



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 9, 2024 – 11:42 AM EST

PDB ID : 6O4P  
Title : The crystal structure of the interleukin 11 alpha receptor  
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Deposited on : 2019-02-28  
Resolution : 3.43 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

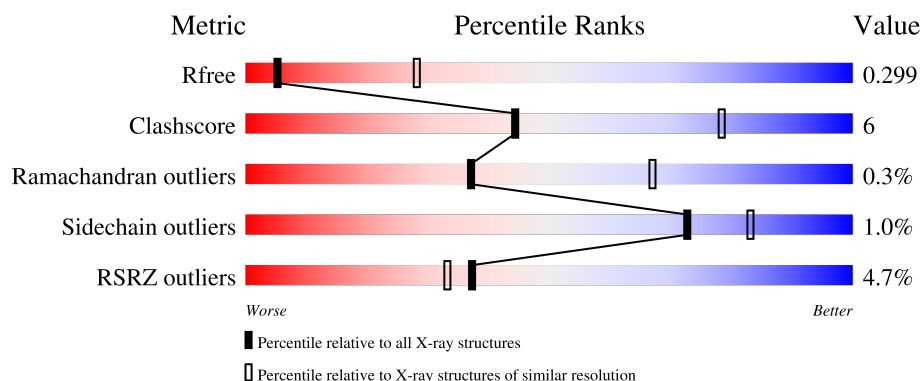
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.43 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))
$R_{free}$	164625	1112 (3.48-3.36)
Clashscore	180529	1144 (3.48-3.36)
Ramachandran outliers	177936	1146 (3.48-3.36)
Sidechain outliers	177891	1146 (3.48-3.36)
RSRZ outliers	164620	1112 (3.48-3.36)

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	349	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>13%</div> <div>15%</div> </div> </div>
1	B	349	<div> <div>3%</div> <div> <div></div> <div>71%</div> <div>11%</div> <div>18%</div> </div> </div>
2	C	4	<div> <div></div> <div> <div>75%</div> <div>25%</div> </div> </div>
3	D	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SO4	A	406	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4580 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 Interleukin-11 receptor subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2253	1432	392	421	8			
1	B	285	Total	C	N	O	S	0	0	0
			2180	1384	381	407	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	226	SER	CYS	conflict	UNP Q14626
A	342	HIS	-	expression tag	UNP Q14626
A	343	HIS	-	expression tag	UNP Q14626
A	344	HIS	-	expression tag	UNP Q14626
A	345	HIS	-	expression tag	UNP Q14626
A	346	HIS	-	expression tag	UNP Q14626
A	347	HIS	-	expression tag	UNP Q14626
A	348	HIS	-	expression tag	UNP Q14626
A	349	HIS	-	expression tag	UNP Q14626
B	226	SER	CYS	conflict	UNP Q14626
B	342	HIS	-	expression tag	UNP Q14626
B	343	HIS	-	expression tag	UNP Q14626
B	344	HIS	-	expression tag	UNP Q14626
B	345	HIS	-	expression tag	UNP Q14626
B	346	HIS	-	expression tag	UNP Q14626
B	347	HIS	-	expression tag	UNP Q14626
B	348	HIS	-	expression tag	UNP Q14626
B	349	HIS	-	expression tag	UNP Q14626

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



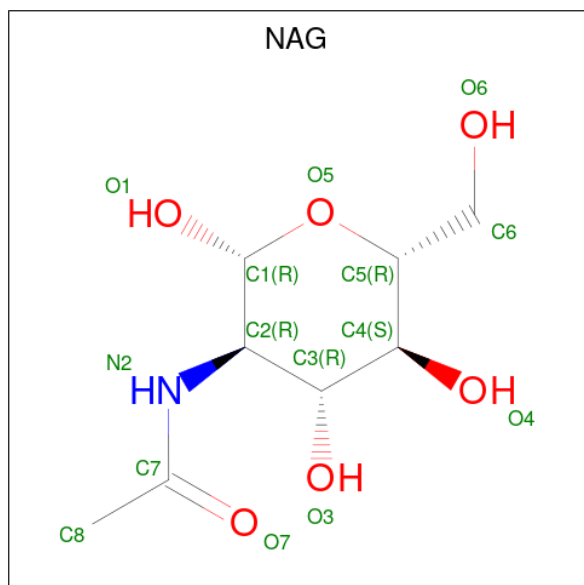
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 3 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
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	171.46Å 171.46Å 107.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.67 – 3.43 45.67 – 3.43	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.67-3.43) 99.5 (45.67-3.43)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.25 (at 3.40Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.244 , 0.298 0.248 , 0.299	Depositor DCC
$R_{free}$ test set	615 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	69.8	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 56.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	4580	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.13% 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: BMA, MAN, NAG, SO4

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	0.24	0/2330	0.43	0/3204
1	B	0.24	0/2254	0.43	0/3098
All	All	0.24	0/4584	0.43	0/6302

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	2253	0	2168	28	0
1	B	2180	0	2090	22	0
2	C	50	0	43	3	0
3	D	28	0	25	2	0
4	A	14	0	13	1	0
5	A	30	0	0	3	0
5	B	25	0	0	1	0
All	All	4580	0	4339	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 6.

The worst 5 of 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:34:PRO:HG2	1:A:75:LEU:HD11	1.71	0.71
1:A:102:ASP:OD2	4:A:401:NAG:H82	1.99	0.62
1:B:211:PRO:HB3	1:B:296:GLY:HA3	1.82	0.61
1:A:93:ARG:NH1	5:A:406:SO4:O2	2.34	0.60
1:B:29:VAL:HG13	1:B:31:ALA:H	1.66	0.60

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	291/349 (83%)	275 (94%)	15 (5%)	1 (0%)	37	67
1	B	281/349 (80%)	269 (96%)	11 (4%)	1 (0%)	30	61
All	All	572/698 (82%)	544 (95%)	26 (4%)	2 (0%)	37	67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	178	PRO
1	A	178	PRO

### 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	244/294 (83%)	241 (99%)	3 (1%)	67	79
1	B	235/294 (80%)	233 (99%)	2 (1%)	75	86
All	All	479/588 (82%)	474 (99%)	5 (1%)	73	83

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	25	CYS
1	A	243	HIS
1	B	4	CYS
1	B	25	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	47	GLN
1	B	17	GLN
1	B	47	GLN
1	B	200	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [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	C	1	1,2	14,14,15	0.33	0	17,19,21	0.54	0
2	NAG	C	2	2	14,14,15	0.42	0	17,19,21	1.33	2 (11%)
2	BMA	C	3	2	11,11,12	0.91	0	15,15,17	1.15	2 (13%)
2	MAN	C	4	2	11,11,12	0.72	0	15,15,17	0.87	1 (6%)
3	NAG	D	1	1,3	14,14,15	0.25	0	17,19,21	0.50	0
3	NAG	D	2	3	14,14,15	0.49	0	17,19,21	1.33	2 (11%)

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

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C2-N2-C7	4.60	129.06	122.90
3	D	2	NAG	C2-N2-C7	4.56	129.02	122.90
2	C	3	BMA	C1-C2-C3	2.37	113.10	109.64
2	C	3	BMA	C2-C3-C4	2.23	114.78	110.86
3	D	2	NAG	C1-C2-N2	2.18	113.88	110.43

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	NAG	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6

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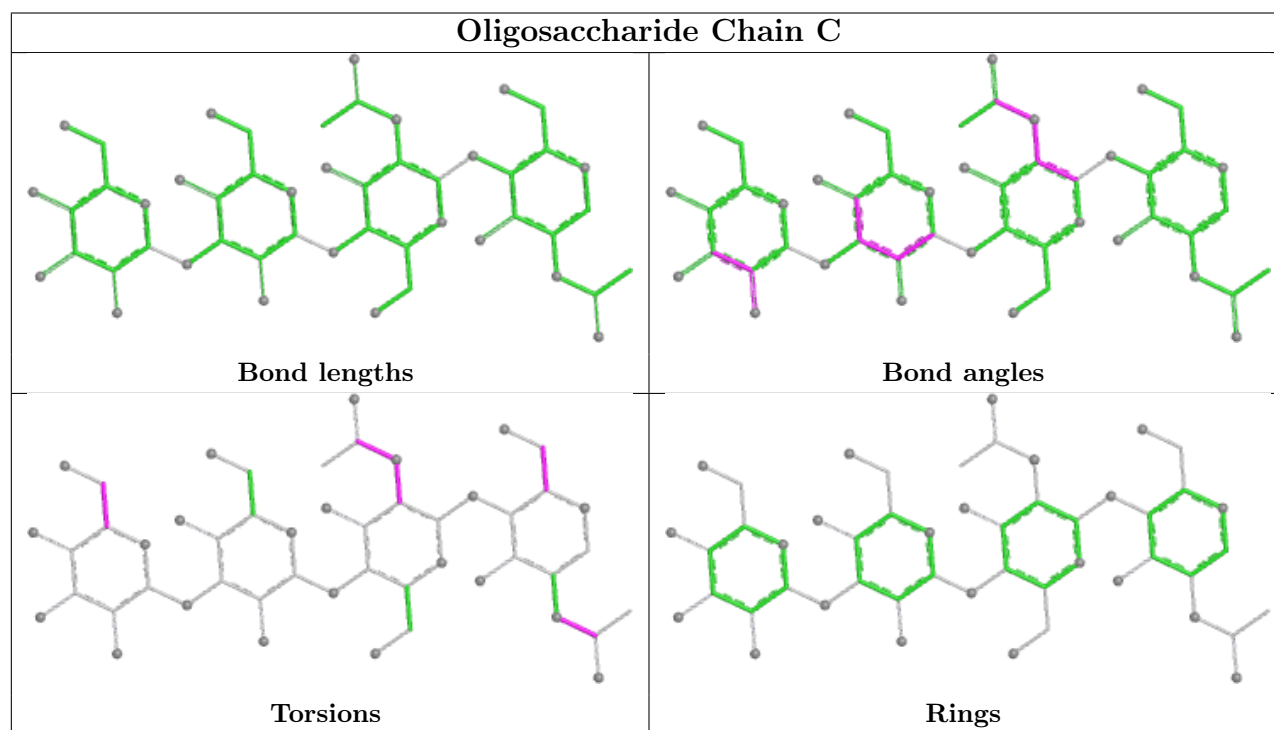
Mol	Chain	Res	Type	Atoms
2	C	4	MAN	C4-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6

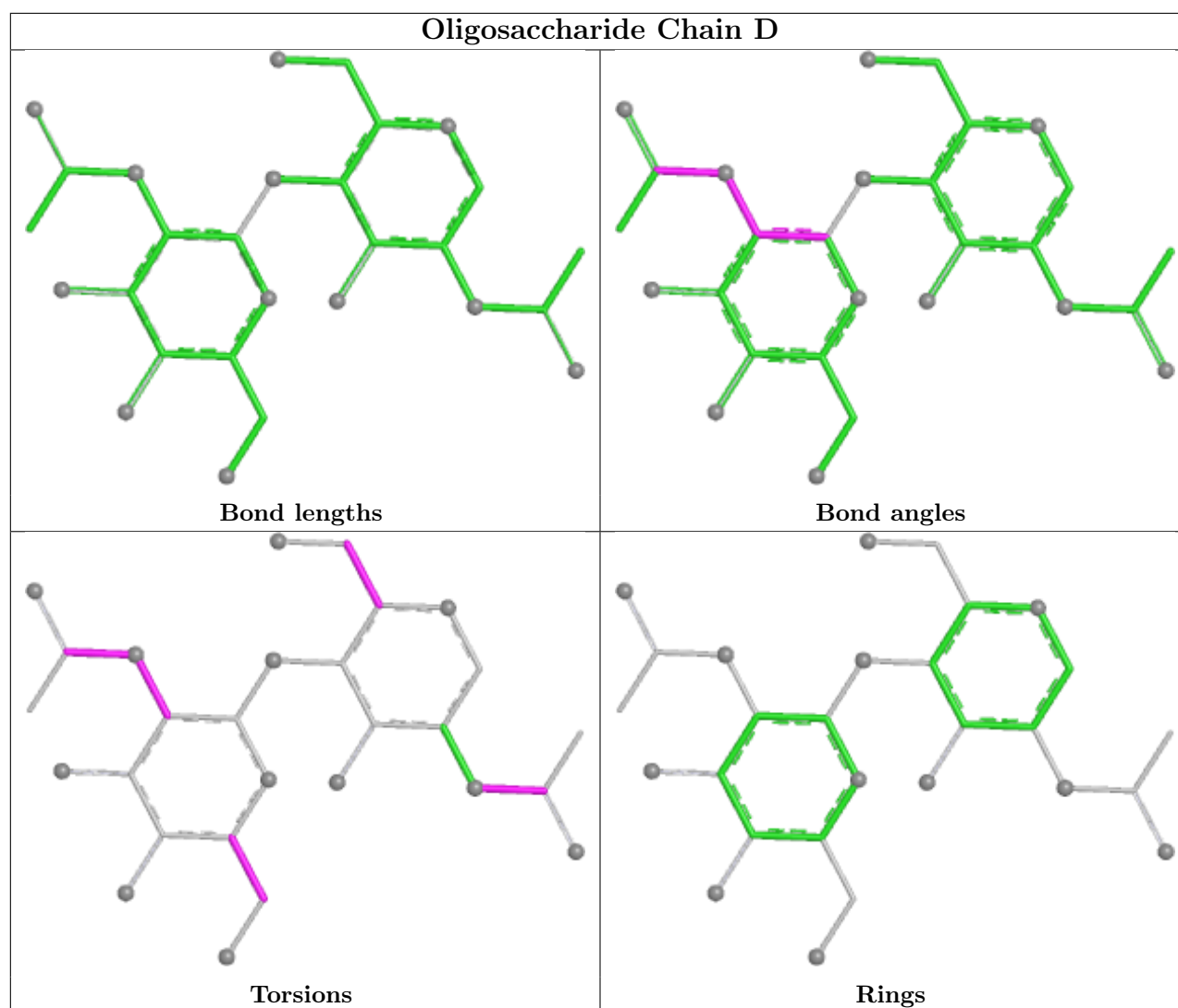
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	2	0
2	C	1	NAG	2	0
3	D	2	NAG	2	0
3	D	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





## 5.6 Ligand geometry [i](#)

12 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	SO4	A	406	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	A	409	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	B	503	-	4,4,4	0.23	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	A	410	-	4,4,4	0.23	0	6,6,6	0.06	0
5	SO4	A	408	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	B	506	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	B	504	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	B	507	-	4,4,4	0.23	0	6,6,6	0.07	0
5	SO4	A	407	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	A	411	-	4,4,4	0.24	0	6,6,6	0.07	0
4	NAG	A	401	1	14,14,15	0.36	0	17,19,21	0.45	0
5	SO4	B	505	-	4,4,4	0.23	0	6,6,6	0.08	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	A	401	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	401	NAG	C4-C5-C6-O6
4	A	401	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	406	SO4	3	0
5	B	503	SO4	1	0
4	A	401	NAG	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	295/349 (84%)	0.31	16 (5%) 32 29	27, 55, 112, 154	0
1	B	285/349 (81%)	0.31	11 (3%) 44 38	28, 63, 113, 168	0
All	All	580/698 (83%)	0.31	27 (4%) 37 33	27, 60, 114, 168	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	79	LEU	5.0
1	A	303	PRO	4.2
1	A	304	ALA	4.1
1	B	242	GLN	3.2
1	B	78	ALA	3.2

### 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.

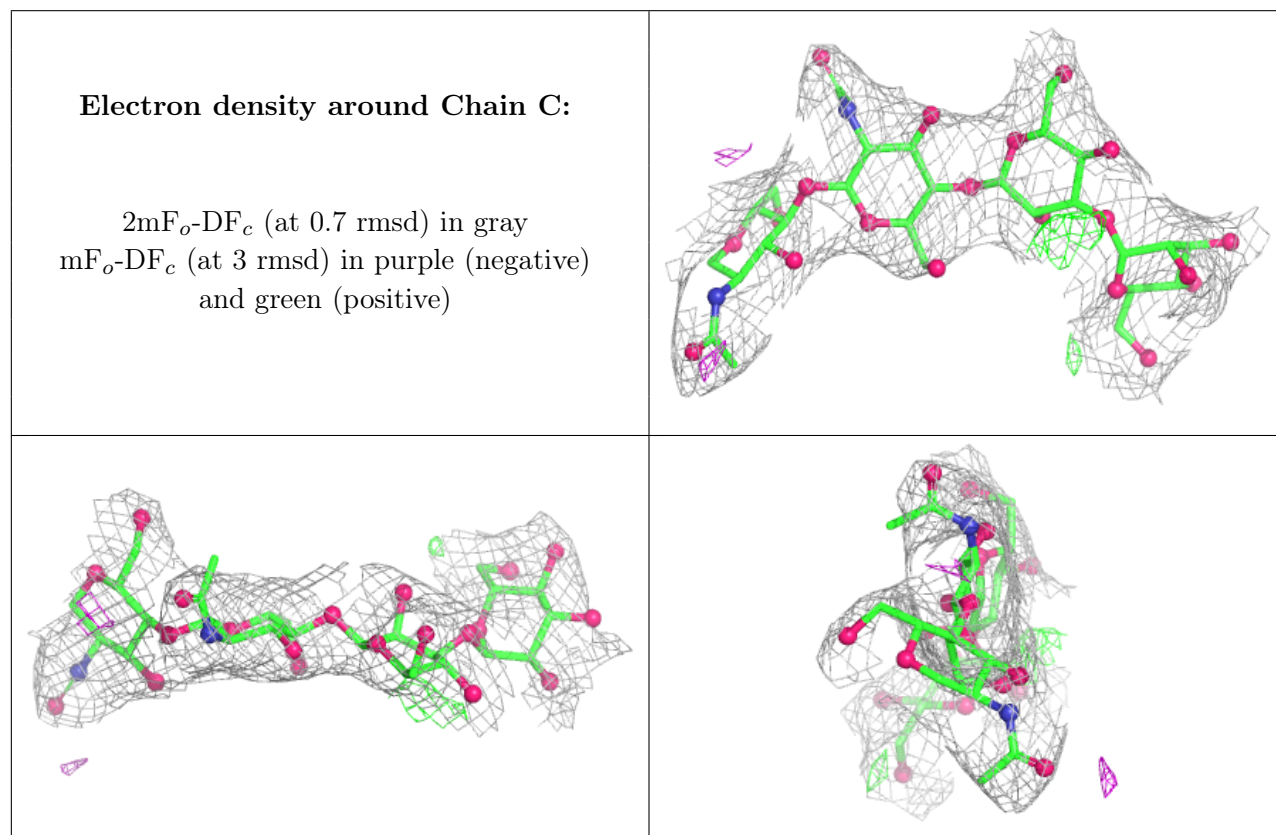
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MAN	C	4	11/12	0.37	0.14	85,97,107,107	0
2	BMA	C	3	11/12	0.65	0.12	89,98,103,107	0
3	NAG	D	2	14/15	0.79	0.15	59,81,89,96	0
3	NAG	D	1	14/15	0.83	0.12	49,60,76,77	0
2	NAG	C	2	14/15	0.89	0.11	62,70,77,81	0

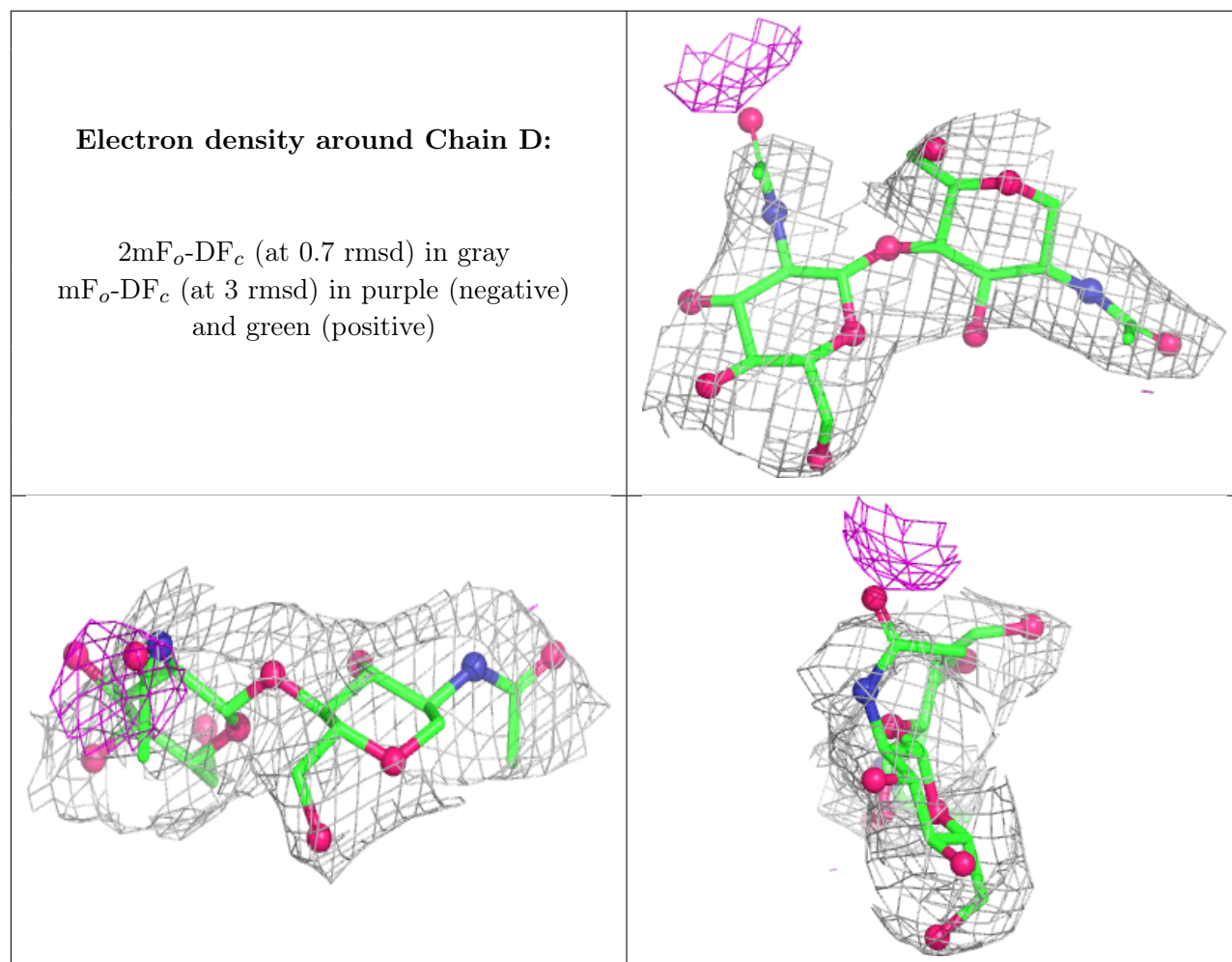
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	C	1	14/15	0.90	0.10	44,49,56,60	0

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 ⓘ

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	NAG	A	401	14/15	0.42	0.19	103,108,116,123	0
5	SO4	A	409	5/5	0.49	0.24	124,127,129,130	0
5	SO4	B	507	5/5	0.49	0.12	188,188,188,189	0
5	SO4	A	410	5/5	0.50	0.23	122,124,126,130	0
5	SO4	A	407	5/5	0.54	0.20	133,135,135,136	0
5	SO4	B	505	5/5	0.57	0.15	121,121,122,123	0
5	SO4	A	408	5/5	0.63	0.30	128,130,131,133	0
5	SO4	B	506	5/5	0.66	0.19	125,126,127,130	0
5	SO4	A	411	5/5	0.70	0.15	100,102,105,111	0
5	SO4	A	406	5/5	0.74	0.14	103,105,109,112	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	SO4	B	503	5/5	0.81	0.14	90,91,95,96	0
5	SO4	B	504	5/5	0.89	0.13	107,109,110,110	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.