



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:50 AM UTC

PDB ID : 6SMV / pdb_00006smv
Title : Structure of HPV49 E6 protein in complex with MAML1 LxxLL motif
Authors : Suarez, I.P.; Cousido-Siah, A.; Bonhoure, A.; Kostmann, C.; Mitschler, A.; Podjarny, A.; Trave, G.
Deposited on : 2019-08-22
Resolution : 2.14 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

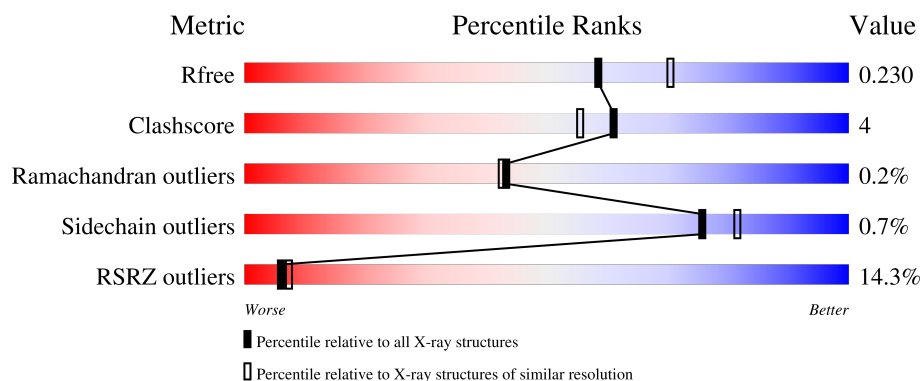
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	14% 87% 10%
2	B	4	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4298 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, Protein E6, Mastermind-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	525	Total	C	N	O	S	0	2	0
			4073	2619	685	750	19			

There are 27 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	LYS	engineered mutation	UNP P0AEX9
A	364	ALA	ASP	engineered mutation	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	1008	ALA	CYS	engineered mutation	UNP P36813
A	1987	GLY	-	linker	UNP P36813
A	1988	SER	-	linker	UNP P36813
A	1989	GLY	-	linker	UNP P36813
A	1990	SER	-	linker	UNP P36813
A	1991	GLY	-	linker	UNP P36813
A	1992	SER	-	linker	UNP P36813
A	1993	GLY	-	linker	UNP P36813
A	1994	SER	-	linker	UNP P36813
A	1995	GLY	-	linker	UNP P36813
A	1996	SER	-	linker	UNP P36813
A	1997	GLY	-	linker	UNP P36813
A	1998	SER	-	linker	UNP P36813
A	1999	ALA	-	linker	UNP P36813
A	2000	ALA	-	linker	UNP P36813

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2001	ALA	-	linker	UNP P36813

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

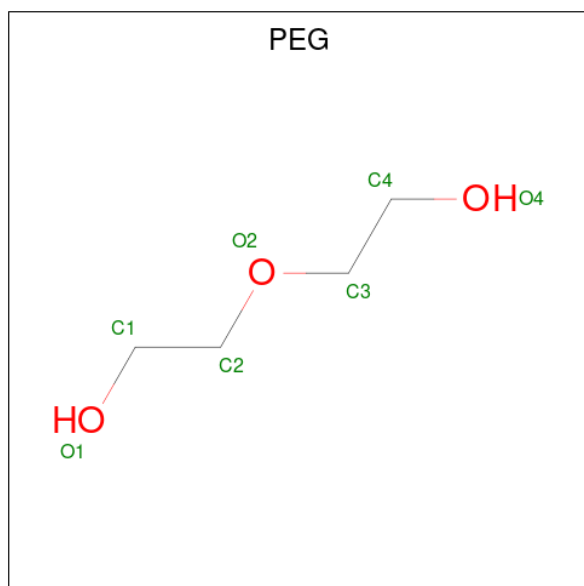


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		

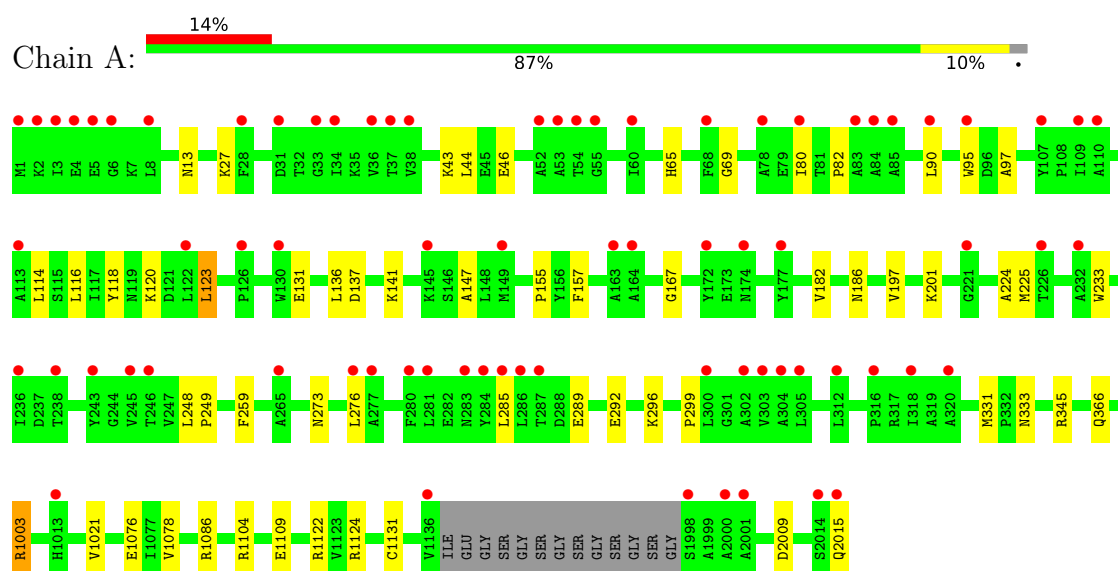
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	171	Total 171	O 171	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: Maltose/maltodextrin-binding periplasmic protein, Protein E6, Mastermind-like protein 1



- Molecule 2: 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 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.91Å 44.54Å 94.24Å 90.00° 99.70° 90.00°	Depositor
Resolution (Å)	46.44 – 2.14 46.44 – 2.14	Depositor EDS
% Data completeness (in resolution range)	97.8 (46.44-2.14) 97.7 (46.44-2.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.18rc1_3769	Depositor
R, R_{free}	0.218 , 0.255 0.222 , 0.230	Depositor DCC
R_{free} test set	1983 reflections (5.89%)	wwPDB-VP
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 65.9	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	4298	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.90% 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: PEG, 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	0.08	0/4177	0.24	0/5674

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	4073	0	3992	34	0
2	B	45	0	39	0	0
3	A	2	0	0	0	0
4	A	7	0	10	1	0
5	A	171	0	0	2	0
All	All	4298	0	4041	34	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 (34) 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:137:ASP:OD2	1:A:141:LYS:NZ	2.21	0.70
1:A:43:LYS:NZ	1:A:46:GLU:OE1	2.29	0.66
1:A:80:ILE:HG22	1:A:82:PRO:HD3	1.79	0.63
1:A:233:TRP:HB2	1:A:299:PRO:HG2	1.82	0.61
1:A:1076:GLU:OE2	1:A:1086:ARG:NH1	2.36	0.57
1:A:1104:ARG:NH1	1:A:2015:GLN:OXT	2.37	0.57
1:A:182:VAL:O	1:A:366:GLN:NE2	2.37	0.56
1:A:1124:ARG:NH1	1:A:2009:ASP:OD1	2.27	0.54
1:A:1078:VAL:HG11	1:A:1086:ARG:HG3	1.90	0.53
1:A:1003[A]:ARG:NH2	5:A:2208:HOH:O	2.41	0.53
1:A:116:LEU:HD22	1:A:249:PRO:HD3	1.91	0.53
1:A:123:LEU:HD11	1:A:136:LEU:HD21	1.91	0.52
1:A:1003[B]:ARG:NH2	5:A:2211:HOH:O	2.43	0.52
1:A:273:ASN:HB3	1:A:276:LEU:HB2	1.90	0.52
1:A:90:LEU:HB2	1:A:95:TRP:HE1	1.76	0.50
1:A:65:HIS:NE2	1:A:331:MET:O	2.42	0.48
1:A:1076:GLU:HG2	1:A:1122:ARG:HH21	1.78	0.47
1:A:27:LYS:NZ	1:A:289:GLU:OE1	2.43	0.47
1:A:116:LEU:HB2	1:A:248:LEU:HD23	1.96	0.47
1:A:131:GLU:OE1	1:A:131:GLU:N	2.47	0.47
1:A:69:GLY:HA3	1:A:333:ASN:O	2.15	0.47
1:A:13:ASN:HA	1:A:44:LEU:HD21	1.98	0.46
1:A:123:LEU:HD12	1:A:224:ALA:HB1	1.98	0.46
1:A:167:GLY:HA2	1:A:186:ASN:HD21	1.81	0.45
1:A:155:PRO:HD3	1:A:345:ARG:HG3	1.98	0.45
1:A:147:ALA:O	1:A:225:MET:N	2.45	0.44
1:A:114:LEU:HD11	1:A:157:PHE:HA	2.01	0.43
1:A:197:VAL:HG12	1:A:201:LYS:HE3	2.01	0.43
1:A:1021:VAL:HG13	4:A:2104:PEG:H21	2.00	0.43
1:A:182:VAL:C	1:A:366:GLN:HE22	2.24	0.42
1:A:65:HIS:CD2	1:A:97:ALA:HB1	2.55	0.42
1:A:1109:GLU:OE2	1:A:1131:CYS:HB2	2.20	0.41
1:A:292:GLU:O	1:A:296:LYS:HG3	2.21	0.40
1:A:118:TYR:CE2	1:A:120:LYS:HG2	2.55	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	523/538 (97%)	508 (97%)	14 (3%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	LEU

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	411/428 (96%)	407 (99%)	4 (1%)	68	74

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

Mol	Chain	Res	Type
1	A	123	LEU
1	A	259	PHE
1	A	1003[A]	ARG
1	A	1003[B]	ARG

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 ⓘ

4 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	1.26	1 (8%)	17,17,17	0.95	0
2	GLC	B	2	2	11,11,12	2.67	7 (63%)	15,15,17	1.03	1 (6%)
2	GLC	B	3	2	11,11,12	2.65	5 (45%)	15,15,17	1.47	3 (20%)
2	GLC	B	4	2	11,11,12	2.91	7 (63%)	15,15,17	1.24	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	-	2/2/19/22	0/1/1/1
2	GLC	B	3	2	-	0/2/19/22	0/1/1/1
2	GLC	B	4	2	-	1/2/19/22	0/1/1/1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4	GLC	O5-C5	6.59	1.56	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	GLC	O5-C5	6.19	1.55	1.43
2	B	3	GLC	O5-C5	6.16	1.55	1.43
2	B	4	GLC	O5-C1	3.83	1.50	1.43
2	B	2	GLC	C2-C3	-3.20	1.47	1.52
2	B	3	GLC	C2-C3	-3.05	1.47	1.52
2	B	4	GLC	O2-C2	3.04	1.49	1.43
2	B	3	GLC	C6-C5	-2.89	1.42	1.51
2	B	4	GLC	C2-C3	-2.82	1.48	1.52
2	B	2	GLC	C6-C5	-2.72	1.42	1.51
2	B	3	GLC	O2-C2	2.55	1.48	1.43
2	B	4	GLC	C1-C2	-2.55	1.46	1.52
2	B	1	GLC	O5-C5	2.24	1.49	1.44
2	B	4	GLC	C6-C5	-2.21	1.44	1.51
2	B	4	GLC	O4-C4	2.14	1.48	1.43
2	B	2	GLC	O3-C3	2.10	1.48	1.43
2	B	2	GLC	C1-C2	-2.07	1.47	1.52
2	B	3	GLC	O5-C1	2.06	1.47	1.43
2	B	2	GLC	O2-C2	2.03	1.47	1.43
2	B	2	GLC	O4-C4	2.02	1.48	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	GLC	C3-C4-C5	3.02	115.70	110.23
2	B	3	GLC	C2-C3-C4	2.82	115.82	110.86
2	B	4	GLC	C1-O5-C5	2.74	115.86	112.19
2	B	4	GLC	C1-C2-C3	2.58	113.40	109.64
2	B	3	GLC	C1-C2-C3	2.41	113.16	109.64
2	B	2	GLC	C3-C4-C5	2.04	113.93	110.23

There are no chirality outliers.

All (3) torsion outliers are listed below:

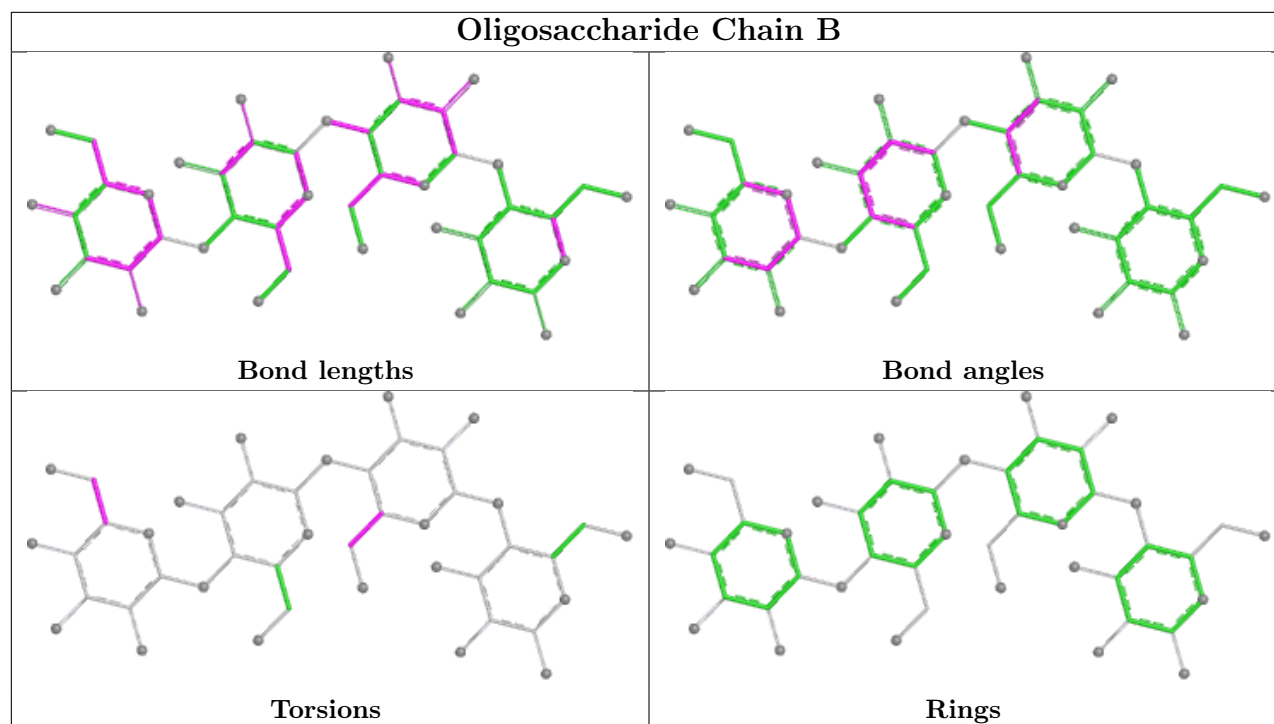
Mol	Chain	Res	Type	Atoms
2	B	4	GLC	O5-C5-C6-O6
2	B	2	GLC	C4-C5-C6-O6
2	B	2	GLC	O5-C5-C6-O6

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](#)

Of 3 ligands modelled in this entry, 2 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	$\# Z > 2$
4	PEG	A	2104	-	6,6,6	0.50	0	5,5,5	0.29	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
4	PEG	A	2104	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2104	PEG	C1-C2-O2-C3
4	A	2104	PEG	O2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2104	PEG	1	0

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	525/538 (97%)	0.92	75 (14%) 6 7	23, 74, 151, 195	2 (0%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	95	TRP	5.6
1	A	1998	SER	5.0
1	A	276	LEU	4.7
1	A	284	TYR	4.4
1	A	1136	VAL	4.3
1	A	281	LEU	4.3
1	A	38	VAL	3.8
1	A	286	LEU	3.7
1	A	285	LEU	3.6
1	A	277	ALA	3.5
1	A	280	PHE	3.3
1	A	37	THR	3.3
1	A	85	ALA	3.2
1	A	6	GLY	3.2
1	A	5	GLU	3.2
1	A	174	ASN	3.2
1	A	36	VAL	3.2
1	A	126	PRO	3.0
1	A	68	PHE	3.0
1	A	302	ALA	3.0
1	A	109	ILE	3.0
1	A	107	TYR	3.0
1	A	54	THR	3.0
1	A	110	ALA	2.9
1	A	60	ILE	2.9
1	A	2014	SER	2.9
1	A	245	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	287	THR	2.8
1	A	90	LEU	2.8
1	A	305	LEU	2.8
1	A	221	GLY	2.8
1	A	232	ALA	2.8
1	A	3	ILE	2.7
1	A	236	ILE	2.7
1	A	80	ILE	2.7
1	A	2	LYS	2.7
1	A	312	LEU	2.7
1	A	318	ILE	2.7
1	A	226	THR	2.6
1	A	31	ASP	2.6
1	A	303	VAL	2.6
1	A	78	ALA	2.6
1	A	164	ALA	2.6
1	A	8	LEU	2.6
1	A	34	ILE	2.6
1	A	172	TYR	2.6
1	A	243	TYR	2.6
1	A	4	GLU	2.5
1	A	122	LEU	2.5
1	A	28	PHE	2.5
1	A	84	ALA	2.4
1	A	265	ALA	2.4
1	A	145	LYS	2.4
1	A	304	ALA	2.4
1	A	320	ALA	2.4
1	A	130	TRP	2.4
1	A	2015	GLN	2.3
1	A	1013	HIS	2.3
1	A	246	THR	2.3
1	A	52	ALA	2.3
1	A	238	THR	2.3
1	A	300	LEU	2.3
1	A	316	PRO	2.2
1	A	83	ALA	2.2
1	A	1	MET	2.1
1	A	283	ASN	2.1
1	A	163	ALA	2.1
1	A	53	ALA	2.1
1	A	113	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	2000	ALA	2.1
1	A	33	GLY	2.0
1	A	149	MET	2.0
1	A	2001	ALA	2.0
1	A	55	GLY	2.0
1	A	177	TYR	2.0

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

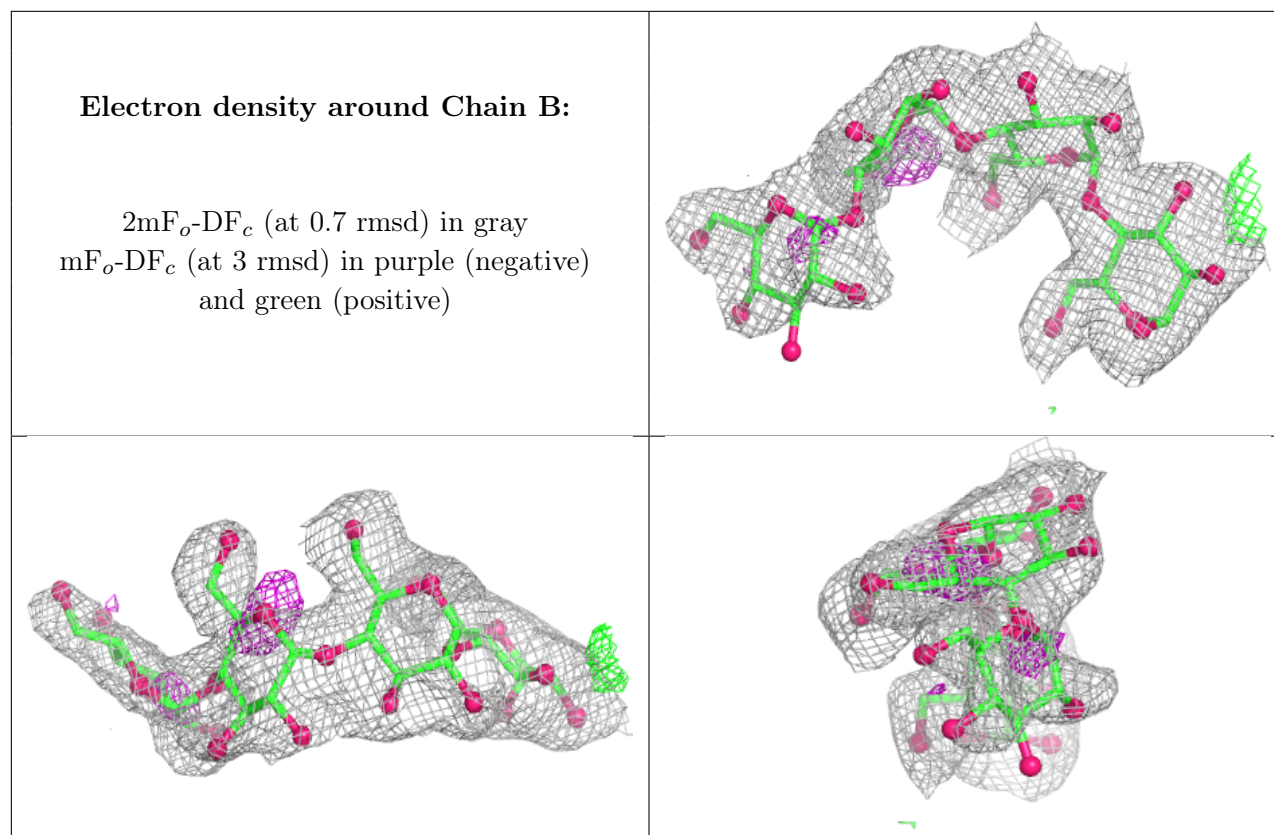
There are no non-standard protein/DNA/RNA residues in this entry.

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(Å ²)	Q<0.9
2	GLC	B	4	11/12	0.70	0.14	93,96,99,99	0
2	GLC	B	3	11/12	0.81	0.15	66,78,85,93	0
2	GLC	B	1	12/12	0.89	0.10	47,57,61,62	0
2	GLC	B	2	11/12	0.90	0.09	50,58,62,65	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
4	PEG	A	2104	7/7	0.84	0.15	63,67,73,74	0
3	ZN	A	2101	1/1	0.96	0.05	51,51,51,51	0
3	ZN	A	2102	1/1	0.97	0.05	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.