



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 16, 2023 – 11:04 PM EDT

PDB ID : 2ESC  
Title : Crystal structure of a 40 KDa protective signalling protein from Bovine (SPC-40) at 2.1 Å resolution  
Authors : Kumar, J.; Ethayathulla, A.S.; Srivastav, D.B.; Sharma, S.; Srinivasan, A.; Singh, T.P.  
Deposited on : 2005-10-26  
Resolution : 2.10 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.

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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

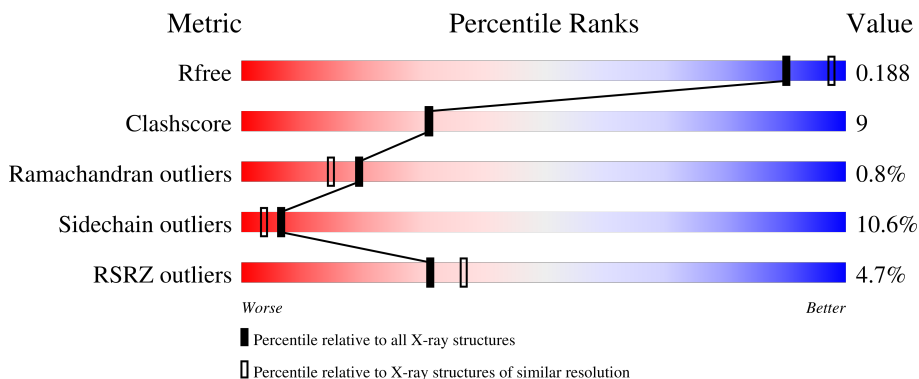
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

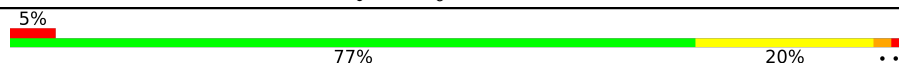
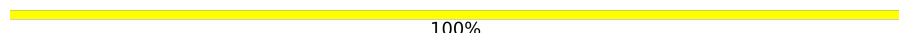
The reported resolution of this entry is 2.10 Å.

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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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  $\geq 3$ , 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	361	
2	B	6	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	B	3	-	-	-	X
2	MAN	B	4	X	-	-	X
2	MAN	B	5	X	-	-	X
2	MAN	B	6	-	-	-	X

## 2 Entry composition [i](#)

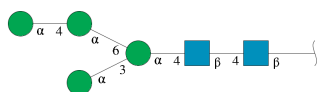
There are 3 unique types of molecules in this entry. The entry contains 3193 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chitinase-3-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	361	2874	1834	503	528	9	0	0	0

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-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	6	72	40	2	30	0	0	0

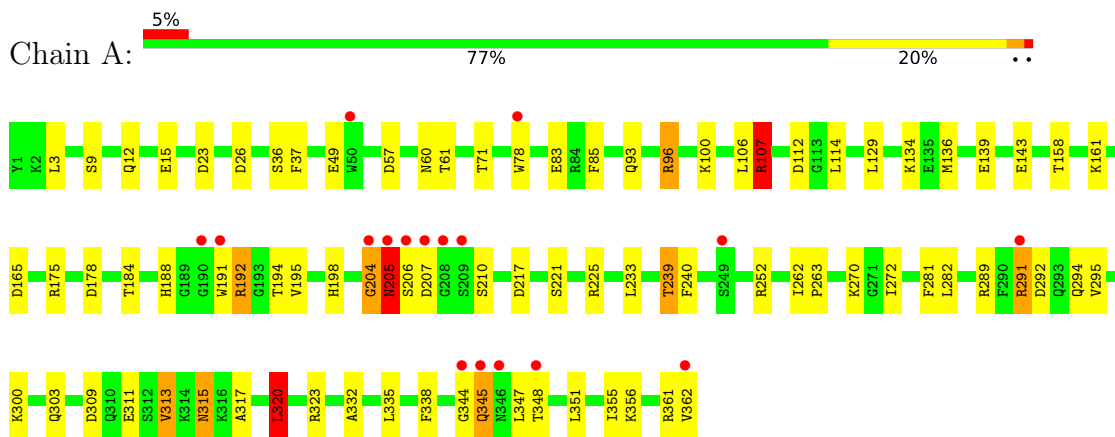
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	247	Total	O	0	0
			247	247		

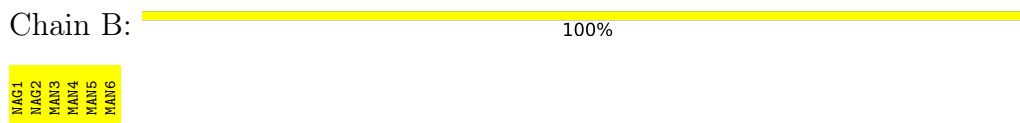
### 3 Residue-property plots [i](#)

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: Chitinase-3-like protein 1



- Molecule 2: alpha-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-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 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.68Å 67.42Å 106.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.86 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.8 (20.00-2.10) 97.9 (19.86-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 2.09Å)	Xtrriage
Refinement program	REFMAC 5.0, CNS 1.1	Depositor
R, $R_{free}$	0.173 , 0.220 0.180 , 0.188	Depositor DCC
$R_{free}$ test set	1281 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.8	Xtrriage
Anisotropy	0.072	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 46.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3193	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% 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: 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	0.70	0/2951	0.95	9/4002 (0.2%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	ARG	NE-CZ-NH1	9.97	125.29	120.30
1	A	107	ARG	NE-CZ-NH2	-8.62	115.99	120.30
1	A	320	LEU	CA-CB-CG	8.20	134.15	115.30
1	A	217	ASP	CB-CG-OD2	7.59	125.13	118.30
1	A	178	ASP	CB-CG-OD2	7.26	124.84	118.30
1	A	112	ASP	CB-CG-OD2	6.31	123.98	118.30
1	A	165	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	26	ASP	CB-CG-OD1	5.61	123.34	118.30
1	A	207	ASP	CB-CG-OD2	5.08	122.88	118.30

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	2874	0	2797	53	0
2	B	72	0	61	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	247	0	0	14	0
All	All	3193	0	2858	53	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 9.

All (53) 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:311:GLU:HG2	3:A:572:HOH:O	1.85	0.76
1:A:348:THR:HG22	3:A:474:HOH:O	1.86	0.75
1:A:317:ALA:HA	1:A:320:LEU:HD13	1.69	0.75
1:A:57:ASP:O	1:A:61:THR:HG23	1.87	0.74
1:A:292:ASP:HB2	3:A:450:HOH:O	1.87	0.73
1:A:204:GLY:CA	1:A:292:ASP:HB3	2.18	0.73
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.19	0.72
1:A:204:GLY:HA2	1:A:292:ASP:HB3	1.73	0.71
1:A:311:GLU:HG3	3:A:472:HOH:O	1.92	0.69
1:A:348:THR:HG21	3:A:554:HOH:O	1.95	0.66
1:A:100:LYS:CD	3:A:491:HOH:O	2.44	0.66
1:A:100:LYS:HE2	1:A:139:GLU:OE2	1.99	0.63
1:A:205:ASN:HD22	1:A:206:SER:N	1.97	0.62
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.82	0.62
1:A:61:THR:HG22	3:A:545:HOH:O	1.99	0.61
1:A:313:VAL:HG13	1:A:355:ILE:HG13	1.81	0.61
1:A:204:GLY:HA3	1:A:292:ASP:HB3	1.83	0.60
1:A:78:TRP:HH2	3:A:477:HOH:O	1.84	0.60
1:A:15:GLU:HB3	3:A:577:HOH:O	2.04	0.58
1:A:100:LYS:HD2	3:A:491:HOH:O	2.02	0.57
1:A:263:PRO:HD3	1:A:270:LYS:HG2	1.86	0.56
1:A:83:GLU:H	1:A:83:GLU:CD	2.10	0.55
1:A:281:PHE:O	1:A:300:LYS:HE3	2.07	0.54
1:A:262:ILE:H	1:A:303:GLN:HE22	1.55	0.54
1:A:262:ILE:H	1:A:303:GLN:NE2	2.05	0.54
1:A:114:LEU:HD22	1:A:136:MET:HE3	1.91	0.52
1:A:291:ARG:HG3	1:A:292:ASP:N	2.25	0.52
1:A:107:ARG:HD3	1:A:143:GLU:OE2	2.10	0.51
1:A:198:HIS:H	1:A:198:HIS:CD2	2.30	0.50
1:A:96:ARG:HD2	3:A:610:HOH:O	2.12	0.50
1:A:313:VAL:HG13	1:A:355:ILE:CG1	2.42	0.49
1:A:239:THR:HG23	1:A:239:THR:O	2.13	0.48

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:GLY:O	1:A:345:GLN:O	2.31	0.48
1:A:239:THR:HG21	1:A:332:ALA:O	2.14	0.47
1:A:100:LYS:HE2	1:A:139:GLU:CD	2.35	0.47
1:A:294:GLN:NE2	1:A:315:ASN:OD1	2.47	0.47
1:A:323:ARG:NH1	3:A:468:HOH:O	2.35	0.47
1:A:188:HIS:CD2	1:A:192:ARG:HD2	2.51	0.46
1:A:263:PRO:HD3	1:A:270:LYS:CG	2.44	0.46
1:A:134:LYS:HE3	1:A:134:LYS:HB2	1.78	0.45
1:A:205:ASN:HD22	1:A:205:ASN:C	2.19	0.45
1:A:270:LYS:HE3	1:A:270:LYS:HB2	1.74	0.45
1:A:356:LYS:NZ	3:A:433:HOH:O	2.51	0.44
1:A:9:SER:O	1:A:12:GLN:HG2	2.18	0.44
1:A:188:HIS:HE1	1:A:194:THR:O	2.01	0.44
1:A:240:PHE:HB3	1:A:335:LEU:HD13	2.00	0.44
1:A:221:SER:OG	1:A:323:ARG:NH2	2.51	0.44
1:A:49:GLU:OE2	3:A:603:HOH:O	2.21	0.43
1:A:289:ARG:NH2	1:A:309:ASP:OD2	2.48	0.42
1:A:36:SER:HA	1:A:37:PHE:HA	1.88	0.42
1:A:281:PHE:O	1:A:300:LYS:CE	2.68	0.41
1:A:338:PHE:O	1:A:348:THR:OG1	2.34	0.41
1:A:60:ASN:ND2	1:A:71:THR:OG1	2.54	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	359/361 (99%)	346 (96%)	10 (3%)	3 (1%)	19 15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
1	A	345	GLN
1	A	204	GLY

### 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	303/303 (100%)	271 (89%)	32 (11%)	<b>6</b> <b>4</b>

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	23	ASP
1	A	85	PHE
1	A	93	GLN
1	A	96	ARG
1	A	106	LEU
1	A	107	ARG
1	A	129	LEU
1	A	158	THR
1	A	161	LYS
1	A	175	ARG
1	A	184	THR
1	A	191	TRP
1	A	192	ARG
1	A	195	VAL
1	A	205	ASN
1	A	210	SER
1	A	225	ARG
1	A	233	LEU
1	A	239	THR
1	A	252	ARG
1	A	272	ILE
1	A	282	LEU
1	A	291	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	295	VAL
1	A	313	VAL
1	A	315	ASN
1	A	320	LEU
1	A	347	LEU
1	A	351	LEU
1	A	361	ARG
1	A	362	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	188	HIS
1	A	198	HIS
1	A	205	ASN
1	A	294	GLN
1	A	303	GLN
1	A	310	GLN
1	A	315	ASN

### 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](#)

6 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	2,1	14,14,15	0.84	1 (7%)	17,19,21	1.71	3 (17%)
2	NAG	B	2	2	14,14,15	0.80	1 (7%)	17,19,21	3.70	8 (47%)
2	MAN	B	3	2	11,11,12	1.16	0	15,15,17	2.84	4 (26%)
2	MAN	B	4	2	11,11,12	0.76	0	15,15,17	2.35	6 (40%)
2	MAN	B	5	2	11,11,12	0.47	0	15,15,17	1.35	2 (13%)
2	MAN	B	6	2	11,11,12	0.49	0	15,15,17	2.12	1 (6%)

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	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	3/6/23/26	0/1/1/1
2	MAN	B	3	2	-	2/2/19/22	1/1/1/1
2	MAN	B	4	2	1/1/4/5	2/2/19/22	0/1/1/1
2	MAN	B	5	2	1/1/4/5	2/2/19/22	0/1/1/1
2	MAN	B	6	2	-	0/2/19/22	1/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	O5-C1	-2.17	1.40	1.43
2	B	2	NAG	C1-C2	2.15	1.55	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	O5-C1-C2	8.35	124.48	111.29
2	B	6	MAN	C1-O5-C5	7.68	122.60	112.19
2	B	3	MAN	C6-C5-C4	6.69	128.68	113.00
2	B	4	MAN	C1-O5-C5	6.66	121.21	112.19
2	B	3	MAN	C1-O5-C5	6.41	120.87	112.19
2	B	2	NAG	C1-O5-C5	5.81	120.06	112.19
2	B	2	NAG	O4-C4-C5	-5.26	96.23	109.30
2	B	2	NAG	C4-C3-C2	5.24	118.70	111.02
2	B	2	NAG	O5-C5-C6	4.53	114.30	107.20
2	B	2	NAG	C3-C4-C5	4.47	118.22	110.24
2	B	3	MAN	O3-C3-C4	4.33	120.35	110.35

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	O5-C5-C4	4.16	120.95	110.83
2	B	1	NAG	C2-N2-C7	-4.03	117.17	122.90
2	B	4	MAN	C1-C2-C3	3.25	113.66	109.67
2	B	1	NAG	C8-C7-N2	2.99	121.16	116.10
2	B	4	MAN	O5-C1-C2	-2.90	106.29	110.77
2	B	1	NAG	O5-C1-C2	-2.66	107.09	111.29
2	B	5	MAN	C1-C2-C3	2.63	112.90	109.67
2	B	3	MAN	O5-C5-C6	-2.40	103.44	107.20
2	B	5	MAN	O5-C5-C6	2.40	110.96	107.20
2	B	4	MAN	C2-C3-C4	2.35	114.96	110.89
2	B	4	MAN	O5-C5-C6	2.32	110.84	107.20
2	B	2	NAG	C1-C2-N2	2.29	114.39	110.49
2	B	4	MAN	C3-C4-C5	2.05	113.89	110.24

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	4	MAN	C1
2	B	5	MAN	C1

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	4	MAN	O5-C5-C6-O6
2	B	5	MAN	O5-C5-C6-O6
2	B	3	MAN	O5-C5-C6-O6
2	B	4	MAN	C4-C5-C6-O6
2	B	3	MAN	C4-C5-C6-O6
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	B	2	NAG	C4-C5-C6-O6
2	B	5	MAN	C4-C5-C6-O6

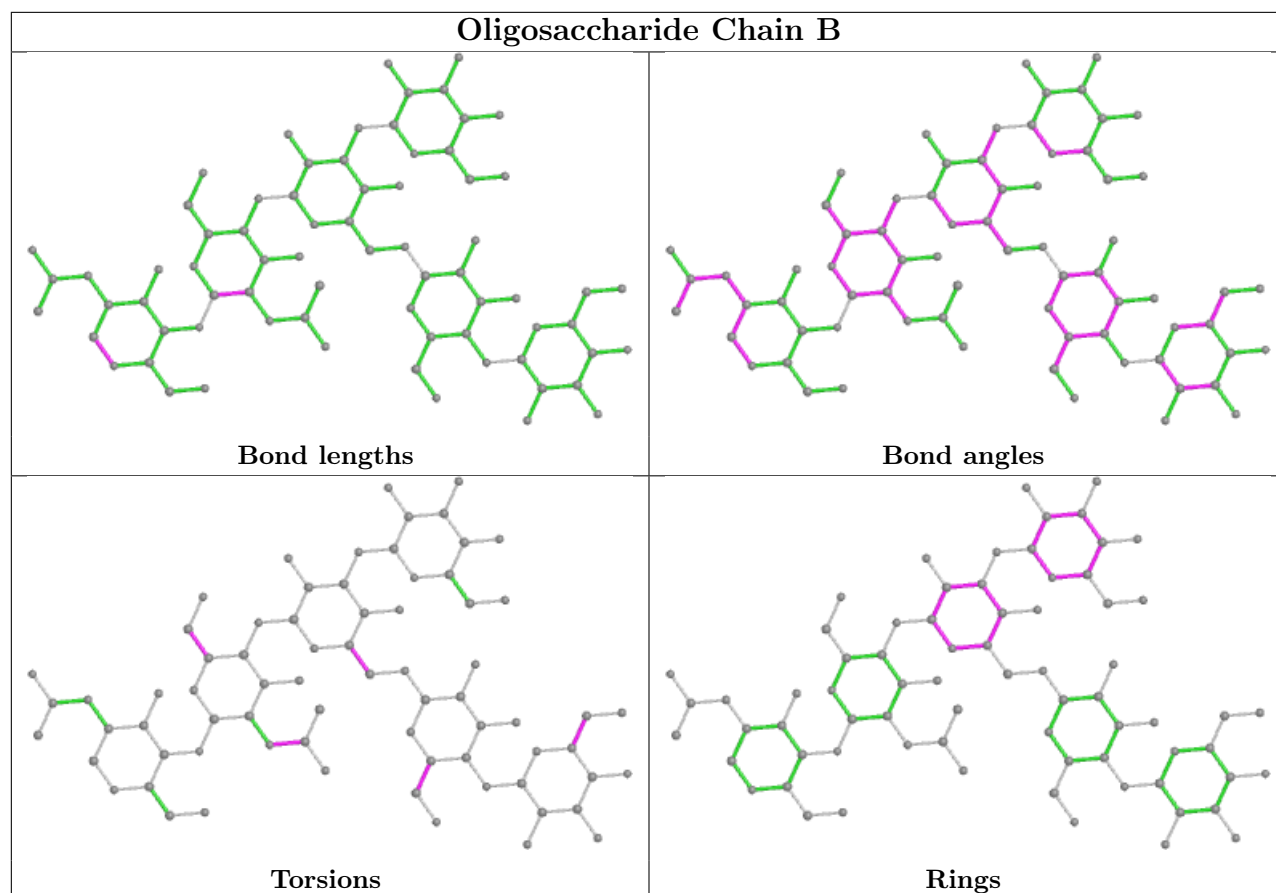
All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	6	MAN	C1-C2-C3-C4-C5-O5
2	B	3	MAN	C1-C2-C3-C4-C5-O5

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](#)

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	361/361 (100%)	-0.12	17 (4%) 31 37	24, 37, 61, 101	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	SER	8.1
1	A	208	GLY	7.4
1	A	207	ASP	6.8
1	A	204	GLY	4.4
1	A	206	SER	4.2
1	A	191	TRP	4.1
1	A	362	VAL	4.1
1	A	205	ASN	4.0
1	A	345	GLN	3.4
1	A	78	TRP	3.2
1	A	50	TRP	3.1
1	A	291	ARG	2.9
1	A	344	GLY	2.5
1	A	249	SER	2.3
1	A	190	GLY	2.3
1	A	346	ASN	2.3
1	A	348	THR	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.

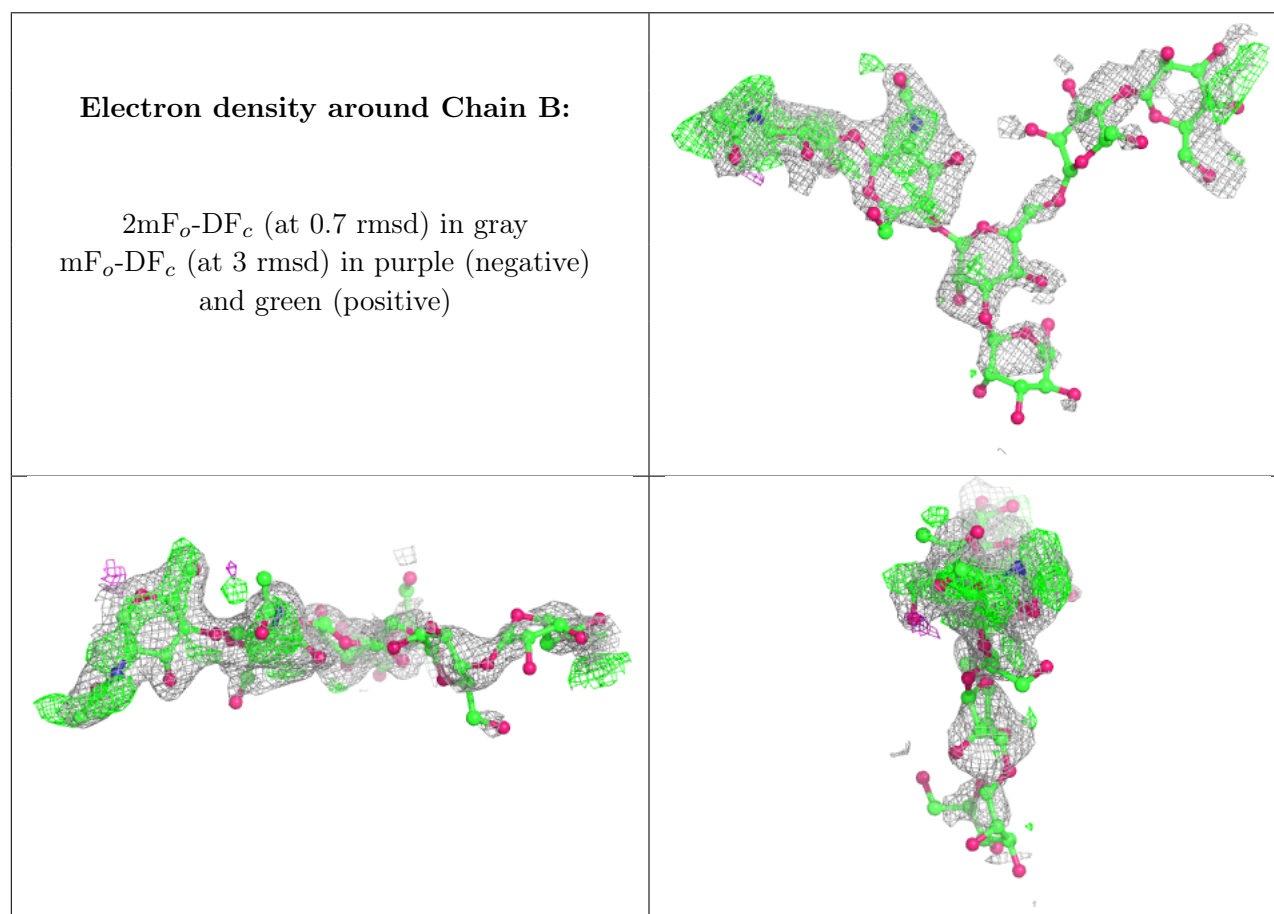
### 6.3 Carbohydrates [i](#)

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, 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	5	11/12	0.37	0.49	46,47,49,49	11
2	MAN	B	4	11/12	0.39	0.49	44,46,48,49	11
2	MAN	B	3	11/12	0.58	0.45	46,46,48,49	11
2	NAG	B	2	14/15	0.64	0.24	52,57,60,60	14
2	MAN	B	6	11/12	0.76	0.60	45,46,48,48	11
2	NAG	B	1	14/15	0.83	0.18	32,34,39,47	14

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](#)

There are no ligands in this entry.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.