



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 11, 2024 – 08:09 PM EDT

PDB ID : 6N35  
Title : Anti-HIV-1 Fab 2G12 + Man1-2 re-refinement  
Authors : Calarese, D.A.; Stanfield, R.L.; Wilson, I.A.  
Deposited on : 2018-11-14  
Resolution : 1.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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>.

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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	:	2.36.2
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)	:	2.36.2

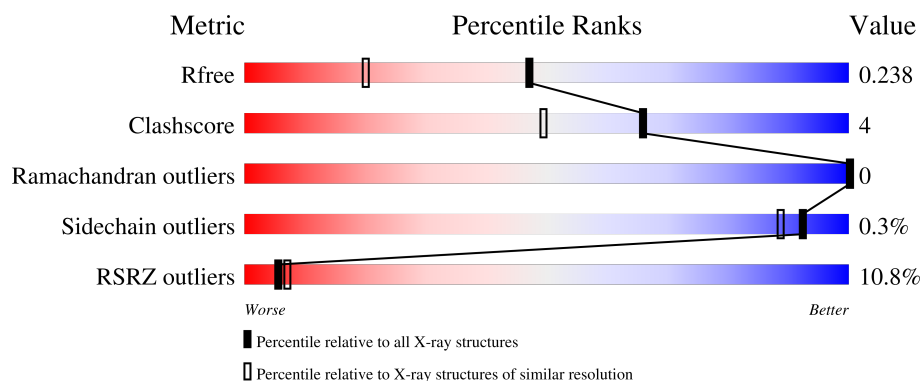
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	K	213	<div> <div>3%</div> <div>94%</div> <div>6%</div> </div>
1	L	213	<div> <div>11%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
2	H	224	<div> <div>9%</div> <div>94%</div> <div>.</div> <div>.</div> </div>
2	M	224	<div> <div>18%</div> <div>92%</div> <div>5%</div> <div>.</div> </div>
3	A	2	<div> <div>100%</div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7170 atoms, of which 20 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 Fab 2G12 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	1	0
			1621	1020	272	323	6			
1	K	213	Total	C	N	O	S	0	1	0
			1638	1029	274	330	5			

- Molecule 2 is a protein called Fab 2G12 heavy chain.

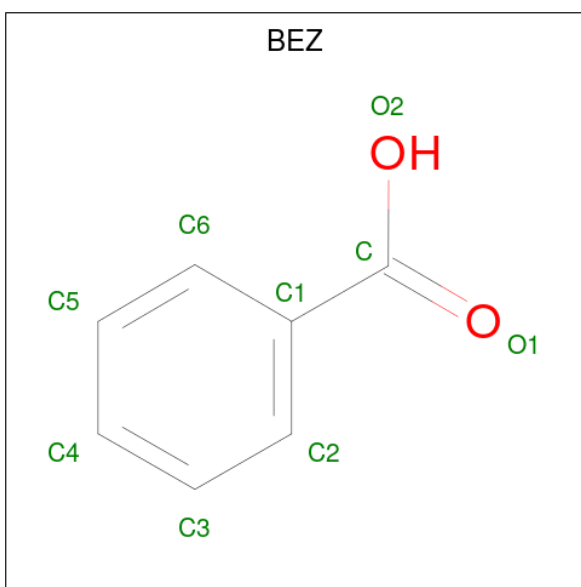
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	218	Total	C	N	O	S	0	1	0
			1640	1034	279	319	8			
2	M	218	Total	C	N	O	S	0	1	0
			1640	1034	279	319	8			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose.



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

- Molecule 4 is BENZOIC ACID (three-letter code: BEZ) (formula: C<sub>7</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total	C	O	0	0
			9	7	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	K	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 6 is alpha-D-mannopyranose (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	M	1	Total	C	H	O	0	0
			24	6	12	6		

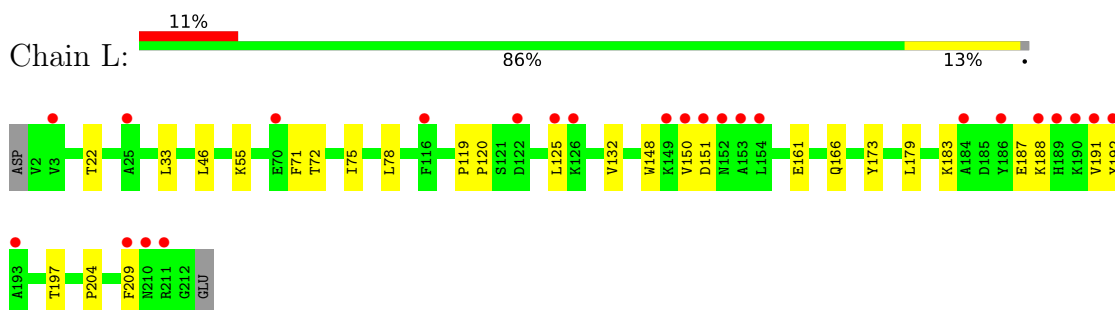
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	L	117	Total	O	0	0
			117	117		
7	H	139	Total	O	0	0
			139	139		
7	K	188	Total	O	0	0
			188	188		
7	M	117	Total	O	0	0
			117	117		

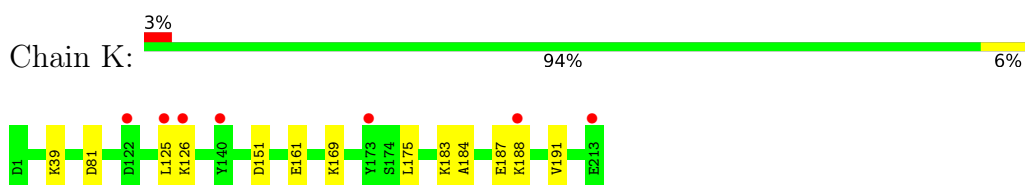
### 3 Residue-property plots

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.

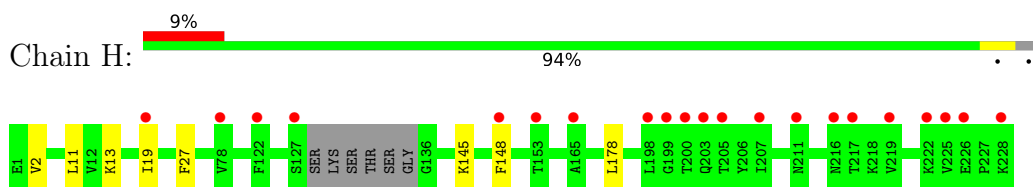
- Molecule 1: Fab 2G12 light chain



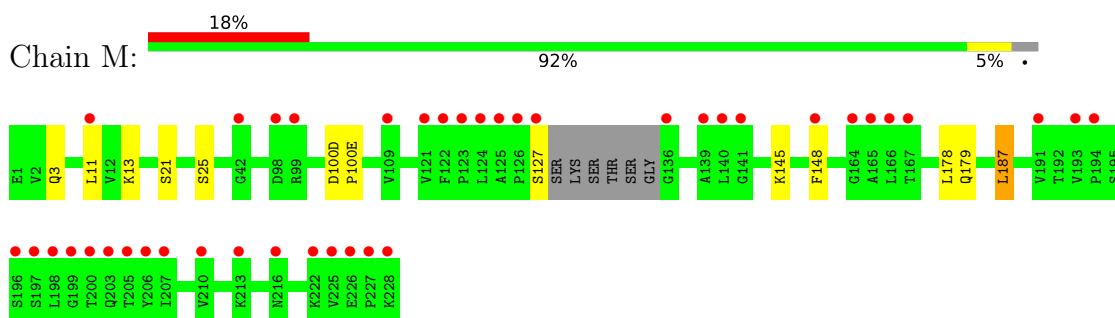
- Molecule 1: Fab 2G12 light chain




- Molecule 2: Fab 2G12 heavy chain



- Molecule 2: Fab 2G12 heavy chain



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain A:  100%

PAN1  
PAN2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.72Å 94.03Å 169.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.30 – 1.75 45.30 – 1.75	Depositor EDS
% Data completeness (in resolution range)	95.0 (45.30-1.75) 95.1 (45.30-1.75)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.13 (at 1.75Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, $R_{free}$	0.206 , 0.238 0.208 , 0.238	Depositor DCC
$R_{free}$ test set	6399 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.9	Xtriage
Anisotropy	0.614	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 47.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7170	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: MAN, GOL, BEZ

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	K	0.50	0/1677	0.63	0/2278
1	L	0.46	0/1660	0.62	0/2254
2	H	0.47	0/1681	0.63	0/2289
2	M	0.50	0/1681	0.66	0/2289
All	All	0.48	0/6699	0.64	0/9110

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	K	1638	0	1598	14	0
1	L	1621	0	1584	22	0
2	H	1640	0	1613	8	0
2	M	1640	0	1613	12	0
3	A	23	0	21	0	0
4	L	9	0	5	0	0
5	K	6	8	8	0	0
6	M	12	12	12	0	0
7	H	139	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	K	188	0	0	5	0
7	L	117	0	0	1	0
7	M	117	0	0	0	0
All	All	7150	20	6454	52	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 (52) 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:H:178:LEU:HD21	2:M:11:LEU:HD11	1.59	0.83
1:L:132:VAL:HG22	1:L:179:LEU:HB3	1.68	0.75
1:L:132:VAL:CG2	1:L:179:LEU:HB3	2.15	0.75
1:L:120:PRO:HD3	1:L:132:VAL:HG12	1.70	0.74
1:L:125:LEU:O	1:L:183:LYS:HD2	1.89	0.73
1:L:33:LEU:HD13	1:L:71:PHE:CG	2.24	0.72
1:K:125:LEU:O	1:K:183:LYS:HD2	1.91	0.70
1:L:188:LYS:HA	1:L:188:LYS:HE2	1.74	0.69
1:K:151:ASP:HA	1:K:191:VAL:CG1	2.24	0.67
1:L:151:ASP:HA	1:L:191:VAL:CG1	2.24	0.66
2:M:187:LEU:C	2:M:187:LEU:HD12	2.15	0.66
1:L:151:ASP:OD1	1:L:191:VAL:HG12	1.95	0.66
1:K:188:LYS:HA	1:K:188:LYS:HE2	1.79	0.64
2:H:145:LYS:HE2	7:K:510:HOH:O	1.99	0.61
2:H:2:VAL:HG13	2:H:27:PHE:CD1	2.34	0.61
2:H:11:LEU:HD11	2:M:178:LEU:HD21	1.81	0.61
2:H:13:LYS:HD2	2:H:148:PHE:CE2	2.36	0.61
2:M:13:LYS:HD2	2:M:148:PHE:CE1	2.38	0.59
2:M:145:LYS:HE3	2:M:179:GLN:OE1	2.03	0.59
1:K:161:GLU:HG3	7:K:518:HOH:O	2.04	0.58
2:H:19:ILE:HD13	2:M:21:SER:HB3	1.87	0.57
1:L:183:LYS:O	1:L:187:GLU:HG3	2.05	0.56
1:K:184:ALA:O	1:K:188:LYS:HG2	2.06	0.56
1:K:169:LYS:HE2	7:K:649:HOH:O	2.07	0.55
1:K:39:LYS:NZ	7:K:503:HOH:O	2.40	0.54
1:L:161:GLU:HG3	7:L:408:HOH:O	2.08	0.53
1:K:39:LYS:NZ	1:K:81:ASP:OD1	2.41	0.53
1:L:166:GLN:HG3	1:L:173:TYR:CZ	2.44	0.52
2:H:2:VAL:HG13	2:H:27:PHE:CE1	2.43	0.52
2:M:187:LEU:HD12	2:M:187:LEU:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:132:VAL:HG21	1:L:179:LEU:HD23	1.94	0.50
2:M:13:LYS:HE3	2:M:148:PHE:CE2	2.48	0.48
2:M:3:GLN:HB2	2:M:25:SER:HB2	1.96	0.48
1:K:151:ASP:OD1	1:K:191:VAL:HG12	2.14	0.48
1:K:151:ASP:HA	1:K:191:VAL:HG12	1.96	0.47
1:L:33:LEU:HD13	1:L:71:PHE:CD1	2.48	0.47
1:L:132:VAL:HG23	1:L:148:TRP:CH2	2.50	0.47
2:H:178:LEU:HD21	2:M:11:LEU:CD1	2.37	0.46
2:M:187:LEU:C	2:M:187:LEU:CD1	2.84	0.46
1:L:75:ILE:HG21	1:L:78:LEU:HD23	1.99	0.45
1:L:151:ASP:HA	1:L:191:VAL:HG12	1.96	0.45
1:K:126:LYS:HA	1:K:126:LYS:CE	2.48	0.44
1:L:151:ASP:H	1:L:191:VAL:HG13	1.81	0.44
1:L:197:THR:HG22	1:L:204:PRO:HB3	1.99	0.44
1:K:183:LYS:O	1:K:187:GLU:HG3	2.19	0.43
1:L:150:VAL:HG22	1:L:192:TYR:CD2	2.54	0.42
1:K:169:LYS:NZ	7:K:508:HOH:O	2.49	0.42
1:L:22:THR:HG22	1:L:72:THR:HG22	2.01	0.41
2:M:100(D):ASP:HB3	2:M:100(E):PRO:HD2	2.03	0.41
1:L:46:LEU:HD23	1:L:55:LYS:HD2	2.03	0.41
1:K:175:LEU:C	1:K:175:LEU:HD23	2.41	0.41
1:L:119:PRO:HB3	1:L:209:PHE:CE1	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	K	212/213 (100%)	205 (97%)	7 (3%)	0	100	100
1	L	210/213 (99%)	205 (98%)	5 (2%)	0	100	100
2	H	215/224 (96%)	211 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	M	215/224 (96%)	211 (98%)	4 (2%)	0	100	100
All	All	852/874 (98%)	832 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	185/184 (100%)	185 (100%)	0	100	100
1	L	183/184 (100%)	183 (100%)	0	100	100
2	H	185/189 (98%)	185 (100%)	0	100	100
2	M	185/189 (98%)	183 (99%)	2 (1%)	73	59
All	All	738/746 (99%)	736 (100%)	2 (0%)	92	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	M	127	SER
2	M	187	LEU

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

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	MAN	A	1	3	12,12,12	1.03	1 (8%)	17,17,17	1.09	1 (5%)
3	MAN	A	2	3	11,11,12	1.10	1 (9%)	15,15,17	1.35	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
3	MAN	A	1	3	-	0/2/22/22	0/1/1/1
3	MAN	A	2	3	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2	MAN	O5-C5	2.83	1.49	1.43
3	A	1	MAN	C4-C3	2.24	1.58	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	MAN	C1-O5-C5	3.73	117.24	112.19
3	A	1	MAN	O2-C2-C3	-2.63	104.27	110.35
3	A	2	MAN	O2-C2-C3	-2.61	104.90	110.14

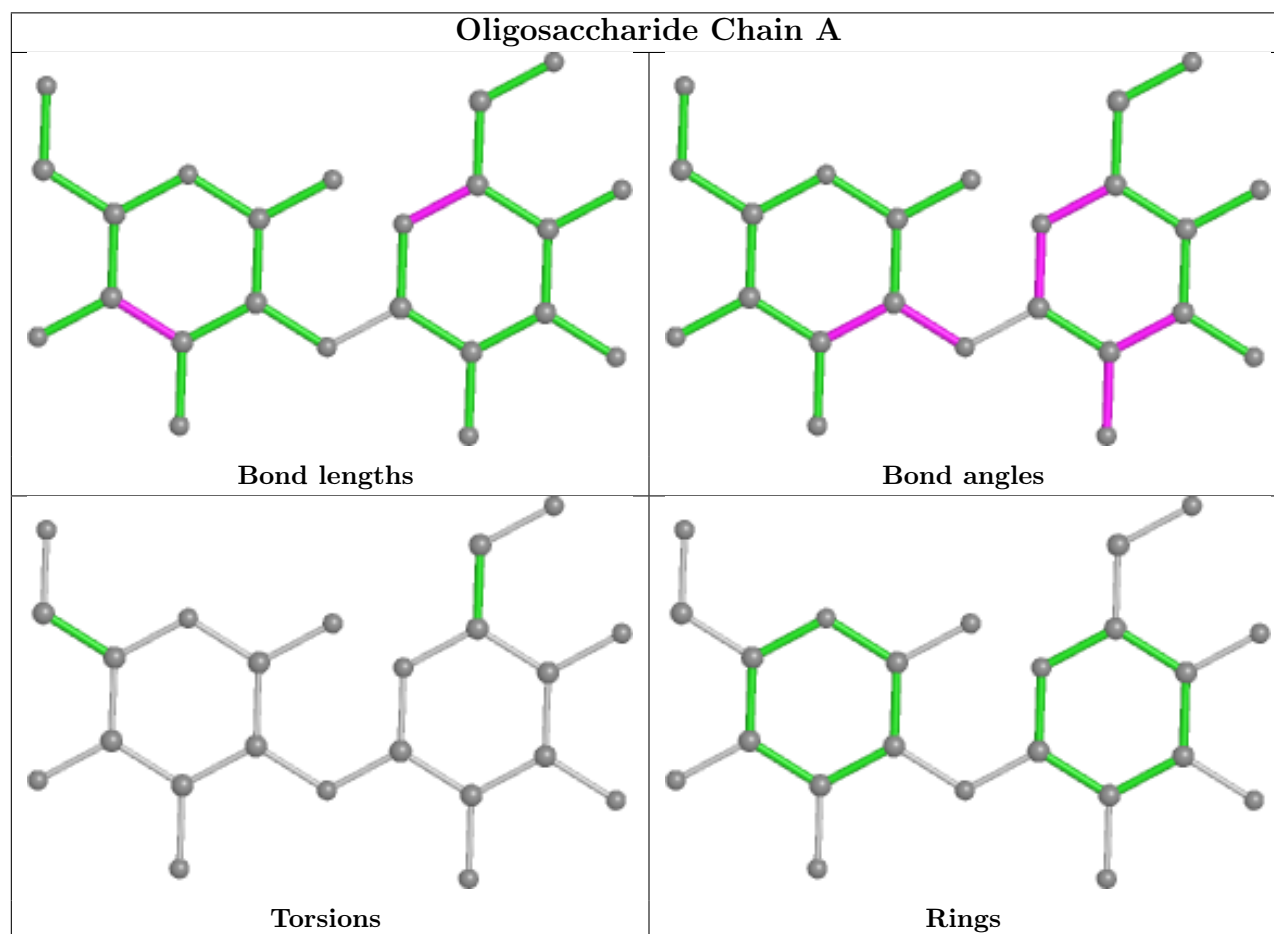
There are no chirality outliers.

There are no torsion outliers.

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](#)

3 ligands 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	$\# Z  > 2$
4	BEZ	L	301	-	9,9,9	0.70	0	11,11,11	1.28	2 (18%)
6	MAN	M	301	-	12,12,12	1.90	2 (16%)	17,17,17	1.03	2 (11%)
5	GOL	K	401	-	5,5,5	0.95	0	5,5,5	0.91	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	BEZ	L	301	-	-	0/4/4/4	0/1/1/1
6	MAN	M	301	-	-	0/2/22/22	0/1/1/1
5	GOL	K	401	-	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	301	MAN	C4-C5	4.57	1.62	1.53
6	M	301	MAN	O5-C5	2.56	1.50	1.44

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	301	BEZ	C6-C1-C2	2.57	122.25	118.59
4	L	301	BEZ	C3-C2-C1	-2.10	117.86	120.34
6	M	301	MAN	O2-C2-C3	-2.10	105.50	110.35
6	M	301	MAN	O4-C4-C5	2.02	114.32	109.30

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	K	213/213 (100%)	0.31	7 (3%) 46 52	26, 35, 59, 78	0
1	L	211/213 (99%)	0.44	24 (11%) 5 6	27, 42, 75, 90	0
2	H	218/224 (97%)	0.53	21 (9%) 8 10	27, 40, 70, 82	0
2	M	218/224 (97%)	0.88	41 (18%) 1 1	25, 40, 76, 88	0
All	All	860/874 (98%)	0.54	93 (10%) 5 7	25, 40, 72, 90	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	200	THR	6.9
2	M	228	LYS	5.8
2	H	200	THR	5.7
2	M	207	ILE	5.6
1	L	191	VAL	5.5
1	L	209	PHE	5.4
1	L	192	TYR	5.3
2	H	199	GLY	5.1
2	H	198	LEU	5.0
2	M	198	LEU	5.0
2	M	197	SER	5.0
2	M	196	SER	5.0
1	L	188	LYS	4.8
2	M	205	THR	4.6
1	L	190	LYS	4.6
2	H	207	ILE	4.5
1	K	126	LYS	4.4
2	M	136	GLY	4.2
2	M	206	TYR	4.2
1	L	184	ALA	4.2
2	M	140	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	L	152	ASN	4.0
2	H	219	VAL	3.7
2	M	199	GLY	3.7
1	L	150	VAL	3.6
2	H	228	LYS	3.6
2	M	213	LYS	3.5
2	M	193	VAL	3.5
2	M	99	ARG	3.4
2	M	165	ALA	3.4
1	L	211	ARG	3.3
1	K	188	LYS	3.3
1	L	153	ALA	3.3
2	M	227	PRO	3.2
2	M	98	ASP	3.2
1	L	126	LYS	3.1
1	L	125	LEU	3.1
2	M	222	LYS	3.1
1	L	210	ASN	3.1
2	M	127	SER	3.0
2	H	127	SER	3.0
2	H	205	THR	3.0
1	L	189	HIS	3.0
2	M	139	ALA	2.9
2	M	125	ALA	2.9
2	H	216	ASN	2.8
1	L	122	ASP	2.8
2	M	210	VAL	2.8
2	M	225	VAL	2.8
1	L	186	TYR	2.8
1	L	149	LYS	2.8
2	H	225	VAL	2.7
1	K	173	TYR	2.7
2	M	166	LEU	2.7
2	H	165	ALA	2.6
2	H	222	LYS	2.6
2	M	148	PHE	2.6
1	K	213	GLU	2.6
2	H	148	PHE	2.6
2	M	141	GLY	2.6
2	M	124	LEU	2.6
2	M	164	GLY	2.5
2	H	122	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	K	125	LEU	2.5
1	L	193	ALA	2.5
2	M	216	ASN	2.5
1	K	140	TYR	2.4
2	M	167	THR	2.4
1	L	70	GLU	2.4
2	H	153	THR	2.4
2	M	226	GLU	2.4
2	M	122	PHE	2.4
1	L	3	VAL	2.3
2	H	211	ASN	2.3
2	M	126	PRO	2.3
1	L	151	ASP	2.3
2	M	42	GLY	2.3
2	M	121	VAL	2.2
1	L	116	PHE	2.2
2	M	109	VAL	2.2
2	H	203	GLN	2.2
2	M	203	GLN	2.2
2	M	191	VAL	2.2
2	H	217	THR	2.2
2	H	78	VAL	2.1
2	H	19	ILE	2.1
2	H	226	GLU	2.0
2	M	194	PRO	2.0
1	L	25	ALA	2.0
1	K	122	ASP	2.0
2	M	123	PRO	2.0
1	L	154	LEU	2.0
2	M	11	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

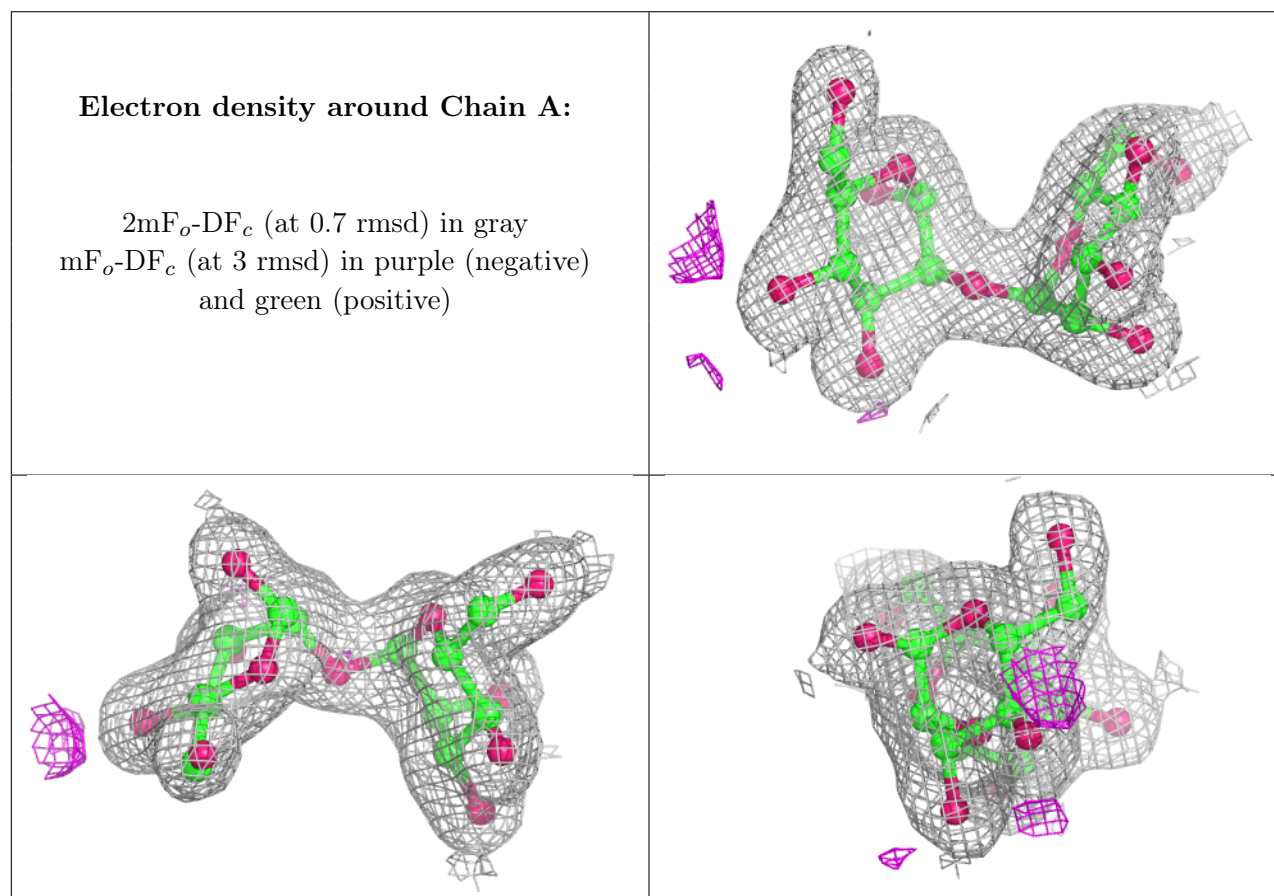
There are no non-standard protein/DNA/RNA residues in this entry.

## 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( $\text{\AA}^2$ )	Q<0.9
3	MAN	A	1	12/12	0.95	0.08	32,39,44,45	0
3	MAN	A	2	11/12	0.96	0.07	30,34,39,39	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
6	MAN	M	301	12/12	0.84	0.24	33,59,73,84	0
5	GOL	K	401	6/6	0.94	0.19	40,56,64,69	0
4	BEZ	L	301	9/9	0.95	0.11	26,30,46,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.