



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:30 PM UTC

PDB ID : 4KRO / pdb_00004kro
Title : Nanobody/VHH domain EgA1 in complex with the extracellular region of EGFR
Authors : Ferguson, K.M.; Schmitz, K.R.
Deposited on : 2013-05-16
Resolution : 3.05 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

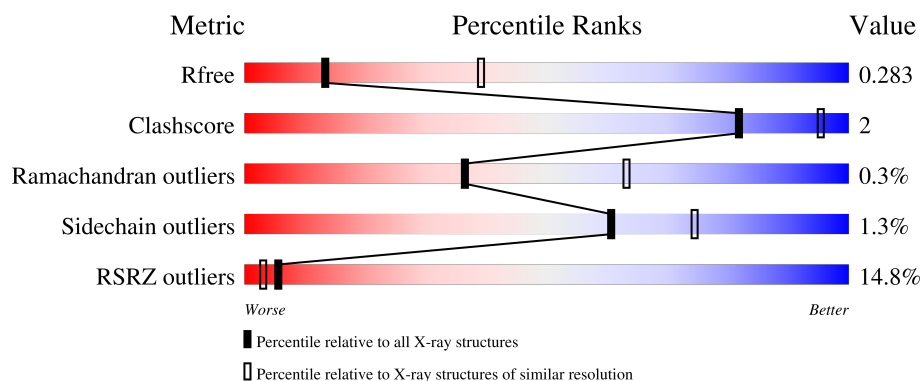
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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 $\leq 5\%$. 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	624	21% 87% 5% 9%
2	B	138	20% 76% 8% 16%
3	C	211	93% 7%
4	D	220	87% 9% .
5	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
5	F	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14907 atoms, of which 6958 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	570	Total	C	H	N	O	S	0	0	0
			7064	2366	3231	683	734	50			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	619	HIS	-	expression tag	UNP P00533
A	620	HIS	-	expression tag	UNP P00533
A	621	HIS	-	expression tag	UNP P00533
A	622	HIS	-	expression tag	UNP P00533
A	623	HIS	-	expression tag	UNP P00533
A	624	HIS	-	expression tag	UNP P00533

- Molecule 2 is a protein called Nanobody/VHH domain EgA1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	116	Total	C	H	N	O	S	0	0	0
			1492	533	656	140	160	3			

- Molecule 3 is a protein called Cetuximab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	211	Total	C	H	N	O	S	0	0	0
			3064	985	1483	267	325	4			

- Molecule 4 is a protein called Cetuximab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	213	Total	C	H	N	O	S	0	0	0
			3088	1009	1499	259	316	5			

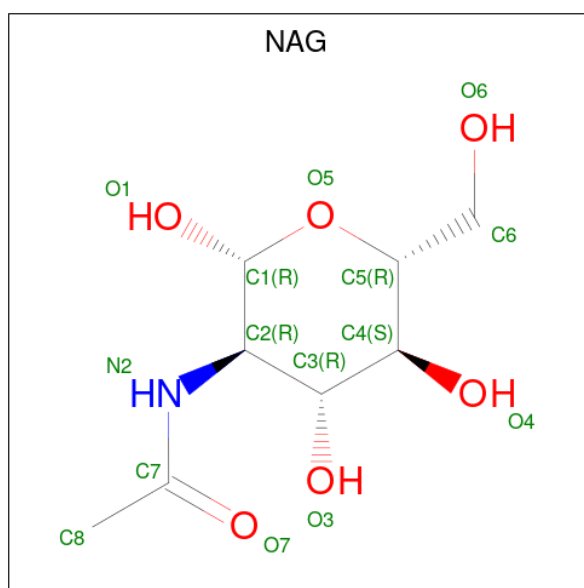
- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a

cetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			
5	F	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
6	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
6	D	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	3	Total	0	0
			3		

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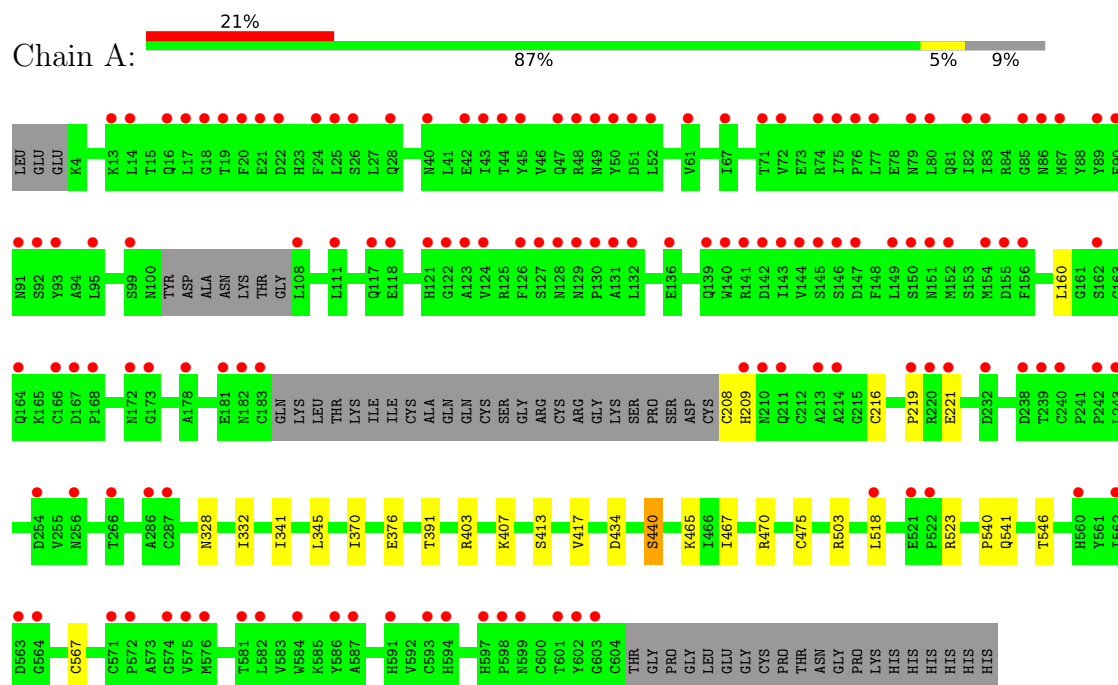
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	3	Total	O	0	0
			3	3		
7	D	6	Total	O	0	0
			6	6		

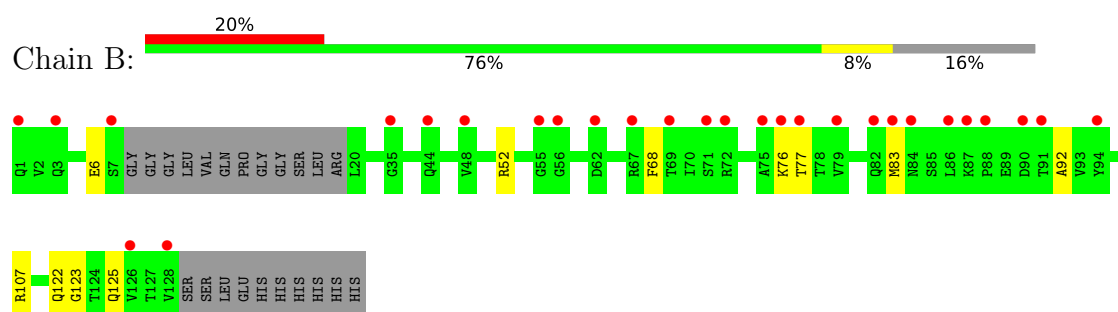
3 Residue-property plots [i](#)

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: Epidermal growth factor receptor



- Molecule 2: Nanobody/VHH domain EgA1

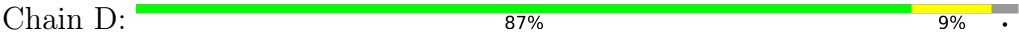


- Molecule 3: Cetuximab light chain





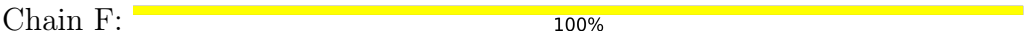
• Molecule 4: Cetuximab heavy chain



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 5: 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	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.21Å 96.29Å 128.10Å 90.00° 100.68° 90.00°	Depositor
Resolution (Å)	38.19 – 3.05 38.19 – 3.05	Depositor EDS
% Data completeness (in resolution range)	98.6 (38.19-3.05) 98.6 (38.19-3.05)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 3.06Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.221 , 0.280 0.225 , 0.283	Depositor DCC
R_{free} test set	1507 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	50.9	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	14907	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NAG

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	0.36	0/3901	0.72	4/5343 (0.1%)
2	B	0.32	0/859	0.62	0/1177
3	C	0.40	0/1615	0.70	0/2204
4	D	0.43	0/1631	0.71	0/2238
All	All	0.38	0/8006	0.70	4/10962 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	LEU	N-CA-C	-6.35	105.84	113.97
1	A	417	VAL	N-CA-C	5.28	115.87	108.17
1	A	440	SER	N-CA-C	5.12	117.03	108.99
1	A	221	GLU	N-CA-C	-5.07	105.84	112.23

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	3833	3231	3244	12	0
2	B	836	656	693	6	0
3	C	1581	1483	1480	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1589	1499	1495	12	0
5	E	28	25	25	1	0
5	F	28	25	25	1	0
6	A	28	26	26	0	0
6	D	14	13	13	0	0
7	A	3	0	0	0	0
7	C	3	0	0	0	0
7	D	6	0	0	0	0
All	All	7949	6958	7001	37	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 2.

All (37) 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:518:LEU:O	1:A:523:ARG:NH2	2.18	0.77
1:A:407:LYS:NZ	1:A:434:ASP:OD2	2.25	0.69
4:D:203:ASN:N	4:D:203:ASN:OD1	2.30	0.64
2:B:68:PHE:CD1	2:B:83:MET:HA	2.34	0.62
2:B:6:GLU:OE2	2:B:123:GLY:N	2.35	0.60
1:A:208:CYS:N	1:A:216:CYS:SG	2.75	0.59
3:C:80:SER:HA	3:C:106:LEU:HD22	1.85	0.58
1:A:465:LYS:NZ	4:D:103:ASP:OD2	2.40	0.54
2:B:6:GLU:OE2	2:B:122:GLN:N	2.41	0.53
2:B:76:LYS:HA	2:B:77:THR:CB	2.39	0.52
1:A:540:PRO:O	1:A:541:GLN:NE2	2.44	0.51
3:C:37:GLN:O	3:C:45:ARG:N	2.41	0.50
2:B:92:ALA:O	2:B:125:GLN:NE2	2.44	0.49
4:D:1:GLN:OE1	4:D:1:GLN:N	2.45	0.48
4:D:86:GLN:N	4:D:89:ASP:OD2	2.43	0.47
4:D:47:TRP:HZ2	4:D:50:VAL:HG23	1.78	0.47
3:C:108:ARG:NH1	3:C:109:THR:O	2.47	0.47
3:C:158:ASN:OD1	3:C:158:ASN:N	2.46	0.47
3:C:182:SER:OG	3:C:185:ASP:OD1	2.30	0.46
1:A:523:ARG:CB	1:A:546:THR:HG21	2.46	0.46
1:A:440:SER:CB	1:A:467:ILE:HG13	2.46	0.46
1:A:376:GLU:OE1	1:A:403:ARG:NH1	2.48	0.45
4:D:13:GLN:HB2	4:D:16:GLN:HG3	1.99	0.45
3:C:129:THR:OG1	3:C:130:ALA:N	2.50	0.44
4:D:47:TRP:CZ2	4:D:50:VAL:HG23	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:36:TRP:CZ2	4:D:80:PHE:HB2	2.53	0.43
1:A:470:ARG:HG2	1:A:475:CYS:SG	2.58	0.42
4:D:125:PRO:HB3	4:D:151:TYR:HB3	2.02	0.42
4:D:67:LEU:HD11	4:D:80:PHE:CE1	2.55	0.42
3:C:32:ASN:HB3	3:C:91:ASN:HB3	2.02	0.42
4:D:61:THR:N	4:D:62:PRO:CD	2.82	0.41
4:D:50:VAL:HG12	4:D:51:ILE:N	2.37	0.40
1:A:328:ASN:HD22	5:E:1:NAG:C7	2.35	0.40
2:B:52:ARG:NH2	2:B:107:ARG:HA	2.37	0.40
1:A:332:ILE:HG13	1:A:370:ILE:HD12	2.03	0.40
1:A:341:ILE:HD13	1:A:345:LEU:HD13	2.03	0.40
5:F:1:NAG:O4	5:F:2:NAG:H83	2.20	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	564/624 (90%)	496 (88%)	65 (12%)	3 (0%)	24	52
2	B	112/138 (81%)	94 (84%)	18 (16%)	0	100	100
3	C	209/211 (99%)	199 (95%)	10 (5%)	0	100	100
4	D	209/220 (95%)	200 (96%)	9 (4%)	0	100	100
All	All	1094/1193 (92%)	989 (90%)	102 (9%)	3 (0%)	36	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	HIS
1	A	567	CYS
1	A	219	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	352/545 (65%)	349 (99%)	3 (1%)	70	78
2	B	69/114 (60%)	69 (100%)	0	100	100
3	C	176/188 (94%)	174 (99%)	2 (1%)	65	76
4	D	177/190 (93%)	172 (97%)	5 (3%)	38	63
All	All	774/1037 (75%)	764 (99%)	10 (1%)	61	74

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	391	THR
1	A	413	SER
1	A	503	ARG
3	C	39	ARG
3	C	83	ILE
4	D	12	VAL
4	D	25	SER
4	D	105	GLU
4	D	118	SER
4	D	203	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	409	HIS
1	A	483	HIS
1	A	554	ASN
2	B	112	GLN
4	D	177	GLN
4	D	198	GLN

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 ⓘ

4 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$
5	NAG	E	1	5,1	14,14,15	0.42	0	17,19,21	0.36	0
5	NAG	E	2	5	14,14,15	0.40	0	17,19,21	0.41	0
5	NAG	F	1	5,1	14,14,15	0.44	0	17,19,21	0.42	0
5	NAG	F	2	5	14,14,15	0.45	0	17,19,21	0.61	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	E	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	3/6/23/26	0/1/1/1
5	NAG	F	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	F	2	5	-	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 (9) torsion outliers are listed below:

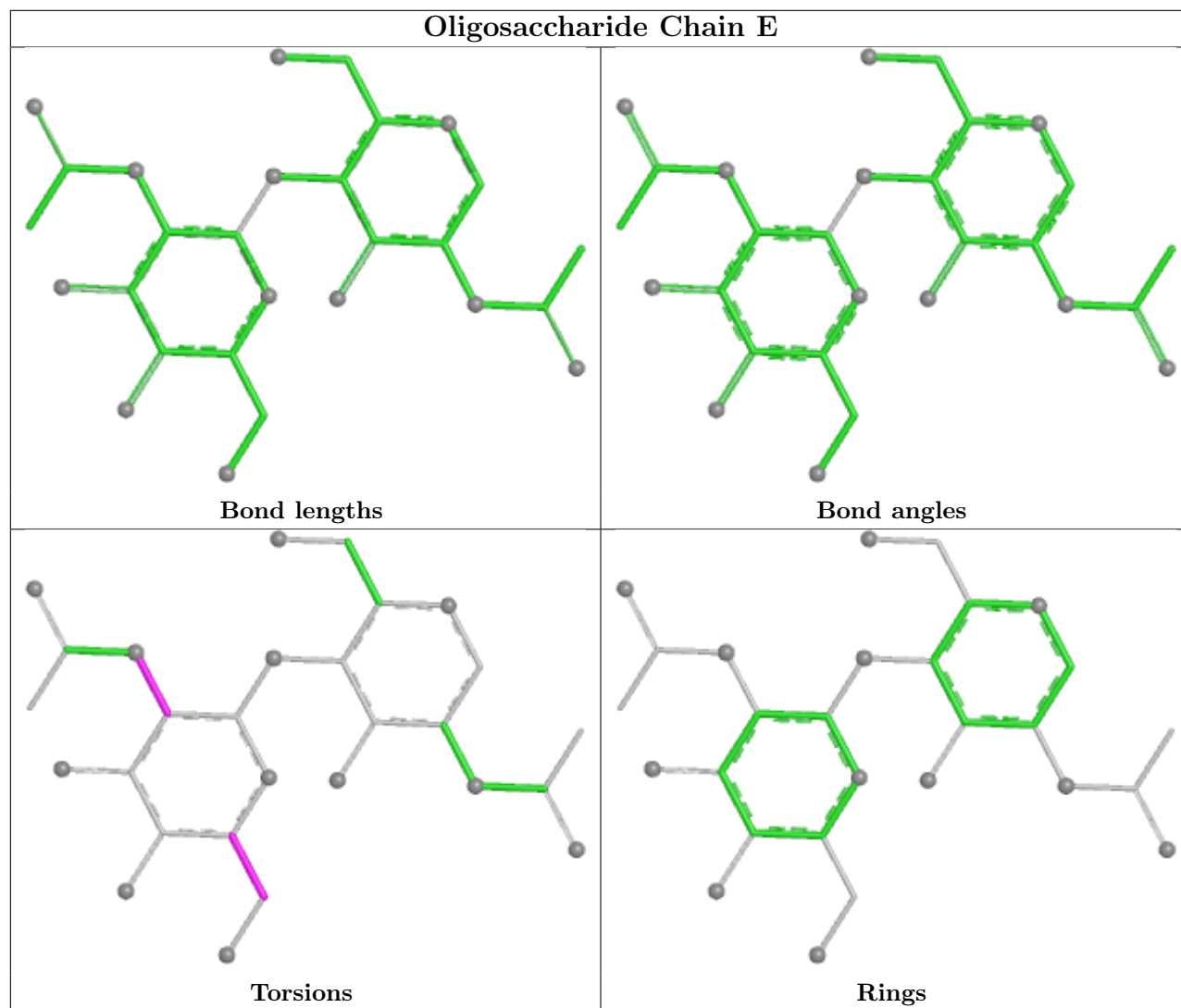
Mol	Chain	Res	Type	Atoms
5	E	2	NAG	C4-C5-C6-O6
5	F	1	NAG	O5-C5-C6-O6
5	E	2	NAG	O5-C5-C6-O6
5	F	1	NAG	C4-C5-C6-O6
5	F	2	NAG	C8-C7-N2-C2
5	F	2	NAG	O7-C7-N2-C2
5	E	2	NAG	C1-C2-N2-C7
5	F	2	NAG	O5-C5-C6-O6
5	F	2	NAG	C4-C5-C6-O6

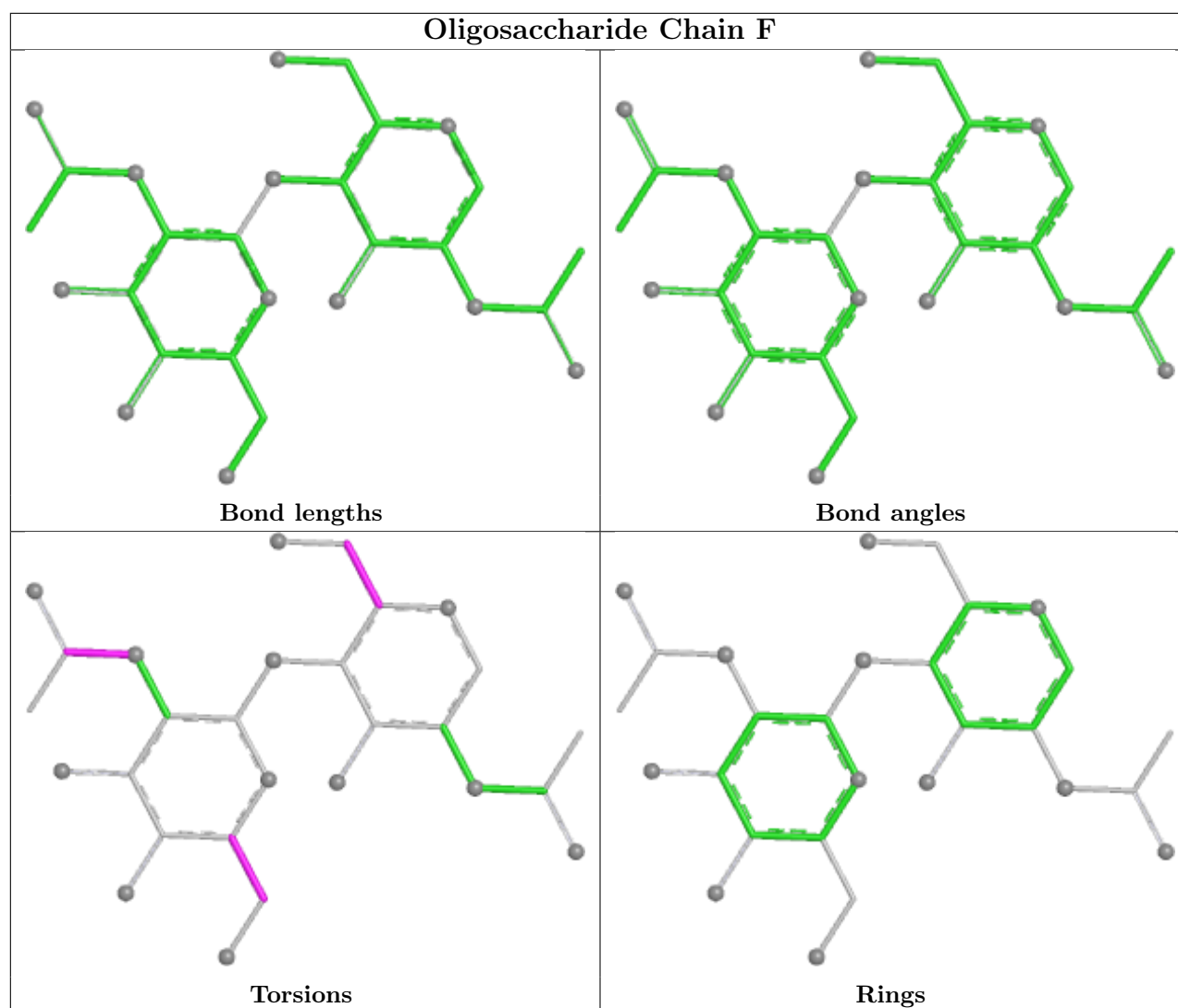
There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1	NAG	1	0
5	F	2	NAG	1	0
5	F	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](#)

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	$\# Z > 2$
6	NAG	A	703	1	14,14,15	0.25	0	17,19,21	0.51	0
6	NAG	D	301	4	14,14,15	0.54	0	17,19,21	1.13	1 (5%)
6	NAG	A	704	1	14,14,15	0.55	0	17,19,21	0.59	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
6	NAG	A	703	1	-	2/6/23/26	0/1/1/1
6	NAG	D	301	4	-	3/6/23/26	0/1/1/1
6	NAG	A	704	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	301	NAG	O5-C5-C4	-2.01	105.94	110.83

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	703	NAG	C8-C7-N2-C2
6	A	703	NAG	O7-C7-N2-C2
6	A	704	NAG	C8-C7-N2-C2
6	A	704	NAG	O7-C7-N2-C2
6	D	301	NAG	C8-C7-N2-C2
6	D	301	NAG	O7-C7-N2-C2
6	D	301	NAG	O5-C5-C6-O6

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, 95th 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 ²)	Q<0.9
1	A	570/624 (91%)	1.02	134 (23%) 2 1	17, 83, 168, 193	0
2	B	116/138 (84%)	1.25	28 (24%) 2 1	40, 94, 120, 129	0
3	C	211/211 (100%)	-0.21	1 (0%) 87 72	15, 32, 53, 74	0
4	D	213/220 (96%)	-0.38	1 (0%) 87 72	15, 28, 50, 78	0
All	All	1110/1193 (93%)	0.54	164 (14%) 5 3	15, 50, 155, 193	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	145	SER	5.9
1	A	593	CYS	5.8
1	A	155	ASP	5.1
1	A	142	ASP	4.8
2	B	7	SER	4.7
2	B	56	GLY	4.4
2	B	91	THR	4.2
2	B	84	ASN	4.2
1	A	560	HIS	4.1
1	A	95	LEU	4.1
2	B	83	MET	4.0
1	A	181	GLU	4.0
2	B	82	GLN	3.9
1	A	45	TYR	3.8
1	A	121	HIS	3.8
2	B	90	ASP	3.8
1	A	586	TYR	3.7
1	A	597	HIS	3.7
2	B	44	GLN	3.7
2	B	76	LYS	3.7
1	A	167	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	598	PRO	3.6
1	A	42	GLU	3.6
1	A	20	PHE	3.5
1	A	571	CYS	3.5
1	A	286	ALA	3.4
1	A	574	GLY	3.4
1	A	139	GLN	3.4
2	B	77	THR	3.4
1	A	584	TRP	3.4
1	A	211	GLN	3.3
1	A	209	HIS	3.3
1	A	128	ASN	3.3
1	A	150	SER	3.3
1	A	93	TYR	3.2
1	A	178	ALA	3.2
1	A	152	MET	3.2
2	B	88	PRO	3.1
1	A	219	PRO	3.1
1	A	71	THR	3.1
1	A	118	GLU	3.1
1	A	86	ASN	3.0
1	A	221	GLU	3.0
1	A	130	PRO	3.0
1	A	48	ARG	3.0
1	A	13	LYS	3.0
1	A	151	ASN	3.0
1	A	172	ASN	3.0
2	B	67	ARG	3.0
1	A	183	CYS	3.0
1	A	24	PHE	3.0
1	A	156	PHE	3.0
1	A	154	MET	3.0
1	A	75	ILE	3.0
1	A	16	GLN	2.9
1	A	117	GLN	2.9
1	A	87	MET	2.9
1	A	587	ALA	2.9
1	A	164	GLN	2.9
2	B	87	LYS	2.9
1	A	76	PRO	2.9
1	A	182	ASN	2.9
1	A	141	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	50	TYR	2.8
1	A	49	ASN	2.8
1	A	599	ASN	2.8
1	A	575	VAL	2.8
2	B	62	ASP	2.8
1	A	91	ASN	2.8
1	A	213	ALA	2.8
1	A	43	ILE	2.8
1	A	143	ILE	2.8
1	A	51	ASP	2.7
1	A	238	ASP	2.7
2	B	35	GLY	2.7
1	A	89	TYR	2.7
1	A	594	HIS	2.7
1	A	240	CYS	2.7
1	A	61	VAL	2.7
1	A	85	GLY	2.7
2	B	94	TYR	2.7
1	A	162	SER	2.7
1	A	25	LEU	2.7
1	A	563	ASP	2.7
1	A	47	GLN	2.6
1	A	147	ASP	2.6
1	A	74	ARG	2.6
1	A	79	ASN	2.6
1	A	173	GLY	2.6
2	B	79	VAL	2.6
1	A	140	TRP	2.5
2	B	3	GLN	2.5
1	A	214	ALA	2.5
1	A	82	ILE	2.5
1	A	108	LEU	2.5
2	B	126	VAL	2.5
1	A	90	GLU	2.5
2	B	128	VAL	2.5
1	A	126	PHE	2.5
1	A	603	GLY	2.5
2	B	71	SER	2.5
2	B	75	ALA	2.5
2	B	72	ARG	2.5
4	D	135	LYS	2.5
1	A	572	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	92	SER	2.4
1	A	232	ASP	2.4
1	A	518	LEU	2.4
2	B	69	THR	2.4
1	A	72	VAL	2.4
1	A	19	THR	2.4
1	A	220	ARG	2.4
1	A	77	LEU	2.4
1	A	601	THR	2.4
1	A	26	SER	2.4
1	A	129	ASN	2.3
1	A	243	LEU	2.3
1	A	111	LEU	2.3
2	B	1	GLN	2.3
2	B	48	VAL	2.3
1	A	99	SER	2.3
1	A	131	ALA	2.3
1	A	256	ASN	2.3
1	A	44	THR	2.3
1	A	132	LEU	2.3
1	A	591	HIS	2.3
1	A	136	GLU	2.2
1	A	168	PRO	2.2
1	A	521	GLU	2.2
1	A	562	ILE	2.2
1	A	210	ASN	2.2
1	A	83	ILE	2.2
1	A	22	ASP	2.2
1	A	80	LEU	2.2
1	A	122	GLY	2.2
1	A	149	LEU	2.2
1	A	576	MET	2.2
1	A	146	SER	2.2
2	B	55	GLY	2.2
1	A	254	ASP	2.2
1	A	40	ASN	2.2
1	A	564	GLY	2.2
1	A	144	VAL	2.1
1	A	127	SER	2.1
3	C	22	SER	2.1
1	A	166	CYS	2.1
1	A	52	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	582	LEU	2.1
1	A	602	TYR	2.1
2	B	86	LEU	2.1
1	A	123	ALA	2.1
1	A	239	THR	2.1
1	A	28	GLN	2.1
1	A	21	GLU	2.1
1	A	124	VAL	2.0
1	A	266	THR	2.0
1	A	287	CYS	2.0
1	A	242	PRO	2.0
1	A	522	PRO	2.0
1	A	14	LEU	2.0
1	A	17	LEU	2.0
1	A	581	THR	2.0
1	A	18	GLY	2.0
1	A	67	ILE	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 ⓘ

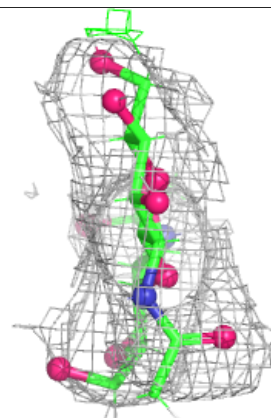
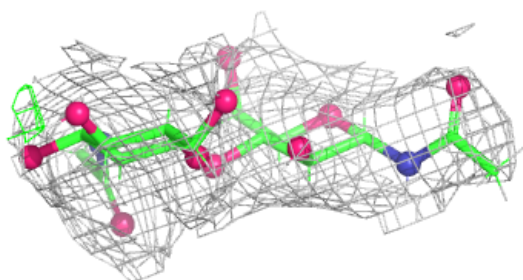
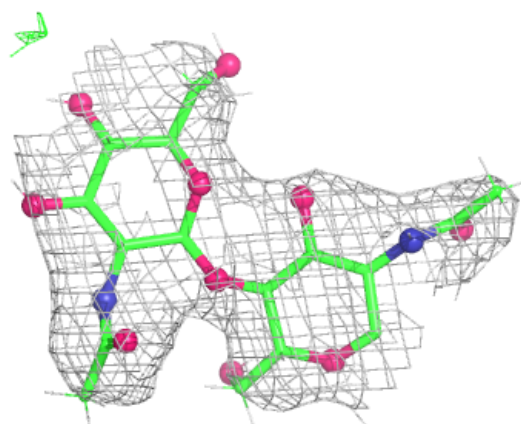
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	F	2	14/15	0.65	0.17	55,81,103,111	0
5	NAG	E	2	14/15	0.72	0.14	54,73,92,103	0
5	NAG	E	1	14/15	0.88	0.13	57,67,78,82	0
5	NAG	F	1	14/15	0.90	0.10	35,48,61,66	0

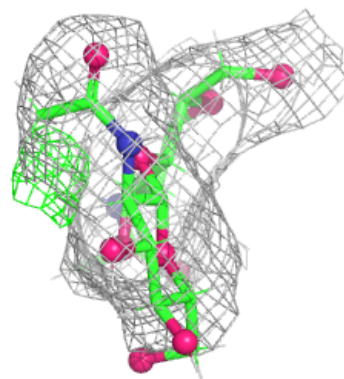
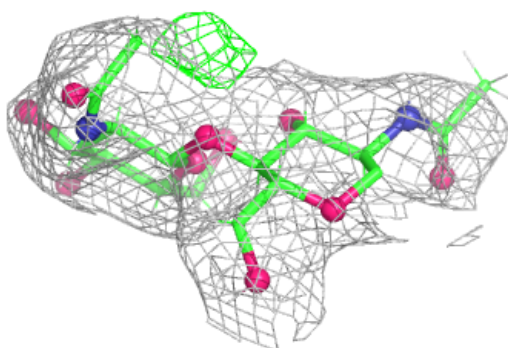
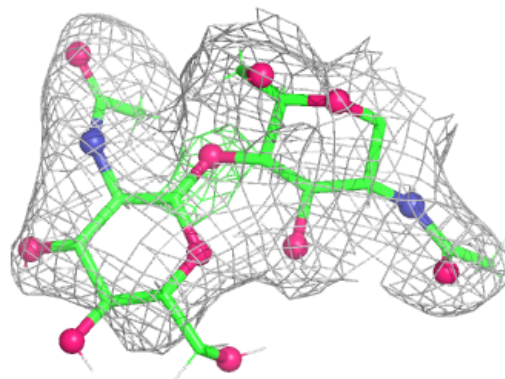
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Chain F:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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, 95th 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	NAG	D	301	14/15	0.44	0.17	55,65,74,89	0
6	NAG	A	704	14/15	0.50	0.15	90,106,126,135	0
6	NAG	A	703	14/15	0.60	0.15	76,87,103,104	0

6.5 Other polymers [i](#)

There are no such residues in this entry.