



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 12:41 PM BST

PDB ID : 4MD5  
Title : Immune Receptor  
Authors : Scally, S.W.; Rossjohn, J.  
Deposited on : 2013-08-22  
Resolution : 1.65 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 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

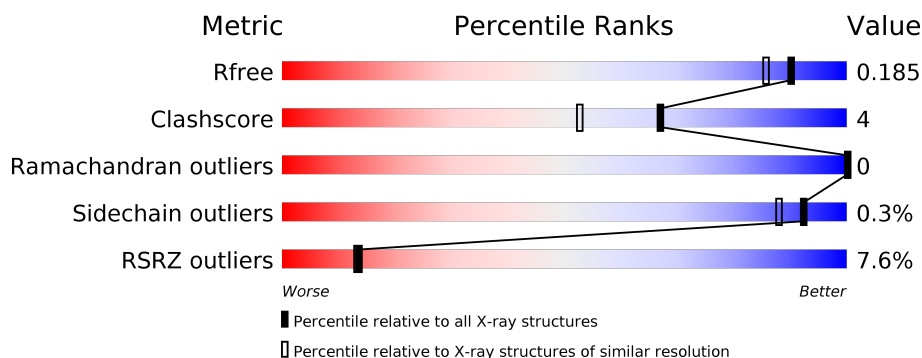
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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	189	<div> <div>7%</div> <div>87%</div> <div>8%</div> <div>5%</div> </div>
2	B	200	<div> <div>8%</div> <div>89%</div> <div>6%</div> <div>5%</div> </div>
3	C	13	<div> <div>85%</div> <div>15%</div> </div>
4	D	2	<div> <div>50%</div> <div>50%</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
5	NAG	B	201	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 3866 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	14	0
			1586	1027	252	301	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	THR	-	expression tag	UNP P01903
A	183	SER	-	expression tag	UNP P01903
A	184	GLY	-	expression tag	UNP P01903
A	185	ASP	-	expression tag	UNP P01903
A	186	ASP	-	expression tag	UNP P01903
A	187	ASP	-	expression tag	UNP P01903
A	188	ASP	-	expression tag	UNP P01903
A	189	LYS	-	expression tag	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-4 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	190	Total	C	N	O	S	0	6	0
			1611	1022	280	303	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P13760
B	0	SER	-	expression tag	UNP P13760
B	71	ARG	LYS	variant	UNP P13760
B	86	VAL	GLY	variant	UNP P13760
B	191	THR	-	expression tag	UNP P13760
B	192	GLY	-	expression tag	UNP P13760
B	193	GLY	-	expression tag	UNP P13760
B	194	ASP	-	expression tag	UNP P13760

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	195	ASP	-	expression tag	UNP P13760
B	196	ASP	-	expression tag	UNP P13760
B	197	ASP	-	expression tag	UNP P13760
B	198	LYS	-	expression tag	UNP P13760

- Molecule 3 is a protein called Citrullinated Vimentin.

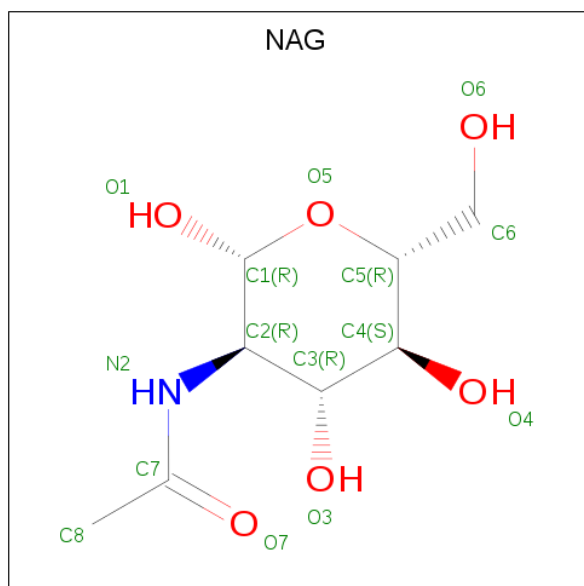
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	2	0
			105	65	22	18			

- 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			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



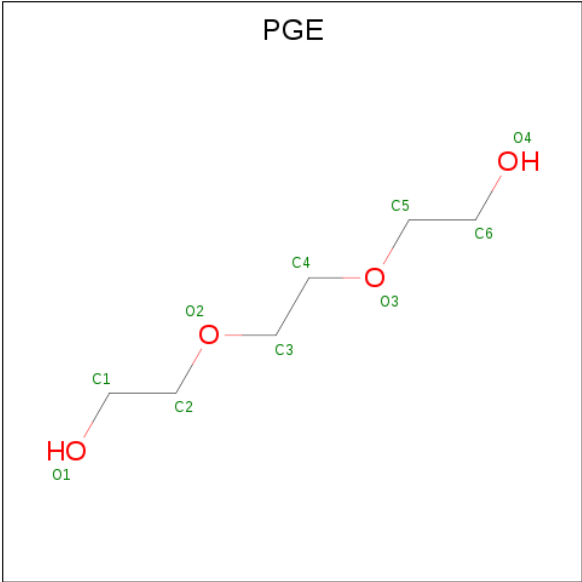
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			10	6	4		

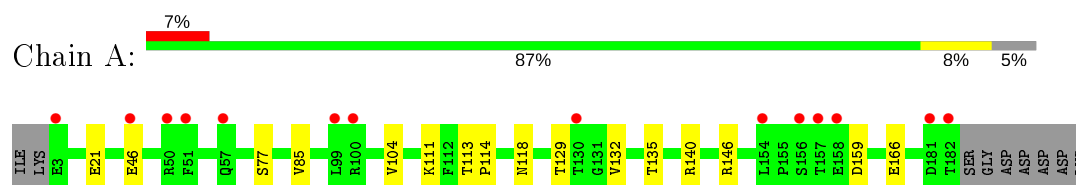
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	246	Total	O	0	0
			246	246		
8	B	203	Total	O	0	0
			203	203		
8	C	17	Total	O	0	0
			17	17		

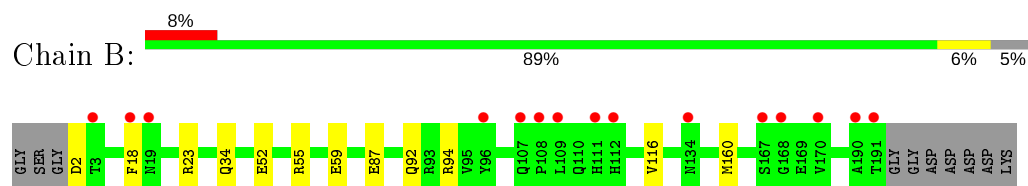
### 3 Residue-property plots [i](#)

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.

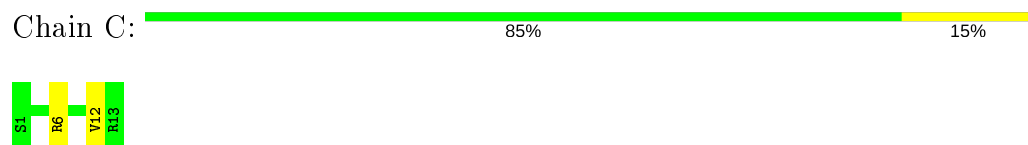
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



- Molecule 2: HLA class II histocompatibility antigen, DRB1-4 beta chain



- Molecule 3: Citrullinated Vimentin



- Molecule 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	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.42Å 183.00Å 77.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.17 – 1.65 32.17 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (32.17-1.65) 100.0 (32.17-1.65)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.82 (at 1.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.163 , 0.186 0.163 , 0.185	Depositor DCC
$R_{free}$ test set	2908 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.5	Xtriage
Anisotropy	0.581	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 51.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3866	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CIR, PGE, NAG, EDO

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	0/1667	0.49	0/2269
2	B	0.30	0/1671	0.51	0/2275
3	C	0.28	0/101	0.60	0/130
All	All	0.29	0/3439	0.51	0/4674

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

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	1586	0	1532	13	0
2	B	1611	0	1517	11	0
3	C	105	0	111	0	0
4	D	28	0	25	2	0
5	A	14	0	13	1	0
5	B	14	0	13	0	0
6	A	20	0	30	2	0
6	B	12	0	18	1	0
7	B	10	0	14	1	0
8	A	246	0	0	4	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	203	0	0	4	0
8	C	17	0	0	1	0
All	All	3866	0	3273	26	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 (26) 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)
7:B:205:PGE:H22	8:B:448:HOH:O	1.57	1.03
2:B:2:ASP:N	4:D:2:NAG:HO6	1.64	0.94
1:A:85:VAL:HG13	6:A:208:EDO:H11	1.60	0.84
2:B:94:ARG:NH2	8:B:398:HOH:O	2.25	0.69
1:A:146[C]:ARG:NH1	8:A:436:HOH:O	2.23	0.62
1:A:104:VAL:HG11	6:B:204:EDO:H11	1.83	0.61
1:A:77:SER:HA	5:A:201:NAG:H82	1.85	0.58
2:B:87[A]:GLU:OE2	2:B:92:GLN:NE2	2.38	0.56
1:A:21[A]:GLU:HG3	8:A:331:HOH:O	2.08	0.53
1:A:111[A]:LYS:HG2	1:A:140:ARG:CZ	2.40	0.51
2:B:34:GLN:NE2	8:B:306:HOH:O	2.41	0.49
2:B:52:GLU:HG2	2:B:55:ARG:CZ	2.43	0.48
2:B:116:VAL:HG22	2:B:160[B]:MET:HG2	1.96	0.47
1:A:46[B]:GLU:H	1:A:46[B]:GLU:CD	2.19	0.45
2:B:52:GLU:HG3	8:B:426:HOH:O	2.17	0.45
2:B:116:VAL:HG22	2:B:160[A]:MET:HG3	2.00	0.44
2:B:18:PHE:CD1	2:B:23:ARG:HG3	2.52	0.44
1:A:111[B]:LYS:HE2	8:A:512:HOH:O	2.17	0.43
1:A:135:THR:HG22	6:A:204:EDO:H21	2.01	0.43
2:B:2:ASP:N	4:D:2:NAG:O6	2.40	0.43
2:B:55:ARG:O	2:B:59[B]:GLU:HG2	2.20	0.41
1:A:118:ASN:HB2	1:A:166[A]:GLU:HB2	2.03	0.41
1:A:159:ASP:O	8:A:372:HOH:O	2.22	0.41
1:A:129:THR:O	1:A:132:VAL:HG22	2.21	0.40
1:A:113:THR:OG1	1:A:114:PRO:HA	2.22	0.40

There are no symmetry-related clashes.

## 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	193/189 (102%)	189 (98%)	4 (2%)	0	100	100
2	B	194/200 (97%)	190 (98%)	4 (2%)	0	100	100
3	C	8/13 (62%)	8 (100%)	0	0	100	100
All	All	395/402 (98%)	387 (98%)	8 (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	A	181/173 (105%)	181 (100%)	0	100	100
2	B	177/179 (99%)	177 (100%)	0	100	100
3	C	12/10 (120%)	11 (92%)	1 (8%)	11	2
All	All	370/362 (102%)	369 (100%)	1 (0%)	92	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	12	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	34	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	$\# Z  > 2$
3	CIR	C	6	3	9,10,11	3.03	3 (33%)	6,11,13	1.42	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	CIR	C	6	3	-	1/8/9/11	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	6	CIR	C7-N6	7.03	1.43	1.34
3	C	6	CIR	C7-N8	4.90	1.44	1.33
3	C	6	CIR	C3-C2	-2.16	1.50	1.53

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	6	CIR	C2-C3-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

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	$\# Z  > 2$
4	NAG	D	1	1,4	14,14,15	0.48	0	17,19,21	0.48	0
4	NAG	D	2	4	14,14,15	0.25	0	17,19,21	0.49	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	NAG	D	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6

*Continued on next page...*

*Continued from previous page...*

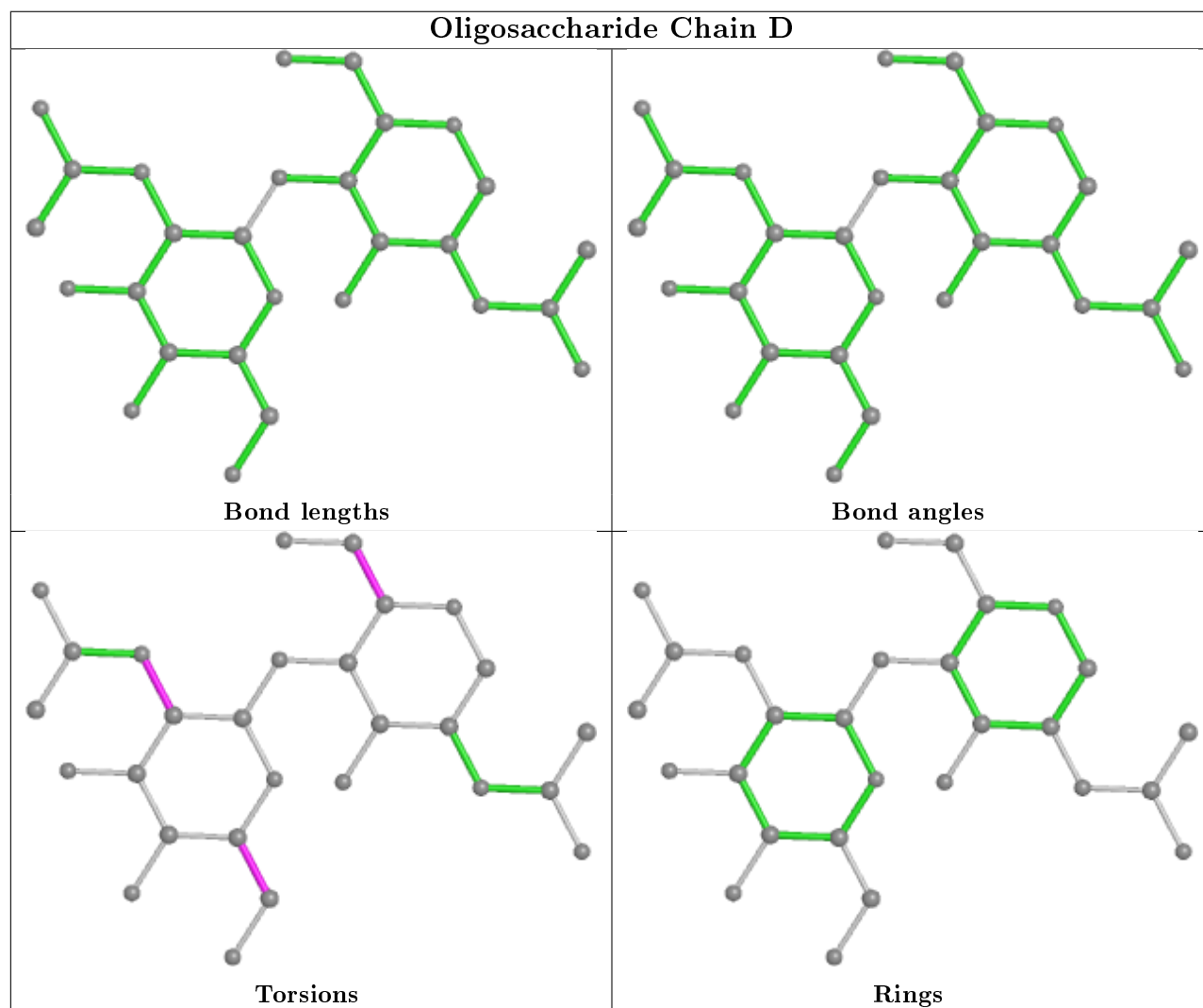
Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
4	D	2	NAG	C3-C2-N2-C7
4	D	2	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	NAG	2	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

11 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	$\# Z  > 2$
5	NAG	B	201	2	14,14,15	0.23	0	17,19,21	0.44	0
5	NAG	A	201	1	14,14,15	0.28	0	17,19,21	0.39	0
6	EDO	A	206	-	3,3,3	0.46	0	2,2,2	0.27	0
6	EDO	B	203	-	3,3,3	0.44	0	2,2,2	0.47	0
6	EDO	A	207	-	3,3,3	0.48	0	2,2,2	0.28	0
7	PGE	B	205	-	9,9,9	0.68	0	8,8,8	0.86	0
6	EDO	B	204	-	3,3,3	0.45	0	2,2,2	0.30	0
6	EDO	A	204	-	3,3,3	0.44	0	2,2,2	0.32	0
6	EDO	A	208	-	3,3,3	0.48	0	2,2,2	0.20	0
6	EDO	A	205	-	3,3,3	0.46	0	2,2,2	0.22	0
6	EDO	B	202	-	3,3,3	0.41	0	2,2,2	0.34	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
5	NAG	B	201	2	-	0/6/23/26	0/1/1/1
5	NAG	A	201	1	-	0/6/23/26	0/1/1/1
6	EDO	A	206	-	-	0/1/1/1	-
6	EDO	B	203	-	-	0/1/1/1	-
6	EDO	A	207	-	-	1/1/1/1	-
7	PGE	B	205	-	-	1/7/7/7	-
6	EDO	B	204	-	-	0/1/1/1	-
6	EDO	A	204	-	-	0/1/1/1	-
6	EDO	A	208	-	-	1/1/1/1	-
6	EDO	A	205	-	-	1/1/1/1	-
6	EDO	B	202	-	-	1/1/1/1	-

There are no bond length outliers.



There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	205	PGE	O1-C1-C2-O2
6	A	208	EDO	O1-C1-C2-O2
6	A	207	EDO	O1-C1-C2-O2
6	B	202	EDO	O1-C1-C2-O2
6	A	205	EDO	O1-C1-C2-O2

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	201	NAG	1	0
7	B	205	PGE	1	0
6	B	204	EDO	1	0
6	A	204	EDO	1	0
6	A	208	EDO	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	180/189 (95%)	0.34	14 (7%) 13 12	8, 17, 41, 64	0
2	B	190/200 (95%)	0.29	15 (7%) 12 12	7, 18, 42, 62	0
3	C	12/13 (92%)	0.20	0 100 100	13, 16, 36, 47	0
All	All	382/402 (95%)	0.32	29 (7%) 13 13	7, 18, 41, 64	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	191	THR	6.9
1	A	51	PHE	6.6
2	B	108	PRO	6.4
1	A	182	THR	6.4
1	A	100	ARG	4.9
2	B	168	GLY	4.3
1	A	181	ASP	4.1
2	B	111	HIS	3.7
1	A	50	ARG	3.5
2	B	109	LEU	3.3
2	B	170	VAL	3.3
2	B	3	THR	3.2
1	A	158	GLU	3.1
2	B	18	PHE	2.9
1	A	130	THR	2.9
1	A	3[A]	GLU	2.8
2	B	134	ASN	2.8
2	B	19	ASN	2.7
1	A	156	SER	2.7
1	A	57	GLN	2.5
1	A	46[A]	GLU	2.4
2	B	112	HIS	2.4
1	A	99	LEU	2.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	B	190	ALA	2.3
2	B	96[A]	TYR	2.3
1	A	157	THR	2.2
1	A	154	LEU	2.1
2	B	167	SER	2.0
2	B	107	GLN	2.0

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

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.

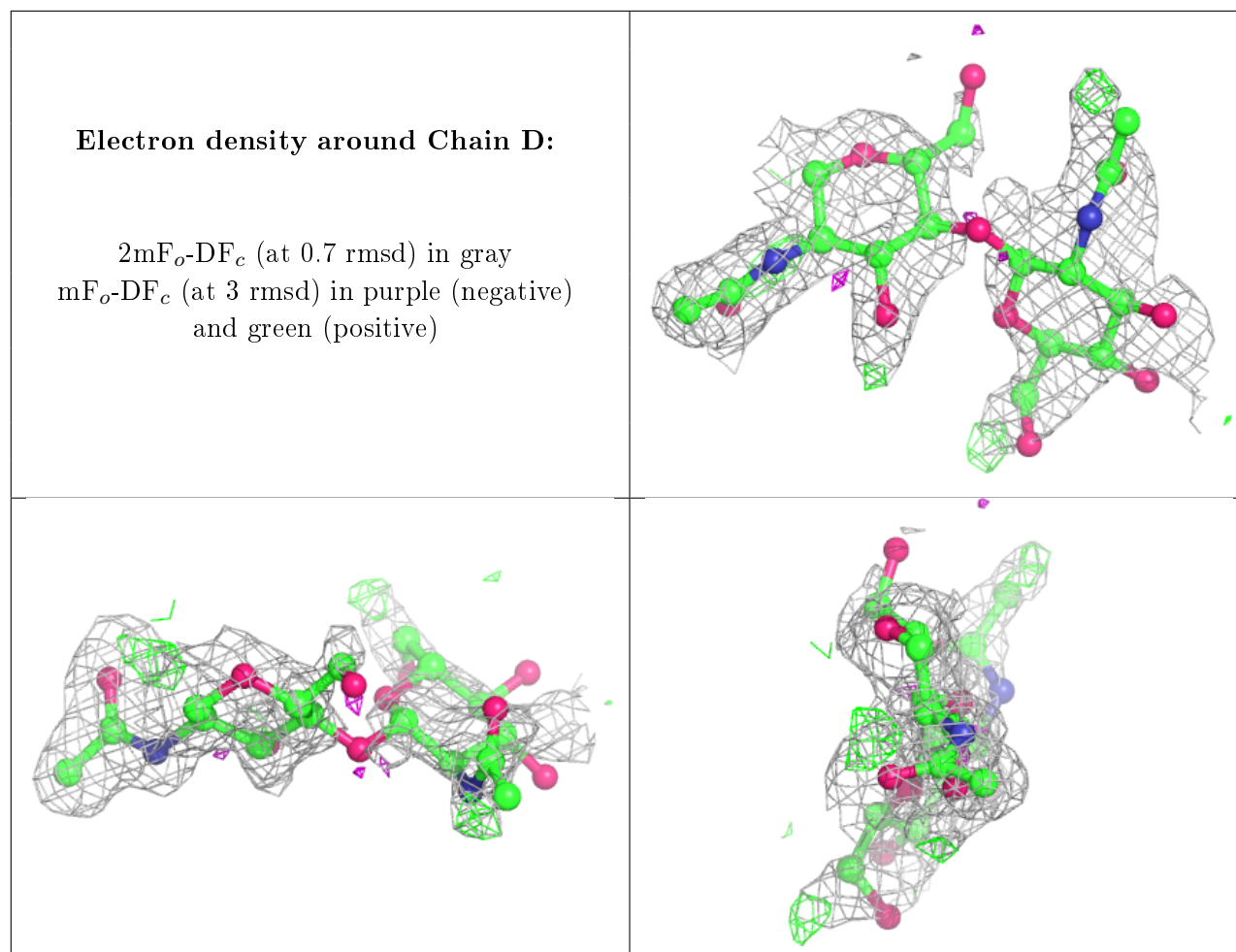
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	CIR	C	6	11/12	0.96	0.13	9,11,23,25	0

## 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
4	NAG	D	2	14/15	0.74	0.48	70,76,81,88	0
4	NAG	D	1	14/15	0.77	0.26	20,38,61,66	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
7	PGE	B	205	10/10	0.69	0.18	26,33,47,51	0
5	NAG	A	201	14/15	0.70	0.31	38,49,60,62	0
6	EDO	A	208	4/4	0.70	0.22	31,43,47,49	0
6	EDO	B	203	4/4	0.71	0.18	42,45,46,48	0
5	NAG	B	201	14/15	0.78	0.50	50,61,68,72	0
6	EDO	A	207	4/4	0.80	0.15	33,34,37,40	0
6	EDO	A	204	4/4	0.86	0.17	46,49,51,64	0
6	EDO	A	206	4/4	0.87	0.12	28,40,49,50	0
6	EDO	B	204	4/4	0.91	0.11	35,36,44,48	0
6	EDO	A	205	4/4	0.91	0.21	19,25,31,34	0
6	EDO	B	202	4/4	0.93	0.14	20,33,35,43	0

## 6.5 Other polymers

There are no such residues in this entry.