1018:GLU:H	2.25	0.45
2:B:1080:SER:HB2	2:B:1081:TYR:H	1.55	0.45
1:A:203:LYS:HA	1:A:203:LYS:HD2	1.68	0.44
2:B:1124:ARG:NH2	5:B:1303:HOH:O	2.27	0.43
2:B:1074:SER:O	2:B:1078:HIS:HB2	2.18	0.43
1:A:176:LYS:HG2	1:A:177:TYR:N	2.34	0.43
1:A:230:PRO:HA	1:A:233:TRP:CE2	2.55	0.42
2:B:1017:THR:HG22	2:B:1017:THR:O	2.19	0.42
1:A:2147:GLU:HB3	1:A:2148:ARG:H	1.64	0.42
1:A:160:PRO:HG3	1:A:258:PRO:HA	2.01	0.41
1:A:348:VAL:HG11	5:A:2434:HOH:O	2.20	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	383/383 (100%)	377 (98%)	6 (2%)	0	100	100
2	B	134/153 (88%)	127 (95%)	7 (5%)	0	100	100
All	All	517/536 (96%)	504 (98%)	13 (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	302/300 (101%)	299 (99%)	3 (1%)	68	56
2	B	130/145 (90%)	127 (98%)	3 (2%)	44	24
All	All	432/445 (97%)	426 (99%)	6 (1%)	59	44

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

Mol	Chain	Res	Type
1	A	141	LYS
1	A	259	PHE
1	A	2141	ASP
2	B	1040	ARG
2	B	1077	ARG
2	B	1080	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	206	ASN

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 ⓘ

5 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	C	1	3	12,12,12	1.26	1 (8%)	17,17,17	0.68	0
3	GLC	C	2	3	11,11,12	2.51	4 (36%)	15,15,17	0.80	0
3	GLC	C	3	3	11,11,12	2.44	6 (54%)	15,15,17	1.08	1 (6%)
3	GLC	C	4	3	11,11,12	2.70	6 (54%)	15,15,17	1.22	1 (6%)
3	GLC	C	5	3	11,11,12	2.60	6 (54%)	15,15,17	0.65	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	GLC	C	1	3	-	0/2/22/22	0/1/1/1
3	GLC	C	2	3	-	0/2/19/22	0/1/1/1
3	GLC	C	3	3	-	0/2/19/22	0/1/1/1
3	GLC	C	4	3	-	0/2/19/22	0/1/1/1
3	GLC	C	5	3	-	2/2/19/22	0/1/1/1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	GLC	O5-C5	6.26	1.55	1.43
3	C	4	GLC	O5-C5	5.92	1.55	1.43
3	C	5	GLC	O5-C5	5.79	1.54	1.43
3	C	3	GLC	O5-C5	5.43	1.54	1.43
3	C	4	GLC	O5-C1	3.30	1.49	1.43
3	C	5	GLC	C2-C3	-3.27	1.47	1.52
3	C	4	GLC	O2-C2	3.11	1.49	1.43
3	C	5	GLC	C6-C5	-2.89	1.42	1.51
3	C	4	GLC	C1-C2	-2.70	1.45	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3	GLC	O2-C2	2.67	1.48	1.43
3	C	1	GLC	O5-C5	2.65	1.50	1.44
3	C	4	GLC	O4-C4	2.64	1.49	1.43
3	C	3	GLC	C2-C3	-2.59	1.48	1.52
3	C	3	GLC	C6-C5	-2.52	1.43	1.51
3	C	2	GLC	O3-C3	2.50	1.49	1.43
3	C	2	GLC	C2-C3	-2.33	1.48	1.52
3	C	4	GLC	C6-C5	-2.24	1.44	1.51
3	C	5	GLC	O3-C3	2.21	1.48	1.43
3	C	5	GLC	O5-C1	2.18	1.47	1.43
3	C	2	GLC	C6-C5	-2.17	1.44	1.51
3	C	5	GLC	O2-C2	2.17	1.47	1.43
3	C	3	GLC	O4-C4	2.10	1.48	1.43
3	C	3	GLC	O3-C3	2.08	1.48	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4	GLC	C1-C2-C3	3.03	114.06	109.64
3	C	3	GLC	C2-C3-C4	2.25	114.82	110.86

There are no chirality outliers.

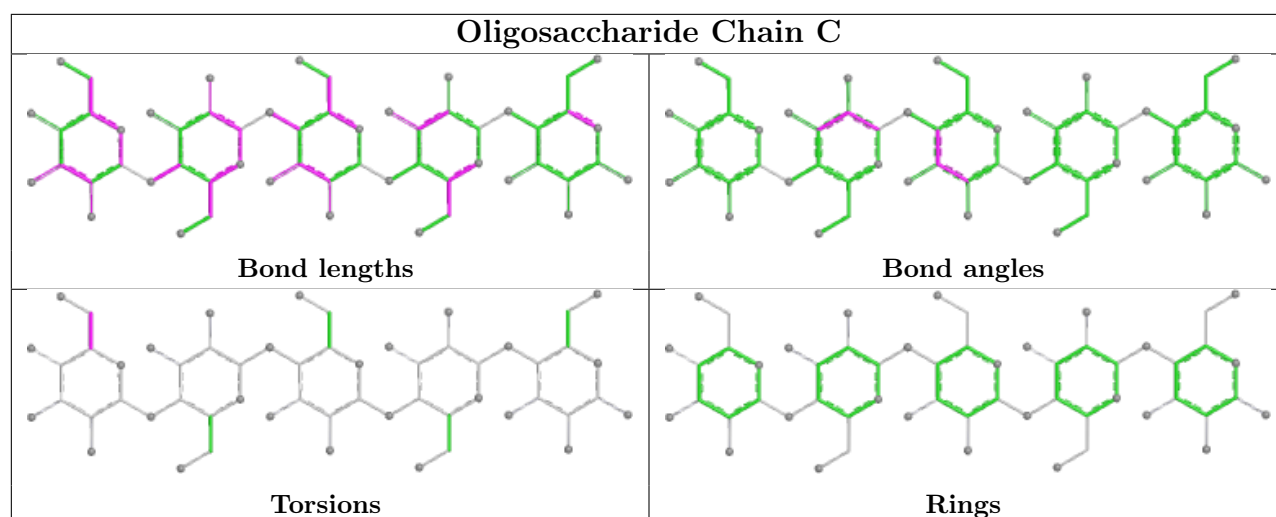
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	5	GLC	O5-C5-C6-O6
3	C	5	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 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 [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	383/383 (100%)	-0.15	4 (1%) 79 84	9, 21, 35, 60	2 (0%)
2	B	136/153 (88%)	0.86	18 (13%) 7 8	18, 36, 60, 72	0
All	All	519/536 (96%)	0.12	22 (4%) 40 46	9, 24, 49, 72	2 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1079	TYR	5.9
1	A	2148	ARG	3.9
2	B	1076	TYR	3.7
2	B	1080	SER	3.1
2	B	1143	SER	3.1
2	B	1077	ARG	3.0
2	B	1119	LEU	3.0
2	B	1017	THR	3.0
1	A	172	TYR	2.6
2	B	1084	TYR	2.6
2	B	1078	HIS	2.5
2	B	1141	ARG	2.5
2	B	1128	ILE	2.4
1	A	174	ASN	2.4
2	B	1095	PRO	2.3
2	B	1020	GLN	2.2
2	B	1092	TYR	2.2
1	A	176	LYS	2.2
2	B	1140	SER	2.2
2	B	1124	ARG	2.1
2	B	1019	LEU	2.1
2	B	1117	ARG	2.0

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

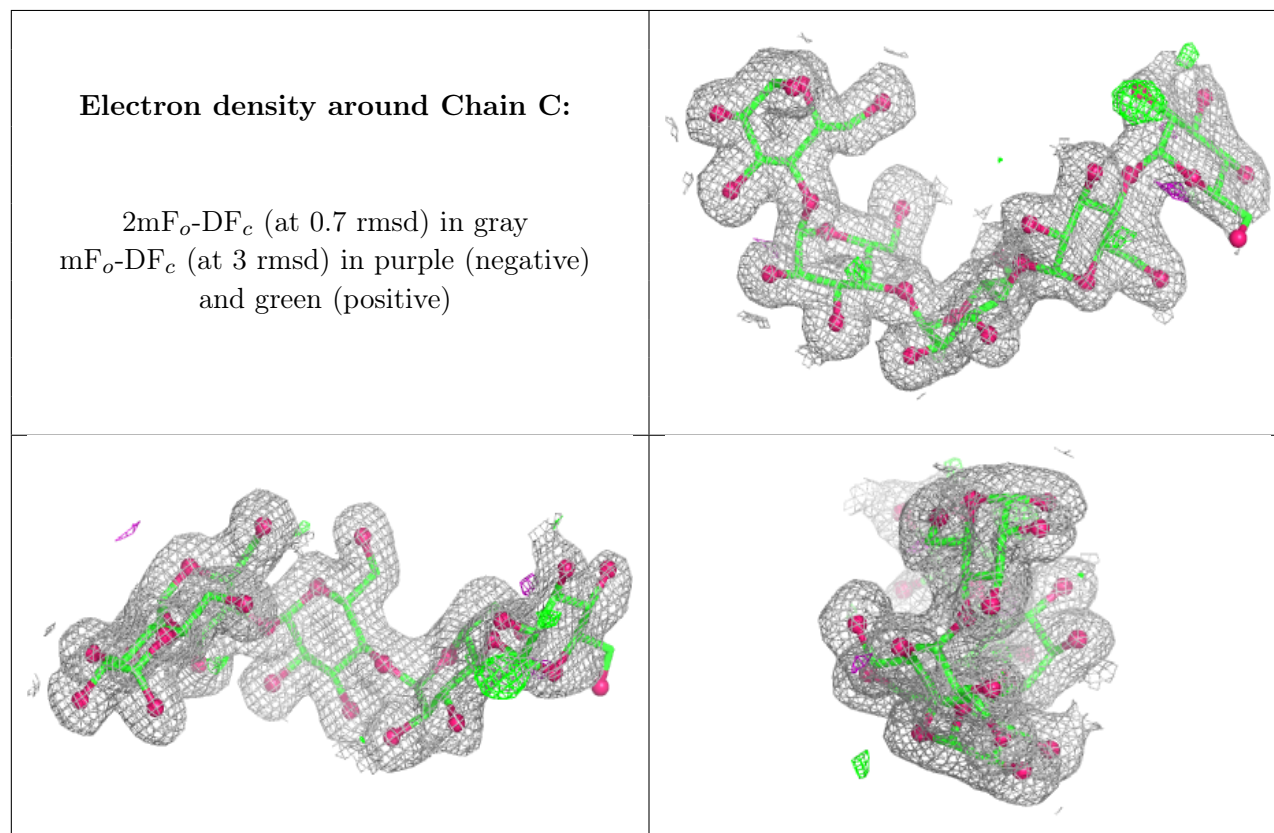
There are no non-standard protein/DNA/RNA residues in this entry.

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	C	5	11/12	0.75	0.15	38,43,51,53	0
3	GLC	C	4	11/12	0.92	0.08	20,27,32,33	0
3	GLC	C	2	11/12	0.97	0.05	11,13,14,14	0
3	GLC	C	3	11/12	0.97	0.04	13,16,18,19	0
3	GLC	C	1	12/12	0.98	0.04	9,13,16,16	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($\text{\AA}^2$)	Q<0.9
4	ZN	B	1200	1/1	0.97	0.08	32,32,32,32	0
4	ZN	B	1201	1/1	0.99	0.03	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.