

Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2024 – 06:40 pm GMT

PDB ID : 8QGX

Title : Complex between human neutrophil elastase with nanobody NbE201 Authors : Morales-Yanez, F.; Redeghieri, P.; Moray, J.; Dumoulin, M.; Kerff, F.

Deposited on : 2023-09-06

Resolution : 2.30 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 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)

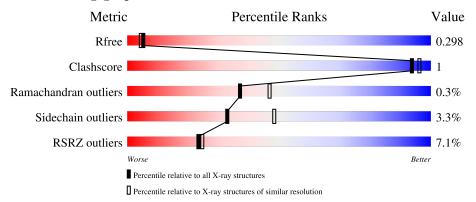
Validation Pipeline (wwPDB-VP) : 2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.30 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
R_{free}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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 >=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 <=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	218	6%	98%					
2	В	129	9%	81%	14%	5%			
3	С	3	33%	67%					
3	D	3	33%	67%					



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5269 atoms, of which 2604 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 Neutrophil elastase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	216	Total 3241	C 1016	H 1624	N 310	O 280	S 11	0	0	0

• Molecule 2 is a protein called NbE201.

Mo	l Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
2	В	123	Total 1851	C 596	H 902	N 163	O 185	S 5	0	0	0

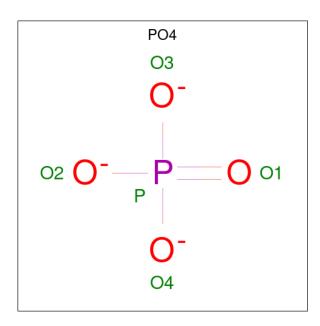
• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[al pha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



	Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace		
	2	2 C	2	Total	С	Н	N	О	0	0	0		
	3	77	22	39	2	14	U	U					
	2	D	D	D	2	Total	С	Н	N	О	0	0	0
	3 D	ა	77	22	39	2	14	0	0				

• Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total (O 4	P 1	0	0

• Molecule 5 is water.

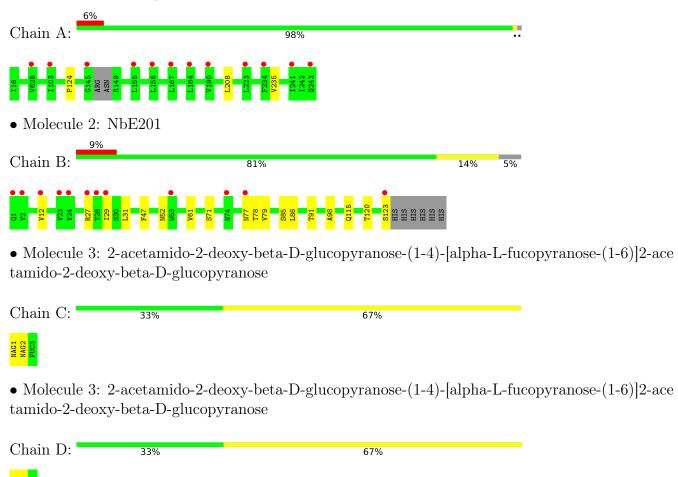
\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	A	15	Total O 15 15	0	0
5	В	3	Total O 3 3	0	0



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: Neutrophil elastase





4 Data and refinement statistics (i)

Property	Value	Source		
Space group	P 21 21 21	Depositor		
Cell constants	64.98Å 73.00Å 84.92Å	Depositor		
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor		
Resolution (Å)	48.54 - 2.30	Depositor		
rtesolution (A)	48.54 - 2.30	EDS		
% Data completeness	99.9 (48.54-2.30)	Depositor		
(in resolution range)	99.9 (48.54-2.30)	EDS		
R_{merge}	0.13	Depositor		
R_{sym}	(Not available)	Depositor		
$< I/\sigma(I) > 1$	1.87 (at 2.29Å)	Xtriage		
Refinement program	BUSTER 2.10.3	Depositor		
P. P.	0.224 , 0.271	Depositor		
R, R_{free}	0.244 , 0.298	DCC		
R_{free} test set	927 reflections (5.00%)	wwPDB-VP		
Wilson B-factor (Å ²)	55.1	Xtriage		
Anisotropy	0.744	Xtriage		
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.41, 59.6	EDS		
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage		
Estimated twinning fraction	No twinning to report.	Xtriage		
F_o, F_c correlation	0.95	EDS		
Total number of atoms	5269	wwPDB-VP		
Average B, all atoms (Å ²)	84.0	wwPDB-VP		

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.02% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: PO4, NAG, FUC

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.50	0/1646	0.68	0/2235	
2	В	0.57	0/969	0.72	0/1313	
All	All	0.53	0/2615	0.70	0/3548	

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	1617	1624	1630	2	0
2	В	949	902	923	5	0
3	С	38	39	34	0	0
3	D	38	39	34	0	0
4	A	5	0	0	1	0
5	A	15	0	0	0	0
5	В	3	0	0	0	0
All	All	2665	2604	2621	7	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 1.



All (7) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}({\rm \AA})$	overlap (Å)
2:B:91:THR:HG23	2:B:120:THR:HA	1.94	0.49
2:B:47:PHE:O	2:B:61:VAL:CG2	2.63	0.47
2:B:47:PHE:O	2:B:61:VAL:HG21	2.18	0.42
2:B:31:LEU:HD13	2:B:98:ALA:HB1	2.02	0.42
1:A:124:PRO:O	1:A:235:VAL:HG21	2.20	0.42
2:B:12:VAL:HG11	2:B:86:LEU:HD13	2.03	0.41
1:A:208:LEU:HD12	4:A:301:PO4:O3	2.21	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 Allower		Outliers	Percentiles			
1	A	212/218 (97%)	208 (98%)	4 (2%)	0	1	100	100	
2	В	121/129 (94%)	115 (95%)	5 (4%)	1 (1%)		16	20	
All	All	333/347 (96%)	323 (97%)	9 (3%)	1 (0%)		37	47	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	77	ASN

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	170/172~(99%)	170 (100%)	0	100 100
2	В	102/108~(94%)	93 (91%)	9 (9%)	8 10
All	All	272/280 (97%)	263 (97%)	9 (3%)	33 48

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	27	ARG
2	В	29	ILE
2	В	52	ASN
2	В	71	SER
2	В	78	THR
2	В	79	VAL
2	В	85	SER
2	В	115	GLN
2	В	123	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	Tuno	Chain	Res	Link	Вс	ond leng	ths	В	ond ang	les
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	С	1	3,1	14,14,15	0.45	0	17,19,21	0.88	1 (5%)
3	NAG	С	2	3	14,14,15	0.31	0	17,19,21	0.95	1 (5%)
3	FUC	С	3	3	10,10,11	0.50	0	14,14,16	0.68	0
3	NAG	D	1	3,1	14,14,15	0.26	0	17,19,21	0.72	1 (5%)
3	NAG	D	2	3	14,14,15	0.29	0	17,19,21	1.04	1 (5%)
3	FUC	D	3	3	10,10,11	0.40	0	14,14,16	0.83	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	NAG	С	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	С	2	3	-	0/6/23/26	0/1/1/1
3	FUC	С	3	3	-	-	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	FUC	D	3	3	-	-	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathbf{Ideal}(^{o})$
3	D	2	NAG	C1-O5-C5	3.34	116.71	112.19
3	С	2	NAG	C1-O5-C5	2.59	115.70	112.19
3	С	1	NAG	C1-C2-N2	-2.32	106.53	110.49
3	D	1	NAG	C1-O5-C5	2.19	115.15	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

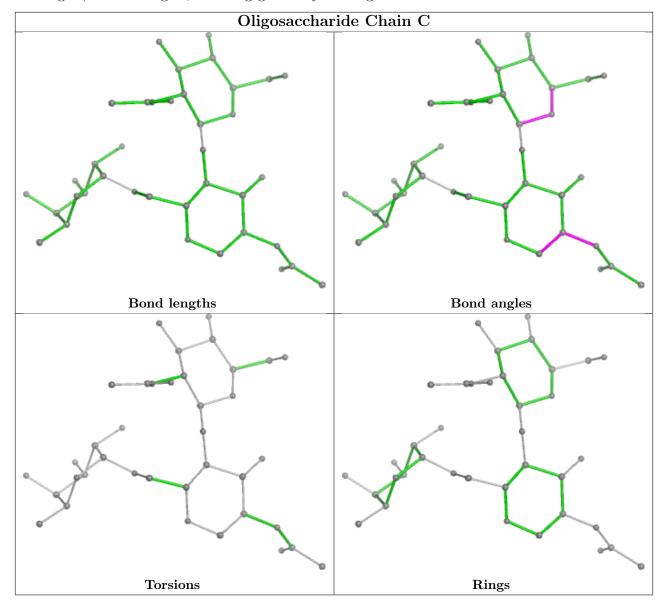
There are no ring outliers.

No monomer is involved in short contacts.

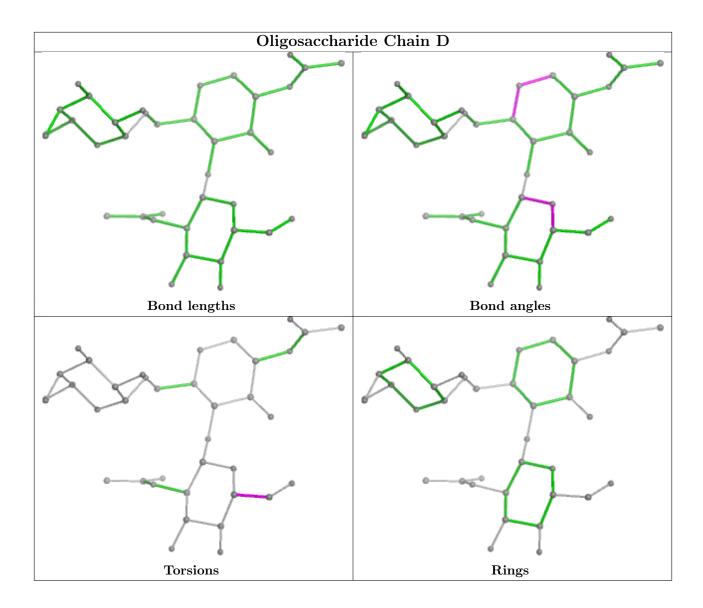
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,



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	Dec	Res Link Bond lengths		${ m gths}$	Bond angles			
MIOI	Туре	Chain	Res	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PO4	A	301	-	4,4,4	2.51	1 (25%)	6,6,6	0.47	0



All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
4	A	301	PO4	P-O1	4.16	1.60	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	301	PO4	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 (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^{th} 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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q < 0.9
1	A	216/218 (99%)	0.53	12 (5%) 31 33	55, 80, 112, 144	0
2	В	123/129 (95%)	0.61	12 (9%) 14 16	57, 84, 116, 137	0
All	All	339/347 (97%)	0.56	24 (7%) 23 25	55, 81, 113, 144	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	145	GLY	5.0
2	В	28	THR	3.6
2	В	53	TRP	3.4
1	A	241	ILE	3.1
1	A	184	LEU	2.9
2	В	123	SER	2.9
1	A	155	LEU	2.8
1	A	62(B)	VAL	2.7
1	A	103	ILE	2.5
1	A	234	PHE	2.4
2	В	29	ILE	2.4
2	В	2	VAL	2.4
2	В	74	ASN	2.4
1	A	158	LEU	2.3
1	A	243	GLN	2.3
2	В	1	GLN	2.3
1	A	223	LEU	2.2
2	В	12	VAL	2.2
2	В	23	VAL	2.2
2	В	27	ARG	2.2
1	A	167	LEU	2.1
1	A	190	VAL	2.1
2	В	24	VAL	2.1
2	В	77	ASN	2.1



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

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

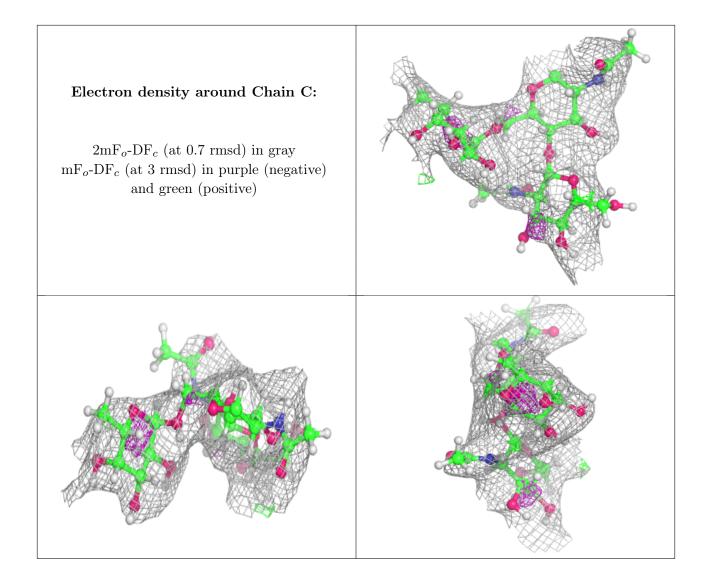
6.3 Carbohydrates (i)

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^{th} 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.

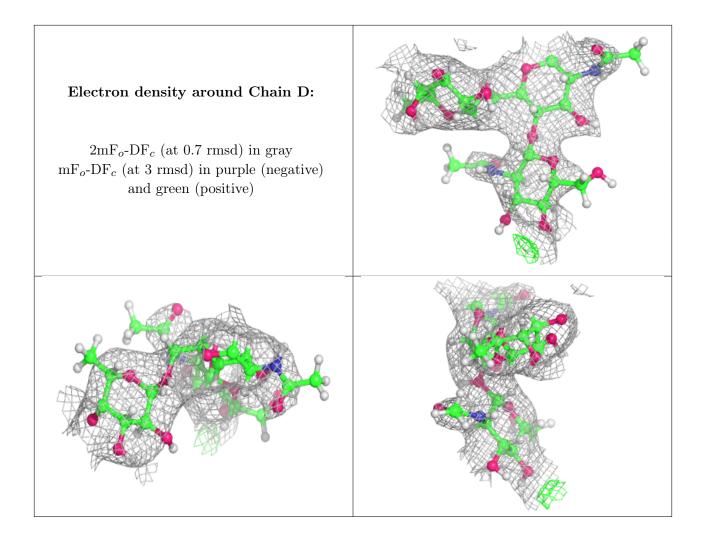
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	NAG	С	2	14/15	0.64	0.13	75,83,89,93	0
3	NAG	D	2	14/15	0.72	0.11	78,89,95,97	0
3	FUC	С	3	10/11	0.81	0.10	66,72,77,81	0
3	NAG	С	1	14/15	0.84	0.10	71,76,82,89	0
3	NAG	D	1	14/15	0.91	0.07	73,80,85,91	0
3	FUC	D	3	10/11	0.91	0.08	69,74,80,82	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^{th} 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	$\operatorname{B-factors}(\mathrm{\AA}^2)$	Q<0.9
4	PO4	A	301	5/5	0.84	0.12	118,121,122,123	0

6.5 Other polymers (i)

There are no such residues in this entry.

