



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 07:22 PM BST

PDB ID : 6EV2  
Title : Crystal structure of antibody against schizophyllan in complex with laminari-hexaose  
Authors : Sung, K.H.; Josewski, J.; Duebel, S.; Blankenfeldt, W.; Rau, U.  
Deposited on : 2017-11-01  
Resolution : 2.40 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

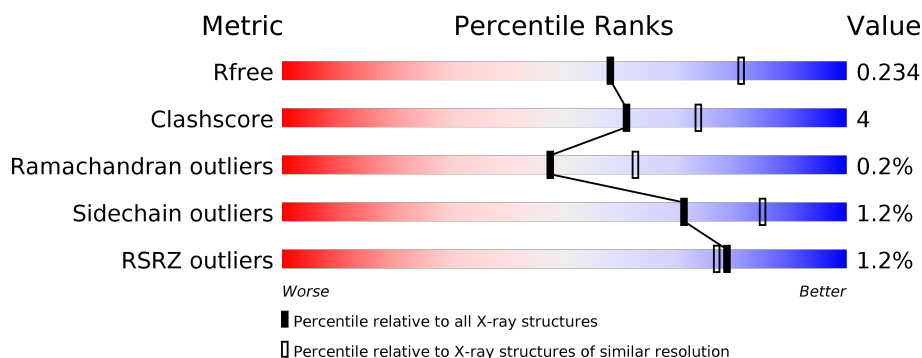
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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.



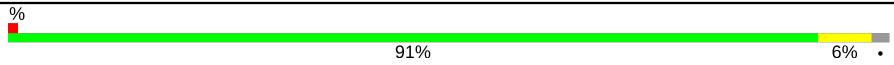
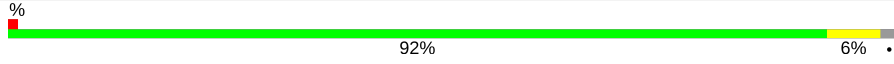
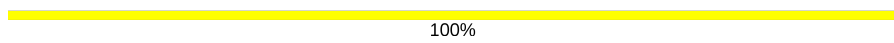
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	222	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 76%; background-color: green;"></div> <div style="width: 23%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>76% 23% ..</div>
1	C	222	<div> <div style="width: 90%; background-color: green;"></div> <div style="width: 9%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>90% 9% .</div>
1	E	222	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 85%; background-color: green;"></div> <div style="width: 12%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>2% 85% 12% .</div>
1	G	222	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 88%; background-color: green;"></div> <div style="width: 9%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>2% 88% 9% .</div>
2	B	217	<div> <div style="width: 86%; background-color: green;"></div> <div style="width: 14%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>86% 14%</div>
2	D	217	<div> <div style="width: 94%; background-color: green;"></div> <div style="width: 6%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>94% 6%</div>

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Mol	Chain	Length	Quality of chain
2	F	217	 91% 6%
2	H	217	 92% 6%
3	I	2	 100%

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
3	BGC	I	1	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13666 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 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1653	1048	267	330	8			
1	C	222	Total	C	N	O	S	0	0	0
			1663	1054	269	332	8			
1	E	214	Total	C	N	O	S	0	0	0
			1615	1027	260	320	8			
1	G	215	Total	C	N	O	S	0	0	0
			1621	1030	261	322	8			

- Molecule 2 is a protein called Light chain.

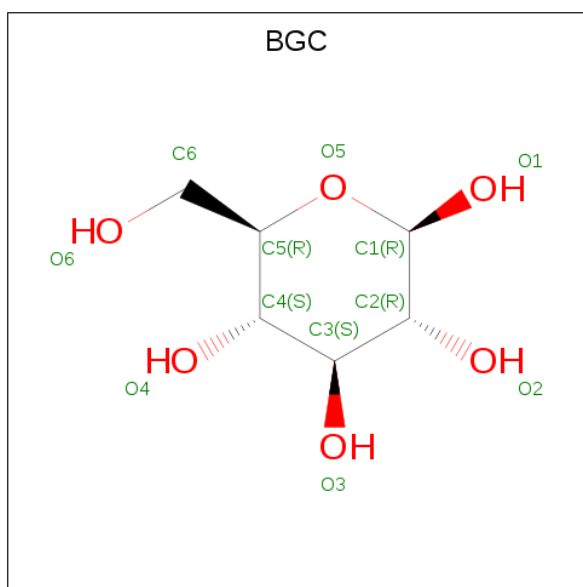
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	217	Total	C	N	O	S	0	0	0
			1650	1027	278	336	9			
2	D	217	Total	C	N	O	S	0	0	0
			1650	1027	278	336	9			
2	F	213	Total	C	N	O	S	0	0	0
			1625	1012	272	332	9			
2	H	213	Total	C	N	O	S	0	0	0
			1625	1012	272	332	9			

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



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

- Molecule 4 is beta-D-glucopyranose (three-letter code: BGC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

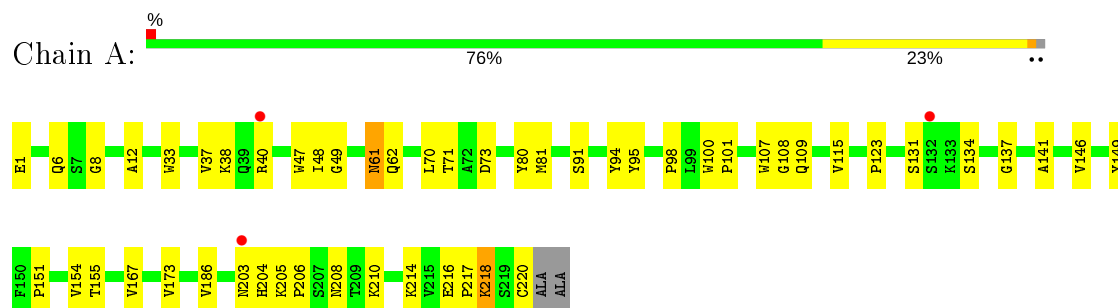
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		
5	B	75	Total	O	0	0
			75	75		
5	C	64	Total	O	0	0
			64	64		
5	D	86	Total	O	0	0
			86	86		
5	E	33	Total	O	0	0
			33	33		
5	F	92	Total	O	0	0
			92	92		
5	G	45	Total	O	0	0
			45	45		
5	H	98	Total	O	0	0
			98	98		

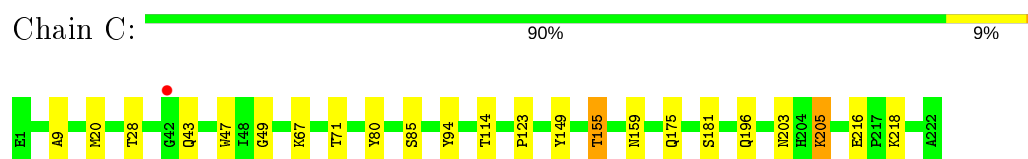
### 3 Residue-property plots

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.

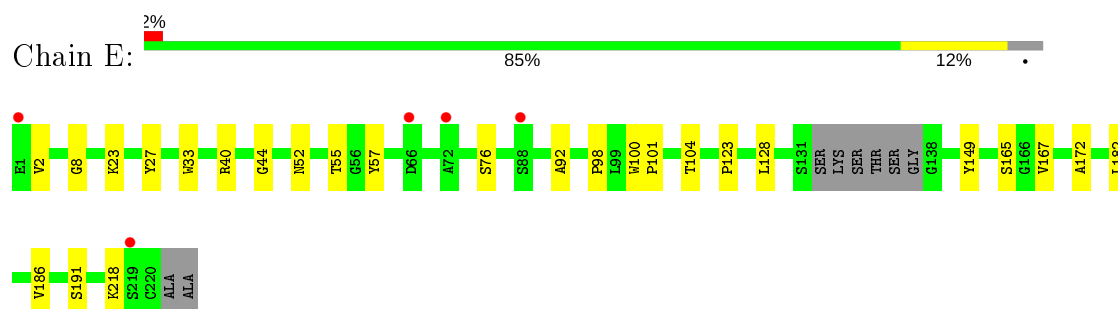
- Molecule 1: Heavy chain



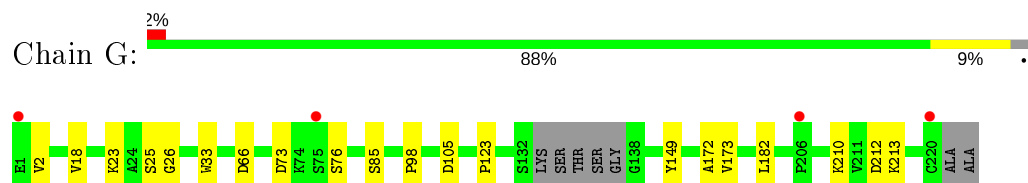
- Molecule 1: Heavy chain




- Molecule 1: Heavy chain

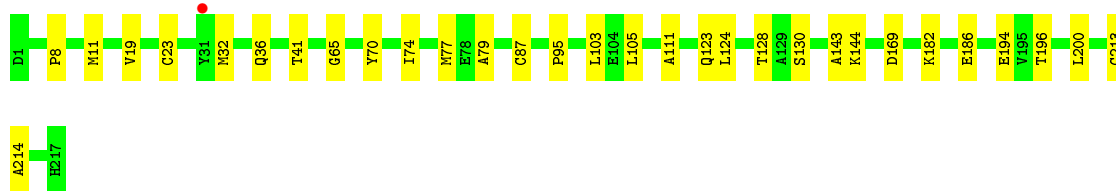


- Molecule 1: Heavy chain



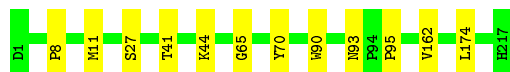
- Molecule 2: Light chain

Chain B:  86% 14%




- Molecule 2: Light chain

Chain D:  94% 6%



- Molecule 2: Light chain

Chain F:  91% 6% .



- Molecule 2: Light chain

Chain H:  92% 6% .



- Molecule 3: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain I:  100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.73Å 131.50Å 91.03Å 90.00° 91.50° 90.00°	Depositor
Resolution (Å)	55.79 – 2.40 91.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (55.79-2.40) 100.0 (91.00-2.40)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.40Å)	Xtriage
Refinement program	PHENIX (1.12 _2829: ???)	Depositor
R, $R_{free}$	0.194 , 0.233 0.194 , 0.234	Depositor DCC
$R_{free}$ test set	3670 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.2	Xtriage
Anisotropy	0.392	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 33.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13666	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.58 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.3404e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: BGC

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	0.29	0/1698	0.53	0/2317
1	C	0.30	0/1708	0.54	0/2331
1	E	0.28	0/1659	0.50	0/2264
1	G	0.29	0/1665	0.51	0/2272
2	B	0.31	0/1688	0.52	0/2292
2	D	0.30	0/1688	0.50	0/2292
2	F	0.30	0/1662	0.51	0/2256
2	H	0.31	0/1662	0.55	0/2256
All	All	0.30	0/13430	0.52	0/18280

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	1653	0	1610	35	0
1	C	1663	0	1620	11	0
1	E	1615	0	1571	17	0
1	G	1621	0	1576	14	0
2	B	1650	0	1590	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1650	0	1590	8	0
2	F	1625	0	1568	11	0
2	H	1625	0	1568	7	0
3	I	23	0	20	0	0
4	A	12	0	11	0	0
5	A	36	0	0	5	0
5	B	75	0	0	4	1
5	C	64	0	0	1	0
5	D	86	0	0	4	2
5	E	33	0	0	5	0
5	F	92	0	0	4	2
5	G	45	0	0	5	0
5	H	98	0	0	1	1
All	All	13666	0	12724	116	3

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 (116) 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)
2:F:57:VAL:O	5:F:301:HOH:O	1.81	0.98
2:D:93:ASN:O	5:D:301:HOH:O	1.89	0.89
1:G:85:SER:OG	5:G:301:HOH:O	1.92	0.87
1:E:191:SER:OG	5:E:302:HOH:O	1.91	0.87
1:E:23:LYS:NZ	1:E:76:SER:O	2.10	0.84
2:D:41:THR:OG1	5:D:302:HOH:O	1.96	0.83
1:A:218:LYS:NZ	1:A:220:CYS:SG	2.52	0.83
1:E:40:ARG:HD2	5:E:310:HOH:O	1.81	0.80
1:A:203:ASN:OD1	1:A:210:LYS:HG3	1.83	0.79
2:B:143:ALA:O	5:B:301:HOH:O	2.02	0.78
1:E:218:LYS:NZ	5:E:304:HOH:O	2.18	0.76
1:A:8:GLY:O	5:A:401:HOH:O	2.08	0.72
1:A:80:TYR:O	5:A:402:HOH:O	2.09	0.71
2:B:41:THR:OG1	5:B:303:HOH:O	2.09	0.70
2:B:194:GLU:OE1	5:B:302:HOH:O	2.09	0.70
1:E:55:THR:HG23	1:E:57:TYR:H	1.57	0.69
1:E:52:ASN:ND2	5:E:301:HOH:O	1.85	0.67
1:G:23:LYS:NZ	1:G:76:SER:OG	2.28	0.67
1:A:134:SER:OG	1:A:141:ALA:O	2.12	0.66
1:C:9:ALA:O	5:C:401:HOH:O	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:27:SER:OG	5:D:303:HOH:O	2.15	0.65
1:G:66:ASP:O	5:G:302:HOH:O	2.14	0.65
1:A:167:VAL:O	5:A:403:HOH:O	2.13	0.65
1:E:8:GLY:O	5:E:303:HOH:O	2.15	0.64
1:E:44:GLY:HA2	2:F:99:ALA:HA	1.78	0.64
1:G:73:ASP:OD1	5:G:303:HOH:O	2.15	0.64
1:A:40:ARG:NH1	1:A:91:SER:O	2.33	0.62
2:B:8:PRO:HG2	2:B:11:MET:HB3	1.80	0.62
2:F:141:ARG:HH21	2:F:162:VAL:HG11	1.65	0.62
1:A:48:ILE:HG21	1:A:81:MET:HE1	1.82	0.61
1:A:6:GLN:HE21	1:A:108:GLY:HA3	1.66	0.60
1:A:218:LYS:HZ2	2:B:213:CYS:HB3	1.67	0.60
1:C:155:THR:HG23	1:C:203:ASN:HB3	1.82	0.59
2:H:8:PRO:HG2	2:H:11:MET:HB3	1.84	0.59
1:E:167:VAL:HG22	1:E:186:VAL:HG22	1.84	0.59
2:D:44:LYS:NZ	5:D:304:HOH:O	2.31	0.58
1:A:37:VAL:HG21	1:A:107:TRP:HZ3	1.69	0.57
1:A:208:ASN:HD22	1:G:23:LYS:HE3	1.69	0.57
1:C:123:PRO:HB3	1:C:149:TYR:HB3	1.88	0.55
1:E:40:ARG:HG2	1:E:92:ALA:HB2	1.89	0.55
2:D:8:PRO:HG2	2:D:11:MET:HB3	1.89	0.54
2:F:148:LYS:NZ	2:F:194:GLU:OE1	2.35	0.54
1:A:37:VAL:HG22	1:A:95:TYR:HB2	1.88	0.54
2:B:32:MET:HE3	2:B:87:CYS:HB2	1.88	0.54
1:A:62:GLN:HG2	5:A:413:HOH:O	2.08	0.54
1:G:212:ASP:OD1	5:G:304:HOH:O	2.18	0.54
1:A:204:HIS:CD2	1:A:206:PRO:HD2	2.42	0.53
1:A:73:ASP:OD2	1:G:210:LYS:NZ	2.40	0.53
2:H:111:ALA:HB1	2:H:200:LEU:HD13	1.92	0.52
1:A:151:PRO:HD2	1:A:206:PRO:HB2	1.92	0.51
2:F:8:PRO:HG2	2:F:11:MET:HB3	1.92	0.51
1:A:218:LYS:HE3	2:B:214:ALA:O	2.11	0.51
2:B:23:CYS:SG	2:B:32:MET:HE2	2.51	0.51
1:C:20:MET:HE1	1:C:94:TYR:HB2	1.91	0.50
1:A:71:THR:OG1	1:A:80:TYR:HB2	2.12	0.50
1:A:214:LYS:HG2	1:A:216:GLU:HG2	1.93	0.50
2:B:123:GLN:HE22	2:B:130:SER:HB2	1.76	0.50
2:F:4:LEU:HD22	2:F:32:MET:HE3	1.94	0.50
2:H:104:GLU:OE2	2:H:141:ARG:NH2	2.45	0.49
2:D:162:VAL:HG22	2:D:174:LEU:HD12	1.94	0.49
2:B:36:GLN:NE2	5:B:310:HOH:O	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:ASN:HD22	1:A:62:GLN:N	2.10	0.48
1:A:6:GLN:O	1:A:109:GLN:NE2	2.44	0.48
1:A:70:LEU:HD21	1:A:81:MET:HE2	1.95	0.48
1:A:173:VAL:HG23	5:A:419:HOH:O	2.13	0.48
1:A:146:VAL:HG11	1:A:154:VAL:HG21	1.96	0.48
2:B:182:LYS:HE3	2:B:186:GLU:OE2	2.13	0.48
1:A:100:TRP:CD2	1:A:101:PRO:HA	2.48	0.48
1:E:123:PRO:HB3	1:E:149:TYR:HB3	1.95	0.48
1:E:33:TRP:O	1:E:98:PRO:HA	2.13	0.48
2:B:144:LYS:HB3	2:B:196:THR:HB	1.95	0.47
1:A:12:ALA:O	1:A:115:VAL:HA	2.15	0.47
1:A:123:PRO:HB3	1:A:149:TYR:HB3	1.96	0.47
2:B:65:GLY:HA3	2:B:70:TYR:HA	1.97	0.46
1:A:47:TRP:CE3	2:B:95:PRO:HD2	2.49	0.46
1:C:47:TRP:CH2	1:C:49:GLY:HA2	2.50	0.46
1:E:2:VAL:HG22	1:E:27:TYR:HB3	1.97	0.46
2:H:158:SER:OG	5:H:301:HOH:O	2.20	0.46
2:B:79:ALA:HA	2:B:105:LEU:HD21	1.97	0.46
1:A:37:VAL:HG21	1:A:107:TRP:CZ3	2.51	0.45
1:A:47:TRP:CH2	1:A:49:GLY:HA2	2.51	0.45
1:C:205:LYS:HE2	1:C:205:LYS:HB2	1.72	0.45
2:D:90:TRP:CE2	2:D:95:PRO:HG3	2.51	0.45
1:E:172:ALA:HB2	1:E:182:LEU:HD23	1.99	0.45
1:C:175:GLN:NE2	1:C:181:SER:HB2	2.31	0.45
1:G:172:ALA:HA	1:G:182:LEU:HB3	1.99	0.44
1:A:38:LYS:HE3	1:A:94:TYR:OH	2.16	0.44
2:B:169:ASP:HA	2:F:15:PRO:HB2	1.99	0.44
2:H:162:VAL:HG22	2:H:174:LEU:HD12	1.99	0.44
2:B:19:VAL:HG22	2:B:74:ILE:HB	1.98	0.44
2:F:12:SER:HB3	5:F:385:HOH:O	2.18	0.44
1:C:71:THR:OG1	1:C:80:TYR:HB2	2.18	0.43
2:F:90:TRP:HB2	5:F:372:HOH:O	2.18	0.43
2:D:65:GLY:HA3	2:D:70:TYR:HA	2.00	0.43
2:H:124:LEU:O	2:H:182:LYS:HD2	2.18	0.43
1:E:172:ALA:HA	1:E:182:LEU:HB3	2.00	0.43
1:G:2:VAL:HA	1:G:26:GLY:HA3	2.01	0.43
2:H:197:HIS:HB3	2:H:200:LEU:HD22	2.00	0.43
2:B:123:GLN:HG2	2:B:128:THR:O	2.19	0.42
1:A:155:THR:OG1	1:A:203:ASN:HB2	2.19	0.42
1:G:33:TRP:O	1:G:98:PRO:HA	2.19	0.42
1:C:43:GLN:OE1	1:C:43:GLN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:105:ASP:OD2	5:G:305:HOH:O	2.22	0.42
1:A:48:ILE:HG21	1:A:81:MET:CE	2.49	0.42
1:E:100:TRP:CG	1:E:101:PRO:HA	2.54	0.42
1:C:67:LYS:NZ	1:C:85:SER:O	2.52	0.42
2:B:124:LEU:O	2:B:182:LYS:HD2	2.20	0.41
2:F:162:VAL:O	5:F:302:HOH:O	2.21	0.41
1:A:33:TRP:O	1:A:98:PRO:HA	2.21	0.41
1:G:213:LYS:HE2	1:G:213:LYS:HB2	1.88	0.41
2:B:77:MET:SD	2:B:103:LEU:HD21	2.60	0.41
1:G:123:PRO:HB3	1:G:149:TYR:HB3	2.02	0.41
1:E:128:LEU:HB3	2:F:117:PHE:CD1	2.55	0.41
1:C:159:ASN:HD21	1:C:196:GLN:HE22	1.68	0.41
2:B:111:ALA:HB1	2:B:200:LEU:HD13	2.03	0.40
1:G:2:VAL:HA	1:G:25:SER:O	2.22	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:329:HOH:O	5:H:379:HOH:O[1_455]	1.71	0.49
5:D:320:HOH:O	5:F:340:HOH:O[1_655]	1.84	0.36
5:D:326:HOH:O	5:F:361:HOH:O[1_655]	2.12	0.08

## 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	218/222 (98%)	210 (96%)	4 (2%)	4 (2%)	8	10
1	C	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
1	E	210/222 (95%)	203 (97%)	7 (3%)	0	100	100
1	G	211/222 (95%)	207 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	215/217 (99%)	209 (97%)	6 (3%)	0	100	100
2	D	215/217 (99%)	211 (98%)	4 (2%)	0	100	100
2	F	211/217 (97%)	206 (98%)	5 (2%)	0	100	100
2	H	211/217 (97%)	205 (97%)	6 (3%)	0	100	100
All	All	1711/1756 (97%)	1666 (97%)	41 (2%)	4 (0%)	47	62

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	131	SER
1	A	137	GLY
1	A	205	LYS
1	A	217	PRO

### 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	187/187 (100%)	183 (98%)	4 (2%)	53	72
1	C	187/187 (100%)	181 (97%)	6 (3%)	39	59
1	E	182/187 (97%)	180 (99%)	2 (1%)	73	87
1	G	183/187 (98%)	181 (99%)	2 (1%)	73	87
2	B	186/186 (100%)	186 (100%)	0	100	100
2	D	186/186 (100%)	186 (100%)	0	100	100
2	F	185/186 (100%)	183 (99%)	2 (1%)	73	87
2	H	185/186 (100%)	183 (99%)	2 (1%)	73	87
All	All	1481/1492 (99%)	1463 (99%)	18 (1%)	71	85

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLU
1	A	61	ASN
1	A	186	VAL
1	A	218	LYS
1	C	28	THR
1	C	114	THR
1	C	155	THR
1	C	205	LYS
1	C	216	GLU
1	C	218	LYS
1	E	104	THR
1	E	165	SER
2	F	90	TRP
2	F	189	LYS
1	G	18	VAL
1	G	173	VAL
2	H	90	TRP
2	H	126	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	39	GLN
1	A	61	ASN
1	A	208	ASN
2	B	37	GLN
2	B	123	GLN
1	C	3	GLN
1	C	5	GLN
1	C	62	GLN
1	C	196	GLN
2	H	137	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 ⓘ

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
3	BGC	I	1	3	12,12,12	1.30	2 (16%)	17,17,17	1.15	3 (17%)
3	BGC	I	2	3	11,11,12	1.72	3 (27%)	15,15,17	1.07	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	BGC	I	1	3	-	2/2/22/22	0/1/1/1
3	BGC	I	2	3	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	2	BGC	O5-C1	4.34	1.50	1.43
3	I	1	BGC	O5-C1	3.07	1.50	1.42
3	I	2	BGC	C2-C3	-2.35	1.49	1.52
3	I	2	BGC	O5-C5	2.17	1.47	1.43
3	I	1	BGC	O3-C3	-2.13	1.38	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1	BGC	O3-C3-C2	2.37	115.84	110.35
3	I	1	BGC	O5-C5-C4	2.04	113.39	109.69
3	I	1	BGC	C3-C4-C5	2.02	113.84	110.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

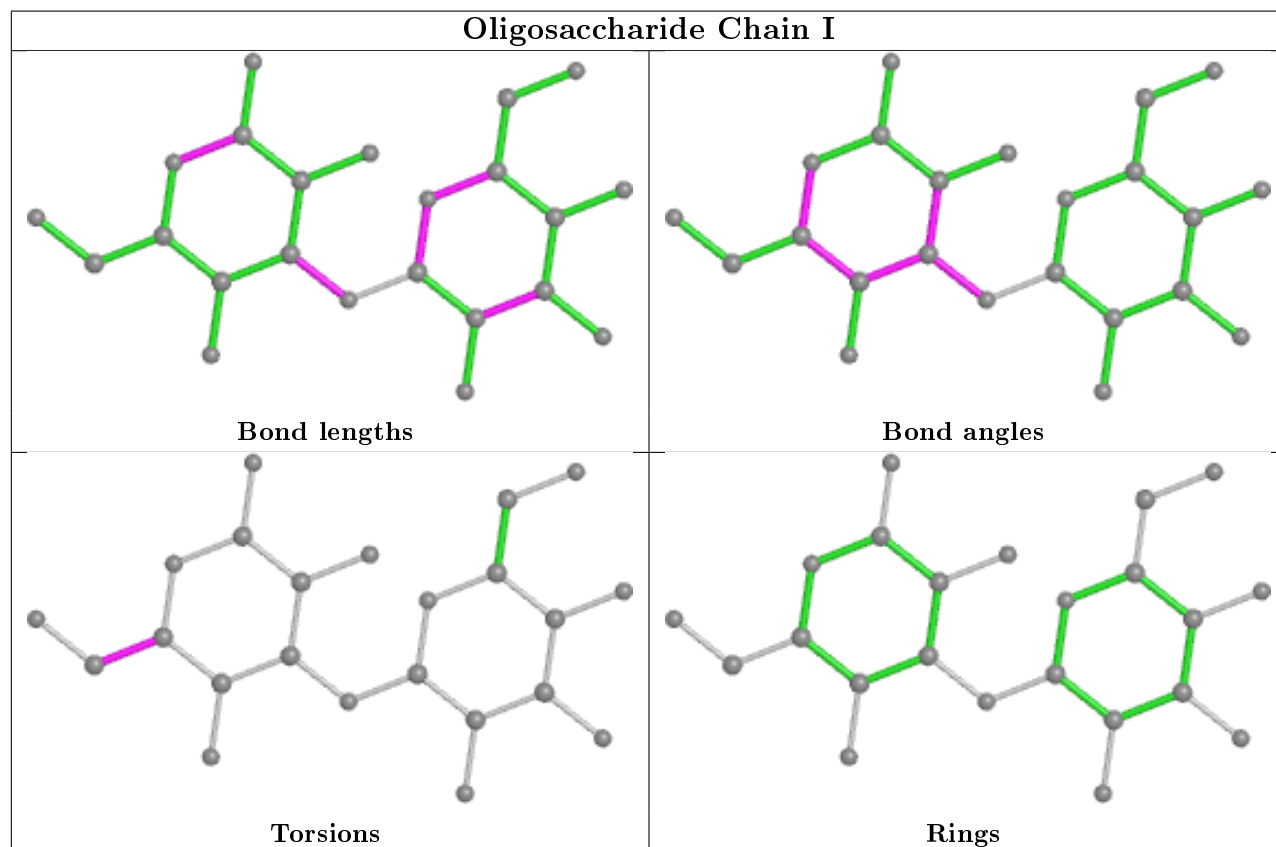


Mol	Chain	Res	Type	Atoms
3	I	1	BGC	O5-C5-C6-O6
3	I	1	BGC	C4-C5-C6-O6

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](#)

1 ligand is 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
4	BGC	A	301	-	12,12,12	1.23	1 (8%)	17,17,17	0.93	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	BGC	A	301	-	-	0/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	301	BGC	O5-C1	3.14	1.50	1.42

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, 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	220/222 (99%)	-0.01	3 (1%) 75 73	43, 64, 95, 110	0
1	C	222/222 (100%)	-0.21	1 (0%) 91 89	35, 55, 82, 104	0
1	E	214/222 (96%)	0.04	5 (2%) 60 58	45, 70, 106, 138	0
1	G	215/222 (96%)	-0.05	4 (1%) 66 64	35, 59, 92, 112	0
2	B	217/217 (100%)	-0.15	1 (0%) 91 89	28, 48, 78, 101	0
2	D	217/217 (100%)	-0.16	0 100 100	30, 46, 70, 87	0
2	F	213/217 (98%)	-0.26	3 (1%) 75 73	30, 50, 76, 120	0
2	H	213/217 (98%)	-0.23	3 (1%) 75 73	29, 46, 76, 115	0
All	All	1731/1756 (98%)	-0.13	20 (1%) 79 77	28, 55, 88, 138	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	213	CYS	5.0
1	A	132	SER	4.4
2	F	90	TRP	4.1
1	G	75	SER	4.0
1	G	220	CYS	3.7
1	C	42	GLY	3.6
2	F	213	CYS	3.3
1	E	1	GLU	3.0
2	F	211	GLY	2.9
1	E	88	SER	2.6
1	A	40	ARG	2.6
1	G	1	GLU	2.5
1	E	66	ASP	2.3
2	B	31	TYR	2.3
2	H	183	ALA	2.2
1	G	206	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
2	H	90	TRP	2.1
1	E	72	ALA	2.1
1	E	219	SER	2.1
1	A	203	ASN	2.0

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

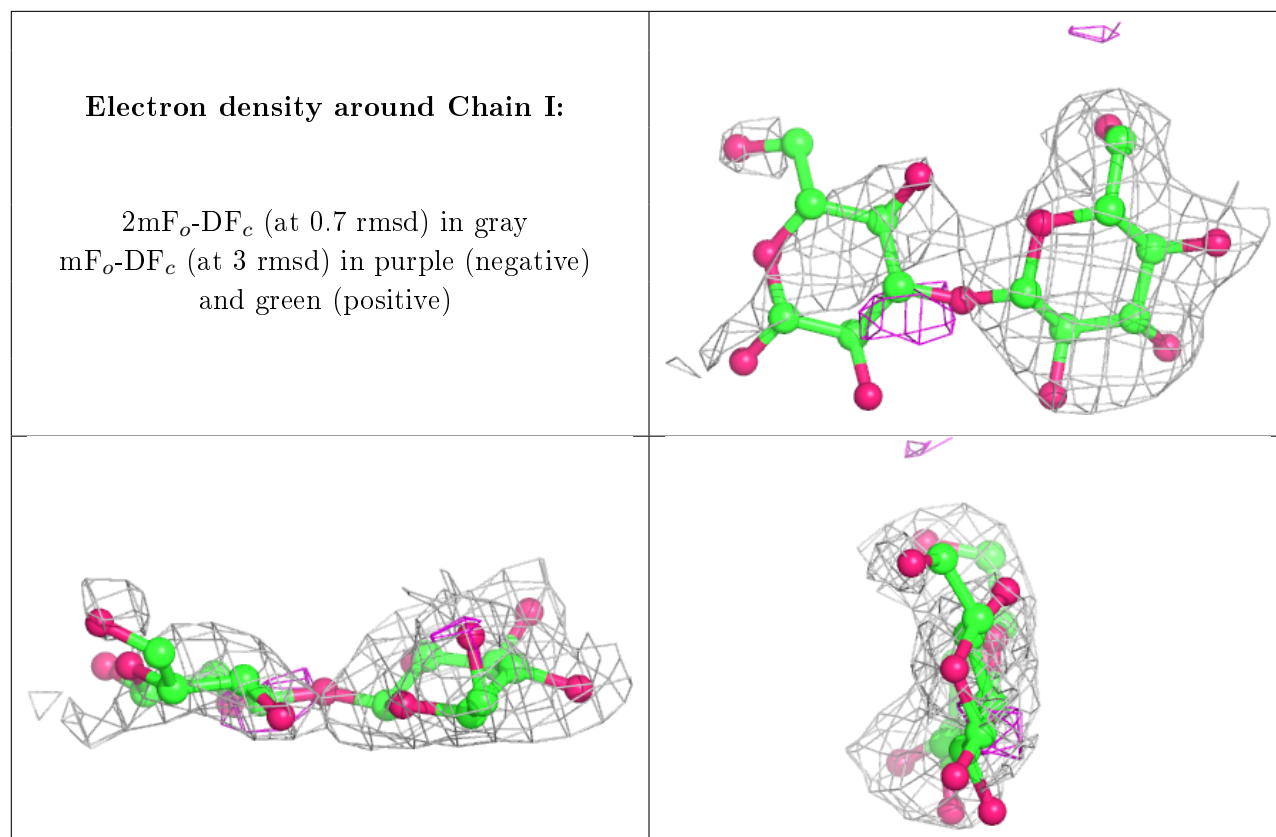
There are no non-standard protein/DNA/RNA residues in this entry.

## 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( $\text{\AA}^2$ )	Q<0.9
3	BGC	I	1	12/12	0.52	0.54	107,119,121,122	0
3	BGC	I	2	11/12	0.87	0.19	69,83,90,96	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, 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( $\text{\AA}^2$ )	Q<0.9
4	BGC	A	301	12/12	0.86	0.18	82,87,91,92	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.