



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 07:19 PM BST

PDB ID : 6EHO  
Title : Dimer of the Sortilin Vps10p domain at low pH  
Authors : Thirup, S.S.; Quistgaard, E.H.; Janulienė, D.; Andersen, J.L.; Nielsen, J.A.  
Deposited on : 2017-09-14  
Resolution : 3.50 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

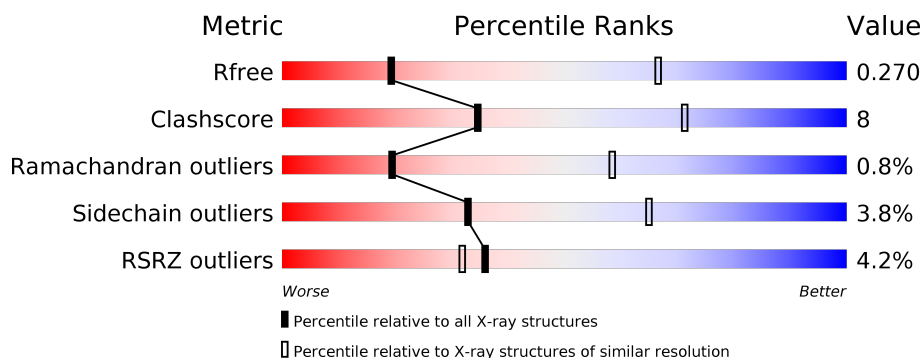
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	723	<div> <div>4%</div> <div> <div></div> <div>68%</div> <div>20%</div> <div>•</div> <div>11%</div> </div> </div>
2	B	5	<div> <div>20%</div> <div>80%</div> </div>
3	C	3	<div> <div>100%</div> </div>
4	D	2	<div> <div>100%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	D	2	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5163 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.

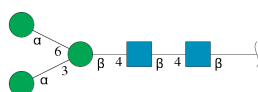
- Molecule 1 is a protein called Sortilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	642	5035	3183	840	983	29	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

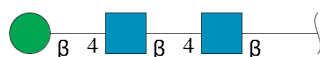
Chain	Residue	Modelled	Actual	Comment	Reference
A	43	GLY	ARG	engineered mutation	UNP Q99523
A	44	GLY	ARG	engineered mutation	UNP Q99523
A	617	MET	VAL	conflict	UNP Q99523

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



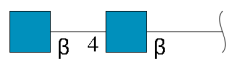
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	5	61	34	2	25	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

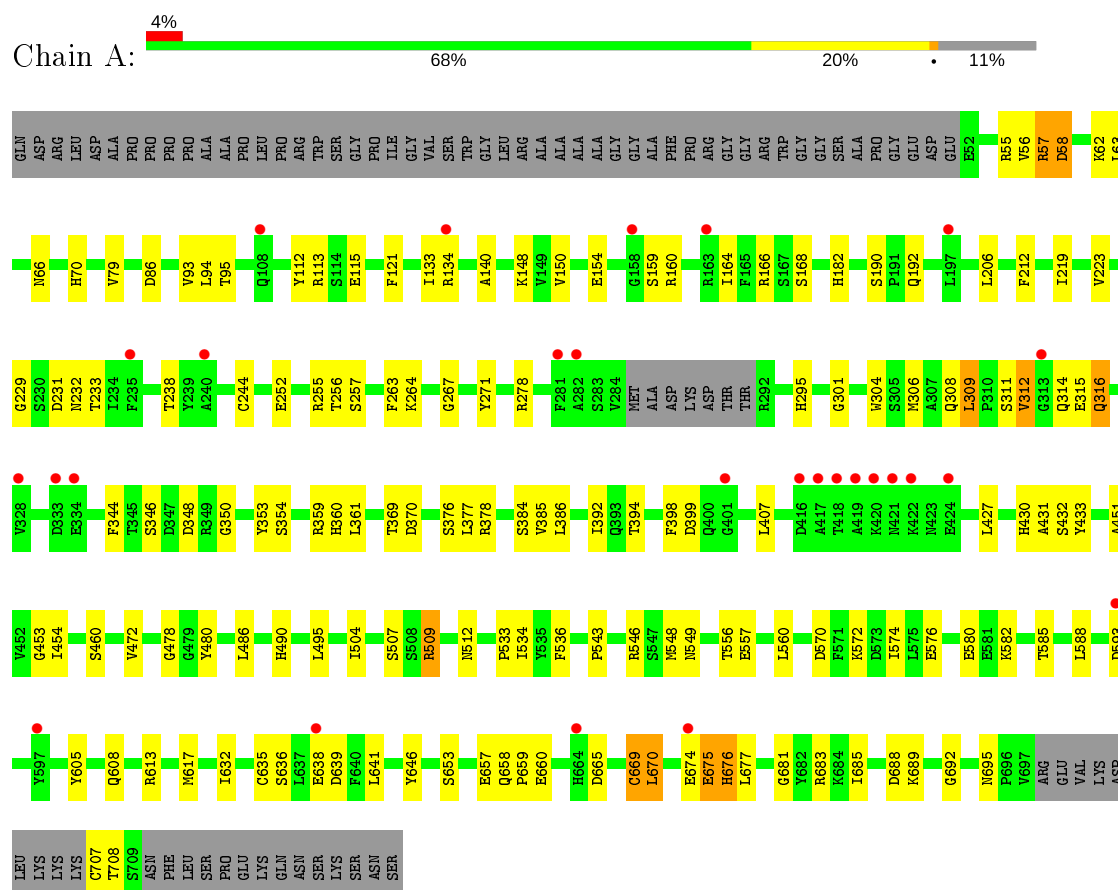


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

### 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: Sortilin



#### • Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:



#### • Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  100%

HA01  
HA02  
BU03

- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

HA01  
HA02

## 4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	189.01Å 189.01Å 189.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.50 – 3.50 94.50 – 3.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (94.50-3.50) 98.6 (94.50-3.50)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 3.49Å)	Xtriage
Refinement program	PHENIX (dev_2614: ???)	Depositor
R, $R_{free}$	0.232 , 0.272 0.231 , 0.270	Depositor DCC
$R_{free}$ test set	566 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	139.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 127.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.033 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	5163	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	146.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: BMA, NAG, MAN

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	0.25	0/5155	0.44	0/6988

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	5035	0	4795	84	0
2	B	61	0	52	1	0
3	C	39	0	34	0	0
4	D	28	0	25	0	0
All	All	5163	0	4906	84	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 8.

All (84) 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:62:LYS:NZ	1:A:576:GLU:OE2	2.14	0.81
1:A:451:ALA:HB1	1:A:454:ILE:HD12	1.75	0.68
1:A:312:VAL:HA	1:A:316:GLN:HG3	1.76	0.68
1:A:534:ILE:HG22	1:A:556:THR:HG22	1.80	0.64
1:A:56:VAL:HG22	1:A:57:ARG:H	1.63	0.64
1:A:658:GLN:O	1:A:660:GLU:N	2.30	0.64
1:A:56:VAL:O	1:A:58:ASP:N	2.30	0.64
1:A:278:ARG:NH2	1:A:348:ASP:O	2.32	0.62
1:A:430:HIS:NE2	1:A:460:SER:OG	2.33	0.61
1:A:605:TYR:HB3	1:A:632:ILE:HD13	1.82	0.60
1:A:134:ARG:HH12	1:A:154:GLU:HG3	1.66	0.60
1:A:206:LEU:HD12	1:A:223:VAL:HG11	1.83	0.59
1:A:635:CYS:N	1:A:692:GLY:O	2.34	0.59
1:A:238:THR:HB	1:A:252:GLU:HG3	1.84	0.59
1:A:150:VAL:HB	1:A:164:ILE:HD11	1.87	0.57
1:A:588:LEU:HD21	1:A:608:GLN:HG2	1.87	0.57
1:A:306:MET:O	1:A:308:GLN:NE2	2.38	0.57
1:A:636:SER:H	1:A:639:ASP:HB2	1.69	0.56
1:A:360:HIS:HA	1:A:385:VAL:HG12	1.86	0.56
1:A:361:LEU:HD21	1:A:386:LEU:HG	1.88	0.55
1:A:674:GLU:HG2	1:A:675:GLU:H	1.70	0.55
1:A:66:ASN:HB3	1:A:570:ASP:HB3	1.88	0.55
1:A:369:THR:O	1:A:432:SER:OG	2.25	0.55
1:A:472:VAL:HB	1:A:486:LEU:HB2	1.89	0.55
1:A:346:SER:HB2	1:A:350:GLY:HA2	1.88	0.55
1:A:309:LEU:HD13	1:A:312:VAL:HG21	1.89	0.54
1:A:548:MET:HE1	1:A:572:LYS:HD3	1.91	0.53
1:A:255:ARG:NH2	1:A:257:SER:OG	2.42	0.53
1:A:384:SER:HA	1:A:394:THR:HA	1.90	0.53
1:A:267:GLY:HA2	1:A:708:THR:OG1	2.09	0.53
1:A:166:ARG:NH1	1:A:212:PHE:O	2.42	0.53
1:A:255:ARG:HH11	1:A:264:LYS:HD3	1.74	0.52
1:A:354:SER:OG	1:A:683:ARG:NH2	2.42	0.52
1:A:140:ALA:HB3	1:A:150:VAL:HG23	1.92	0.51
1:A:93:VAL:HB	1:A:112:TYR:HB2	1.92	0.51
1:A:359:ARG:HB3	1:A:386:LEU:HB2	1.92	0.51
1:A:56:VAL:HG21	1:A:617:MET:HG2	1.92	0.51
1:A:646:TYR:CE1	1:A:657:GLU:HG2	2.47	0.49
1:A:641:LEU:N	1:A:683:ARG:O	2.41	0.49
1:A:376:SER:HB3	1:A:453:GLY:N	2.28	0.49
1:A:399:ASP:OD1	1:A:399:ASP:N	2.44	0.49
1:A:63:LEU:HG	1:A:574:ILE:HD11	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:585:THR:HG23	1:A:613:ARG:HE	1.78	0.49
1:A:580:GLU:HB2	1:A:582:LYS:HG2	1.94	0.48
1:A:190:SER:OG	1:A:232:ASN:OD1	2.28	0.48
1:A:295:HIS:NE2	1:A:707:CYS:HA	2.29	0.48
1:A:344:PHE:HB3	1:A:353:TYR:HB3	1.95	0.48
1:A:641:LEU:O	1:A:683:ARG:N	2.36	0.48
1:A:472:VAL:HG21	1:A:490:HIS:HB2	1.96	0.48
1:A:159:SER:O	1:A:182:HIS:NE2	2.44	0.48
1:A:394:THR:HG23	1:A:407:LEU:HD13	1.97	0.47
1:A:646:TYR:CD1	1:A:681:GLY:HA3	2.49	0.46
1:A:113:ARG:NH1	1:A:115:GLU:OE2	2.49	0.46
1:A:206:LEU:HB2	1:A:223:VAL:HG21	1.96	0.46
1:A:377:LEU:HD12	1:A:478:GLY:HA3	1.97	0.46
1:A:219:ILE:HG23	1:A:263:PHE:CZ	2.51	0.46
1:A:148:LYS:HG2	1:A:168:SER:HA	1.98	0.45
1:A:669:CYS:HB3	1:A:670:LEU:H	1.62	0.45
1:A:86:ASP:HB3	1:A:543:PRO:O	2.17	0.45
1:A:206:LEU:HD22	1:A:219:ILE:HB	1.97	0.45
1:A:301:GLY:O	1:A:304:TRP:NE1	2.50	0.45
1:A:370:ASP:HA	1:A:431:ALA:HB3	1.98	0.45
1:A:56:VAL:HG22	1:A:57:ARG:N	2.32	0.43
1:A:134:ARG:NH1	1:A:154:GLU:HG3	2.32	0.43
1:A:219:ILE:HG23	1:A:263:PHE:HZ	1.84	0.43
1:A:70:HIS:CE1	1:A:121:PHE:HB2	2.54	0.43
1:A:507:SER:HB2	1:A:509:ARG:NH1	2.34	0.42
1:A:192:GLN:HB2	1:A:231:ASP:HA	2.01	0.42
1:A:384:SER:HB3	1:A:392:ILE:HD11	2.01	0.42
1:A:314:GLN:HB3	1:A:315:GLU:H	1.64	0.42
1:A:665:ASP:OD1	1:A:676:HIS:HA	2.20	0.42
1:A:512:ASN:HB3	1:A:533:PRO:HA	2.02	0.42
1:A:229:GLY:N	1:A:233:THR:O	2.53	0.42
1:A:94:LEU:HD11	1:A:133:ILE:HD13	2.01	0.41
1:A:369:THR:HA	1:A:433:TYR:HB2	2.02	0.41
1:A:641:LEU:HB2	1:A:685:ILE:HG12	2.03	0.41
1:A:252:GLU:HA	1:A:267:GLY:O	2.21	0.41
1:A:638:GLU:OE2	1:A:653:SER:OG	2.37	0.41
1:A:398:PHE:HZ	1:A:480:TYR:HB2	1.86	0.40
1:A:394:THR:HG22	1:A:427:LEU:O	2.21	0.40
1:A:685:ILE:HB	1:A:688:ASP:HB2	2.03	0.40
1:A:79:VAL:HG22	1:A:95:THR:HG22	2.02	0.40
1:A:378:ARG:NH2	2:B:1:NAG:H3	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:504:ILE:HG21	1:A:536:PHE:CD1	2.57	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	636/723 (88%)	553 (87%)	78 (12%)	5 (1%)	19 58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	ARG
1	A	311	SER
1	A	659	PRO
1	A	58	ASP
1	A	312	VAL

### 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	557/620 (90%)	536 (96%)	21 (4%)	33 65

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ARG
1	A	160	ARG
1	A	244	CYS
1	A	256	THR
1	A	271	TYR
1	A	309	LEU
1	A	316	GLN
1	A	495	LEU
1	A	509	ARG
1	A	546	ARG
1	A	549	ASN
1	A	557	GLU
1	A	560	LEU
1	A	593	ASP
1	A	669	CYS
1	A	670	LEU
1	A	675	GLU
1	A	676	HIS
1	A	677	LEU
1	A	689	LYS
1	A	695	ASN

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

Mol	Chain	Res	Type
1	A	66	ASN
1	A	68	HIS
1	A	69	GLN
1	A	70	HIS
1	A	490	HIS
1	A	522	GLN
1	A	691	GLN

### 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 ⓘ

10 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	1,2	14,14,15	0.31	0	17,19,21	0.43	0
2	NAG	B	2	2	14,14,15	0.20	0	17,19,21	0.48	0
2	BMA	B	3	2	11,11,12	1.15	1 (9%)	15,15,17	1.26	2 (13%)
2	MAN	B	4	2	11,11,12	1.00	1 (9%)	15,15,17	1.47	2 (13%)
2	MAN	B	5	2	11,11,12	0.82	0	15,15,17	1.22	2 (13%)
3	NAG	C	1	1,3	14,14,15	0.40	0	17,19,21	0.54	0
3	NAG	C	2	3	14,14,15	0.24	0	17,19,21	0.43	0
3	BMA	C	3	3	11,11,12	0.64	0	15,15,17	0.74	0
4	NAG	D	1	1,4	14,14,15	0.50	0	17,19,21	0.59	0
4	NAG	D	2	4	14,14,15	0.22	0	17,19,21	0.47	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	B	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	2/2/19/22	0/1/1/1
2	MAN	B	4	2	-	1/2/19/22	1/1/1/1
2	MAN	B	5	2	-	1/2/19/22	1/1/1/1
3	NAG	C	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
4	NAG	D	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	BMA	C1-C2	2.78	1.58	1.52
2	B	4	MAN	C1-C2	2.60	1.58	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4	MAN	C1-O5-C5	4.02	117.64	112.19
2	B	5	MAN	C1-O5-C5	3.58	117.04	112.19
2	B	4	MAN	O2-C2-C3	-2.38	105.36	110.14
2	B	3	BMA	O2-C2-C3	-2.33	105.48	110.14
2	B	5	MAN	O2-C2-C3	-2.24	105.65	110.14
2	B	3	BMA	C1-C2-C3	-2.21	106.95	109.67

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
2	B	3	BMA	O5-C5-C6-O6
2	B	3	BMA	C4-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	B	4	MAN	O5-C5-C6-O6
2	B	5	MAN	O5-C5-C6-O6

All (2) ring outliers are listed below:

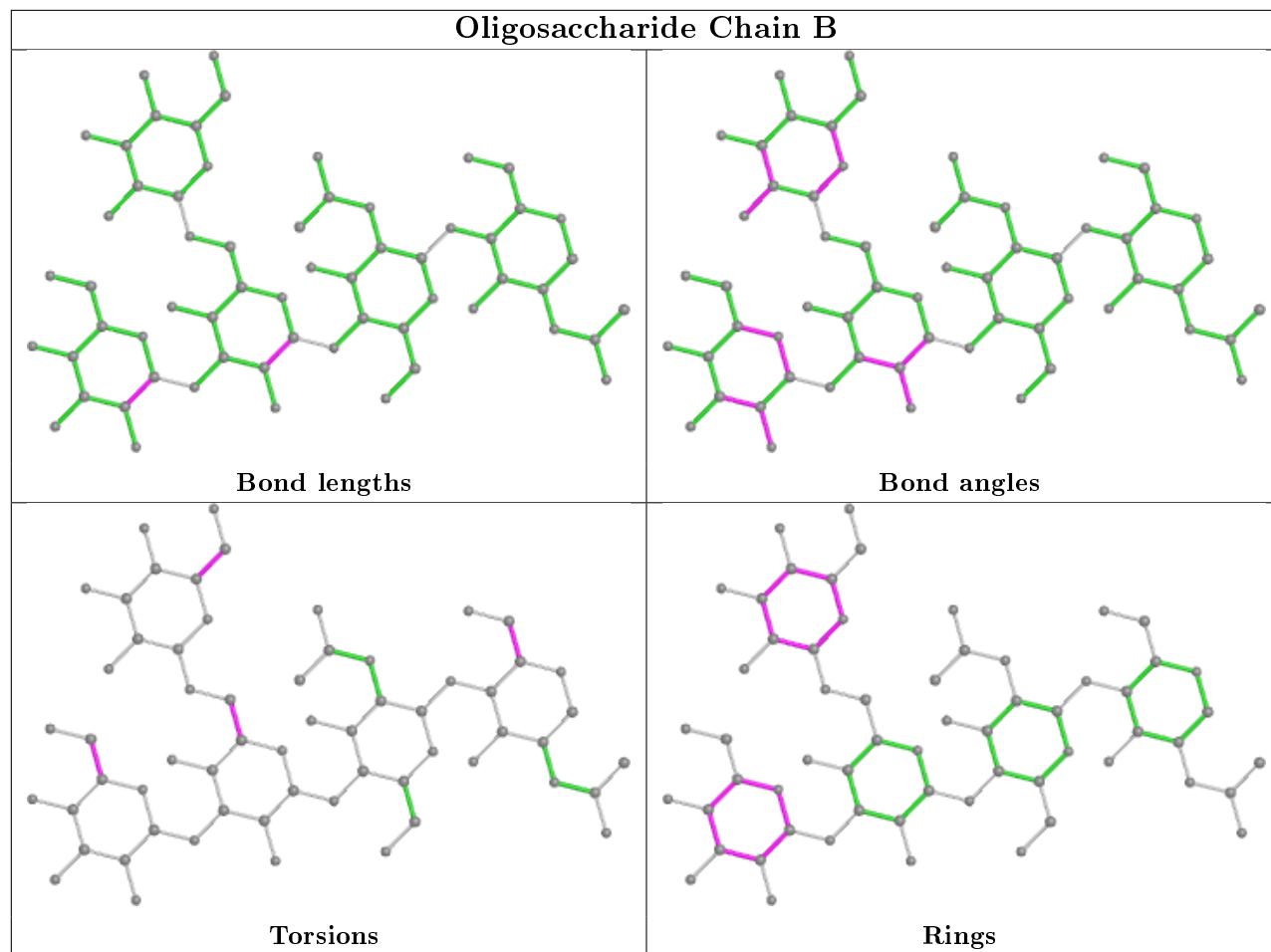
Mol	Chain	Res	Type	Atoms
2	B	4	MAN	C1-C2-C3-C4-C5-O5
2	B	5	MAN	C1-C2-C3-C4-C5-O5

1 monomer is involved in 1 short contact:

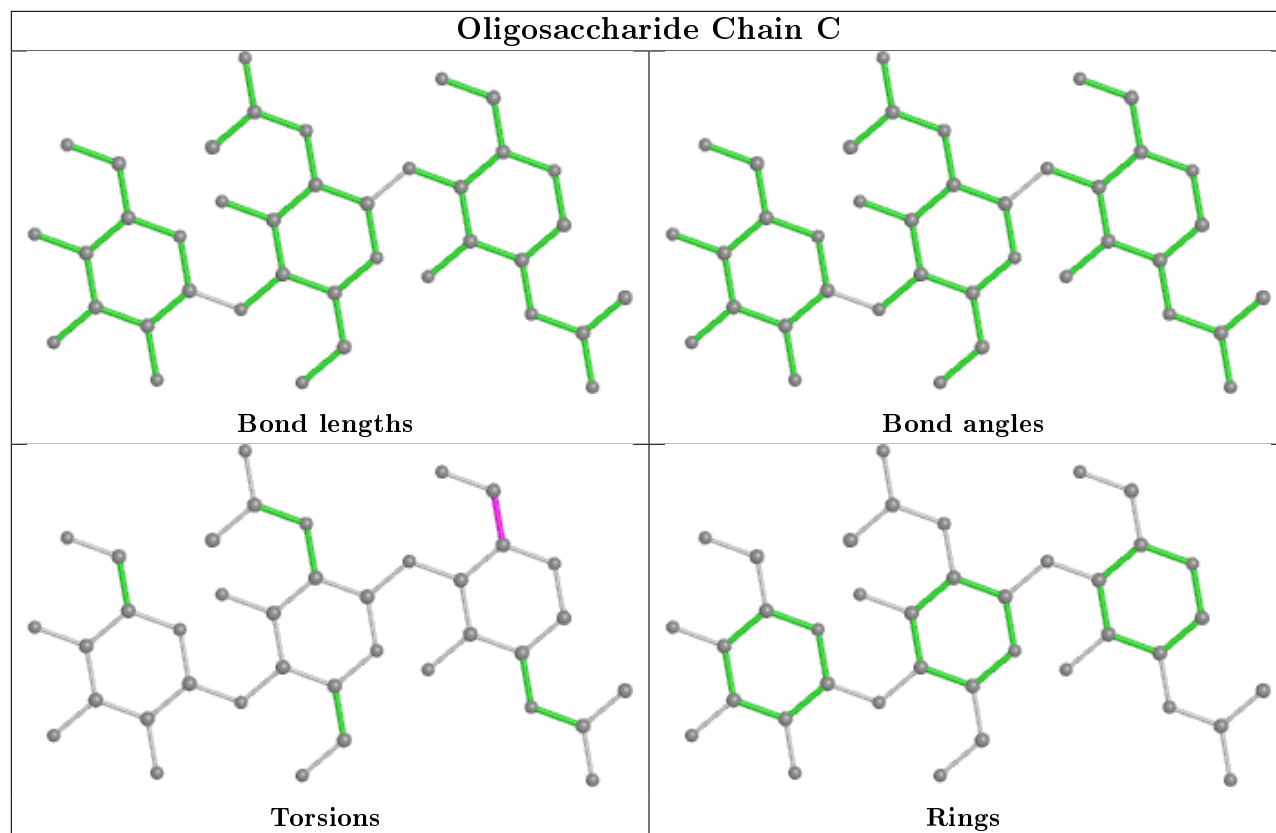
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	1	0

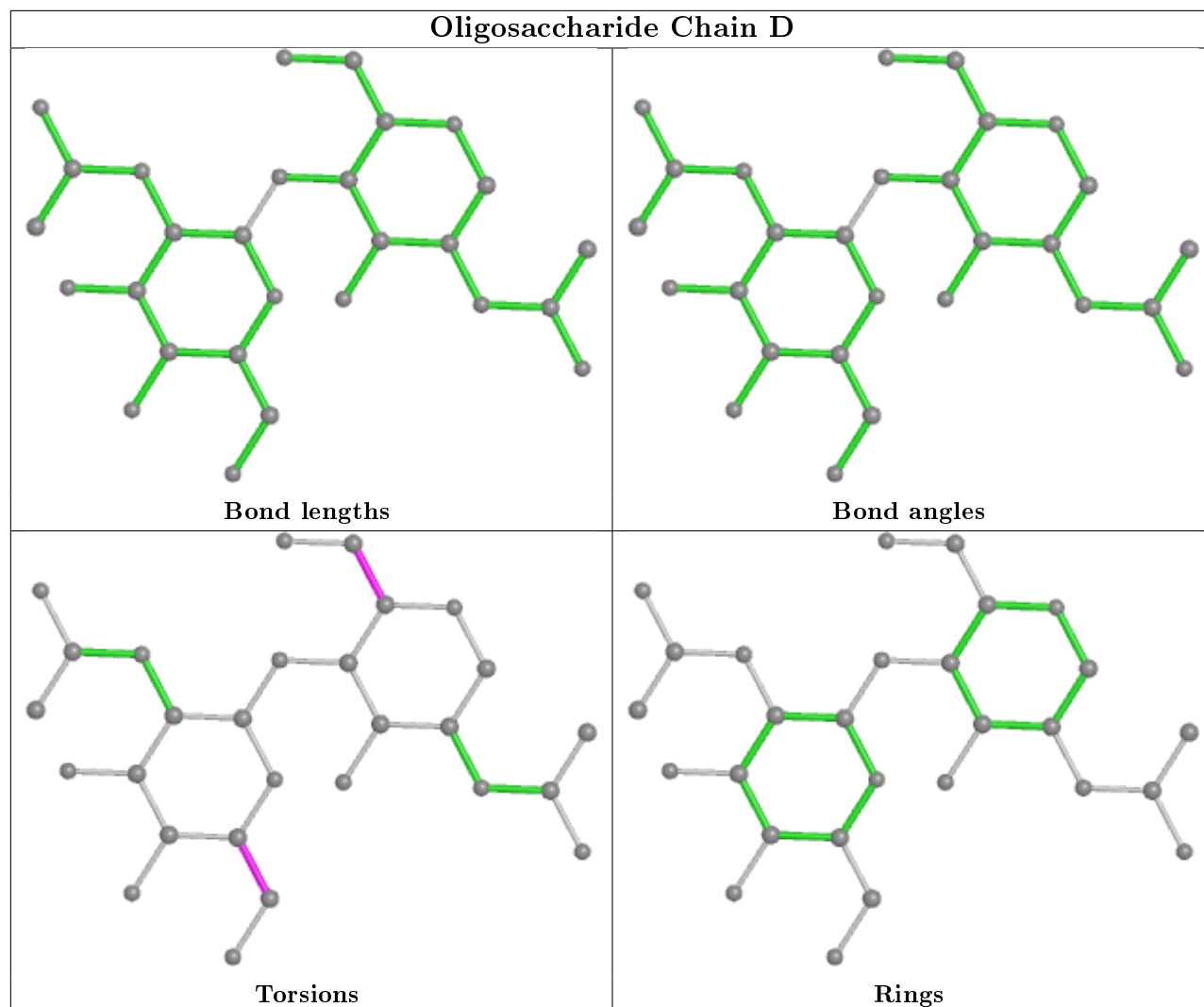
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for oligosaccharide.









## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	642/723 (88%)	0.49	27 (4%) 36 32	83, 143, 201, 248	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	421	ASN	7.1
1	A	419	ALA	5.1
1	A	420	LYS	5.0
1	A	674	GLU	3.6
1	A	424	GLU	3.4
1	A	334	GLU	3.3
1	A	108	GLN	3.2
1	A	163	ARG	3.1
1	A	417	ALA	3.0
1	A	313	GLY	2.8
1	A	597	TYR	2.8
1	A	664	HIS	2.7
1	A	416	ASP	2.7
1	A	158	GLY	2.5
1	A	240	ALA	2.3
1	A	422	LYS	2.3
1	A	401	GLY	2.3
1	A	593	ASP	2.3
1	A	328	VAL	2.1
1	A	235	PHE	2.1
1	A	418	THR	2.1
1	A	282	ALA	2.1
1	A	281	PHE	2.1
1	A	333	ASP	2.0
1	A	134	ARG	2.0
1	A	197	LEU	2.0
1	A	638	GLU	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 ⓘ

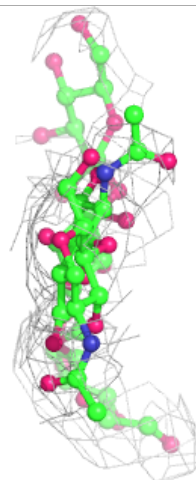
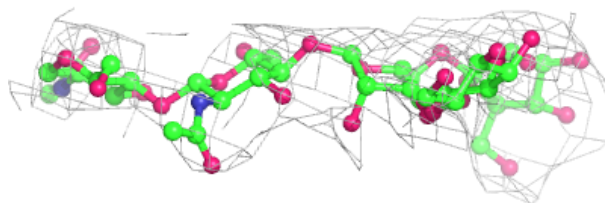
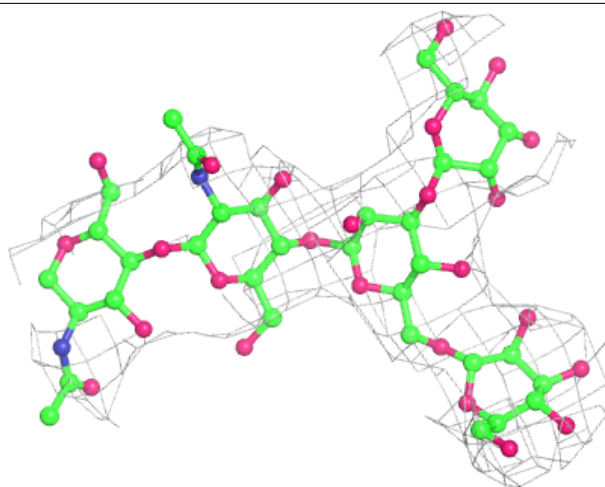
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MAN	B	4	11/12	0.58	0.34	204,209,213,213	0
4	NAG	D	1	14/15	0.73	0.29	180,193,213,217	0
2	BMA	B	3	11/12	0.74	0.18	185,189,198,200	0
4	NAG	D	2	14/15	0.78	0.67	218,224,225,226	0
3	BMA	C	3	11/12	0.80	0.28	180,183,192,196	0
2	MAN	B	5	11/12	0.82	0.20	195,197,198,200	0
2	NAG	B	1	14/15	0.84	0.31	126,143,169,183	0
2	NAG	B	2	14/15	0.85	0.25	159,166,173,185	0
3	NAG	C	2	14/15	0.91	0.25	150,155,165,174	0
3	NAG	C	1	14/15	0.93	0.26	125,137,147,152	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.

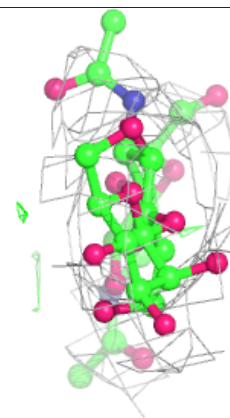
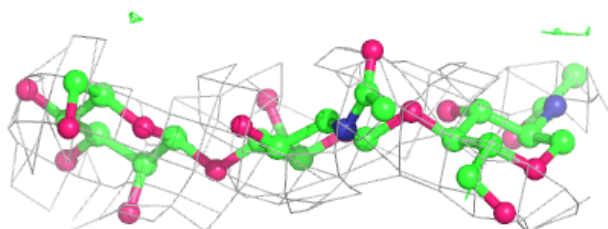
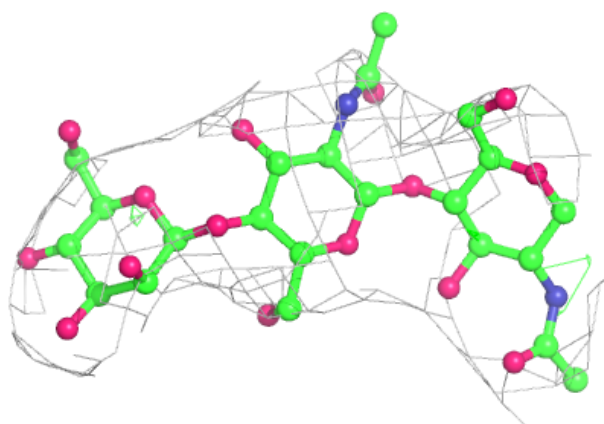
**Electron density around Chain B:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

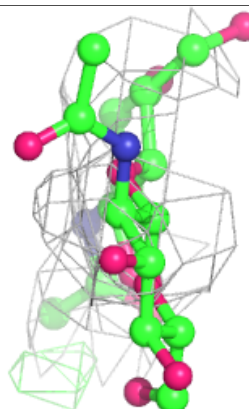
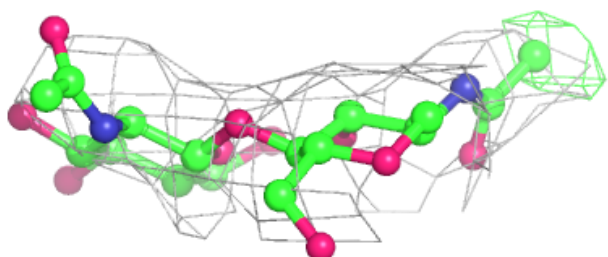
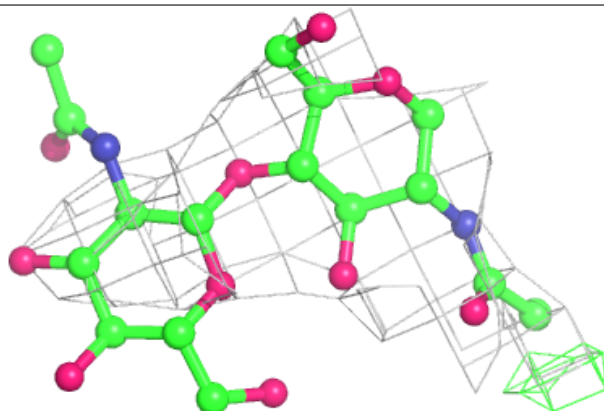


**Electron density around Chain C:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around Chain D:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.