



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 3, 2024 – 02:06 PM EDT

PDB ID : 8V58
Title : Complex of murine cathepsin K with bound heparan sulfate 12mer
Authors : Pedersen, L.C.; Xu, D.; Krahn, J.M.
Deposited on : 2023-11-30
Resolution : 3.10 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

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 : 4.02b-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

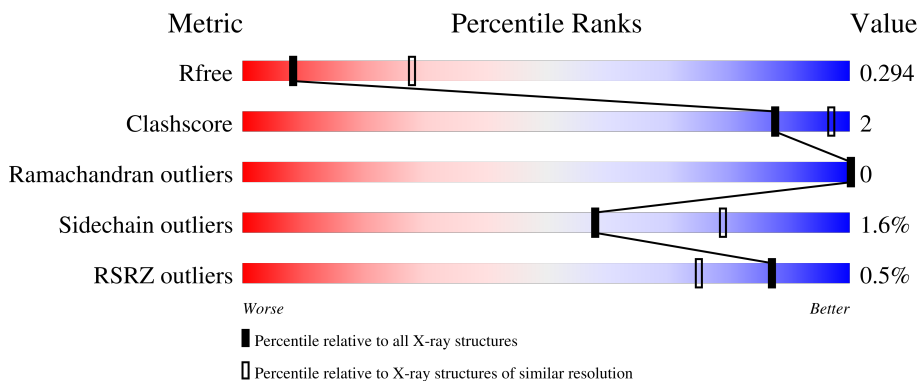
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1351 (3.10-3.10)
Clashscore	180529	1454 (3.10-3.10)
Ramachandran outliers	177936	1391 (3.10-3.10)
Sidechain outliers	177891	1391 (3.10-3.10)
RSRZ outliers	164620	1351 (3.10-3.10)

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	217	 95%
1	B	217	 92% 7%
2	C	8	 12% 88%
3	D	9	 11% 56% 33%

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
3	SGN	D	1	-	-	-	X

2 Entry composition [i](#)

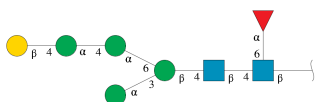
There are 6 unique types of molecules in this entry. The entry contains 6509 atoms, of which 3087 are hydrogens and 0 are deuteriums.

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 Cathepsin K.

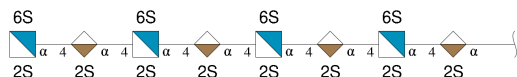
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	215	3123	1008	1510	279	314	12	0	0	0
1	B	215	2967	974	1411	262	308	12	0	0	0

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-4)-alpha-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



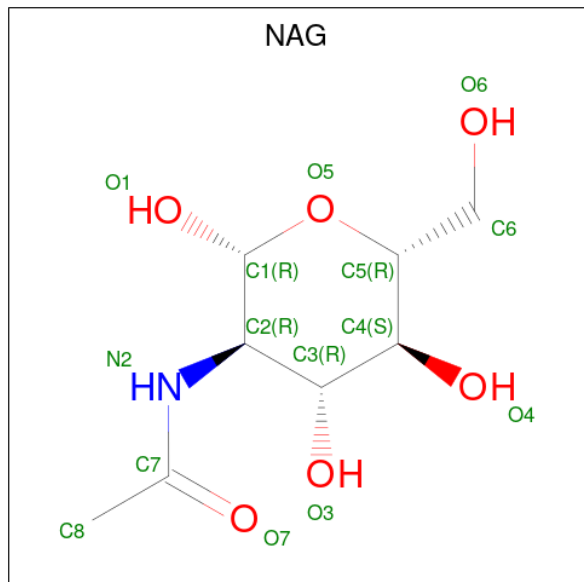
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	C	8	180	52	87	2	39	0	0	0

- Molecule 3 is an oligosaccharide called 2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid.



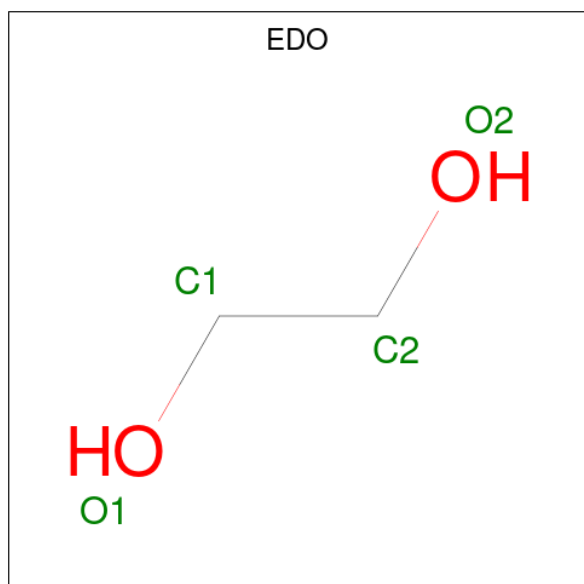
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	D	9	201	48	60	4	77	12	0	0	1

- 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
			Total	C	H	N	O		
4	B	1	27	8	13	1	5	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	B	1	10	2	6	2	0	0

- Molecule 6 is water.

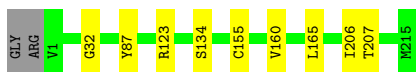
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total O 1 1	0	0

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: Cathepsin K

Chain A:  95%



- Molecule 1: Cathepsin K

Chain B:  92% 7%

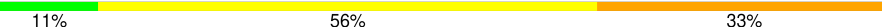


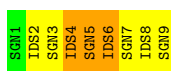
- Molecule 2: beta-D-galactopyranose-(1-4)-alpha-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  12% 88%



- Molecule 3: 2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid

Chain D:  11% 56% 33%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	111.89Å 111.89Å 116.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.87 – 3.10 19.87 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (19.87-3.10) 97.5 (19.87-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 3.09Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.236 , 0.293 0.237 , 0.294	Depositor DCC
R_{free} test set	13222 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	92.5	Xtriage
Anisotropy	0.430	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -h,l,k 0.016 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6509	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IDS, MAN, GAL, FUC, EDO, SGN, NAG, BMA

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	0.47	0/1648	0.73	0/2233
1	B	0.36	0/1589	0.63	0/2160
All	All	0.42	0/3237	0.68	0/4393

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	1613	1510	1512	3	0
1	B	1556	1411	1419	7	0
2	C	93	87	79	0	0
3	D	141	60	45	2	0
4	B	14	13	13	0	0
5	B	4	6	6	0	0
6	B	1	0	0	0	0
All	All	3422	3087	3074	12	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.

The worst 5 of 12 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:B:206:ILE:HG23	1:B:207:THR:HG23	1.81	0.62
1:B:32:GLY:HA3	1:B:165:LEU:HD22	1.87	0.56
1:B:40:LYS:NZ	1:B:127:ARG:O	2.41	0.54
1:B:42:THR:HG22	1:B:43:GLY:H	1.72	0.53
1:A:206:ILE:HG23	1:A:207:THR:HG23	1.92	0.52

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	213/217 (98%)	203 (95%)	10 (5%)	0	100	100
1	B	213/217 (98%)	202 (95%)	11 (5%)	0	100	100
All	All	426/434 (98%)	405 (95%)	21 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	163/172 (95%)	160 (98%)	3 (2%)	54	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	151/172 (88%)	149 (99%)	2 (1%)	65	82
All	All	314/344 (91%)	309 (98%)	5 (2%)	58	79

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

Mol	Chain	Res	Type
1	A	87	TYR
1	A	123	ARG
1	A	155	CYS
1	B	87	TYR
1	B	155	CYS

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](#)

Of 17 monosaccharides modelled in this entry, 16 were used for Mogul analysis.

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	0.66	0	17,19,21	0.75	0
2	NAG	C	2	2	14,14,15	1.05	1 (7%)	17,19,21	1.11	1 (5%)
2	BMA	C	3	2	11,11,12	1.46	2 (18%)	15,15,17	1.87	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	C	4	2	11,11,12	1.45	2 (18%)	15,15,17	1.82	4 (26%)
2	MAN	C	5	2	11,11,12	0.74	0	15,15,17	1.19	2 (13%)
2	GAL	C	6	2	11,11,12	1.16	2 (18%)	15,15,17	1.10	0
2	MAN	C	7	2	11,11,12	0.99	1 (9%)	15,15,17	2.44	4 (26%)
2	FUC	C	8	2	10,10,11	1.35	2 (20%)	14,14,16	1.48	4 (28%)
3	IDS	D	2	3	16,16,17	0.99	1 (6%)	16,24,26	1.31	3 (18%)
3	SGN	D	3	3	19,19,20	0.94	1 (5%)	23,29,31	2.04	4 (17%)
3	IDS	D	4	3	16,16,17	1.08	1 (6%)	16,24,26	1.67	4 (25%)
3	SGN	D	5	3	19,19,20	0.90	0	23,29,31	2.54	6 (26%)
3	IDS	D	6	3	16,16,17	0.92	0	16,24,26	2.03	4 (25%)
3	SGN	D	7	3	19,19,20	1.05	2 (10%)	23,29,31	2.04	5 (21%)
3	IDS	D	8	3	16,16,17	0.86	0	16,24,26	1.81	3 (18%)
3	SGN	D	9	3	19,19,20	0.80	0	23,29,31	1.51	3 (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
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	1/1/1/1
2	MAN	C	4	2	-	1/2/19/22	0/1/1/1
2	MAN	C	5	2	-	1/2/19/22	1/1/1/1
2	GAL	C	6	2	-	0/2/19/22	0/1/1/1
2	MAN	C	7	2	-	2/2/19/22	0/1/1/1
2	FUC	C	8	2	-	-	0/1/1/1
3	IDS	D	2	3	-	0/9/26/29	0/1/1/1
3	SGN	D	3	3	-	2/11/28/31	0/1/1/1
3	IDS	D	4	3	-	3/9/26/29	0/1/1/1
3	SGN	D	5	3	-	6/11/28/31	0/1/1/1
3	IDS	D	6	3	-	1/9/26/29	0/1/1/1
3	SGN	D	7	3	-	3/11/28/31	0/1/1/1
3	IDS	D	8	3	-	5/9/26/29	0/1/1/1
3	SGN	D	9	3	-	2/11/28/31	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	NAG	O5-C1	-3.73	1.37	1.43
2	C	3	BMA	C4-C5	3.14	1.59	1.53
2	C	4	MAN	C1-C2	2.86	1.59	1.52
2	C	8	FUC	C1-C2	2.56	1.58	1.52
2	C	6	GAL	O5-C1	-2.52	1.39	1.43

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	7	MAN	C1-O5-C5	7.55	122.30	112.19
2	C	3	BMA	C1-O5-C5	6.28	120.61	112.19
3	D	5	SGN	O1S-S1-O2S	-6.13	106.71	120.36
3	D	5	SGN	O6-C6-C5	6.03	118.31	107.57
3	D	7	SGN	O1S-S1-O2S	-6.01	107.00	120.36

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	3	SGN	C4-C5-C6-O6
3	D	3	SGN	O5-C5-C6-O6
3	D	4	IDS	C3-C2-O2-S
3	D	4	IDS	C4-C5-C6-O6A
3	D	4	IDS	C4-C5-C6-O6B

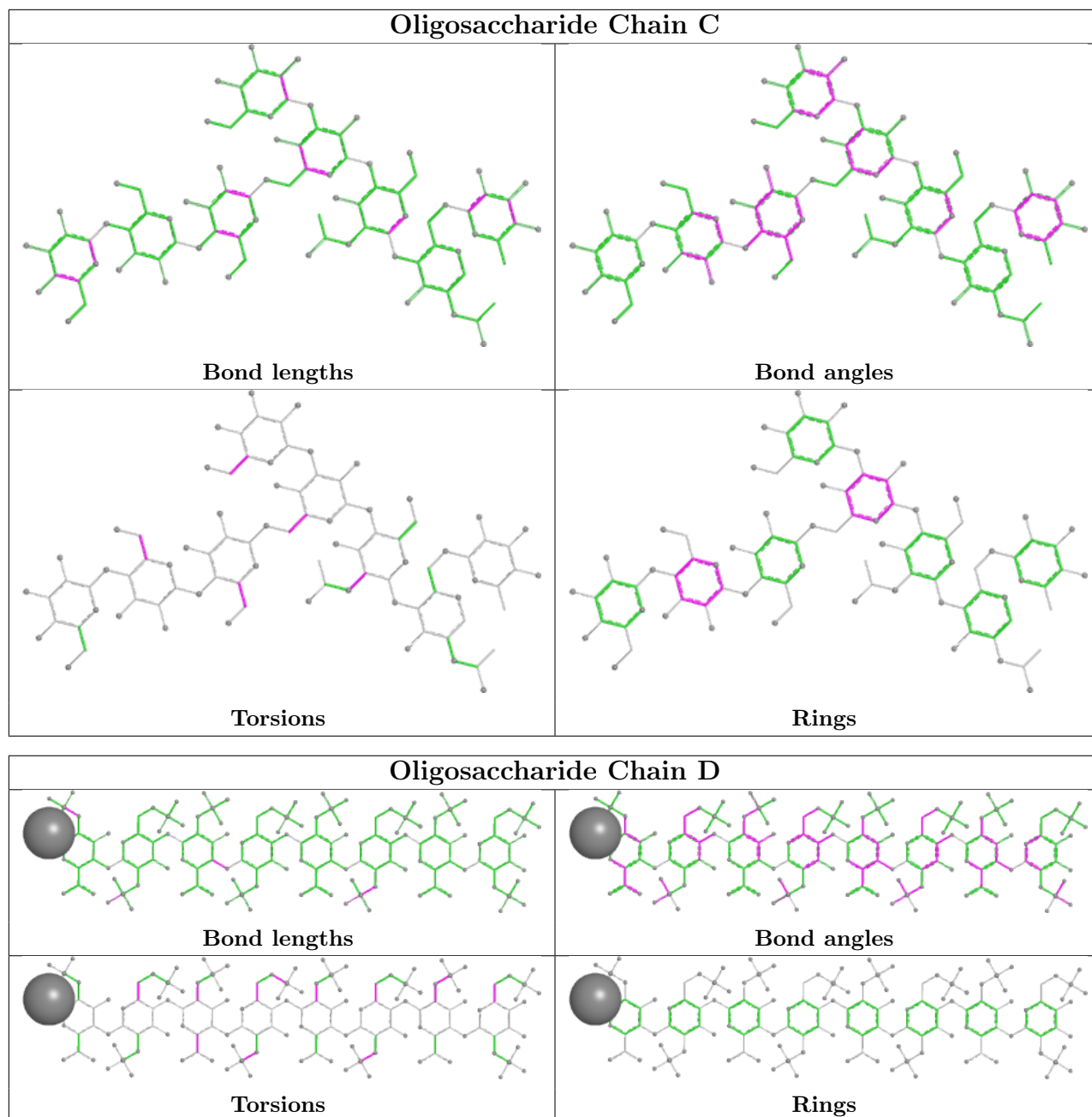
All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	3	BMA	C1-C2-C3-C4-C5-O5
2	C	5	MAN	C1-C2-C3-C4-C5-O5

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	6	IDS	1	0
3	D	4	IDS	1	0
3	D	5	SGN	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](#)

2 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	EDO	B	402	-	3,3,3	0.47	0	2,2,2	0.31	0
4	NAG	B	401	1	14,14,15	0.32	0	17,19,21	0.93	1 (5%)

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	EDO	B	402	-	-	1/1/1/1	-
4	NAG	B	401	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(°)
4	B	401	NAG	C2-N2-C7	2.65	126.46	122.90

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	401	NAG	C8-C7-N2-C2
4	B	401	NAG	O7-C7-N2-C2
5	B	402	EDO	O1-C1-C2-O2

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 [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, 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	215/217 (99%)	-0.26	0 100 100	92, 108, 125, 137	0
1	B	215/217 (99%)	-0.19	2 (0%) 81 66	110, 139, 168, 178	0
All	All	430/434 (99%)	-0.23	2 (0%) 87 75	92, 121, 162, 178	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	159	ASN	2.3
1	B	144	PHE	2.3

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, 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.

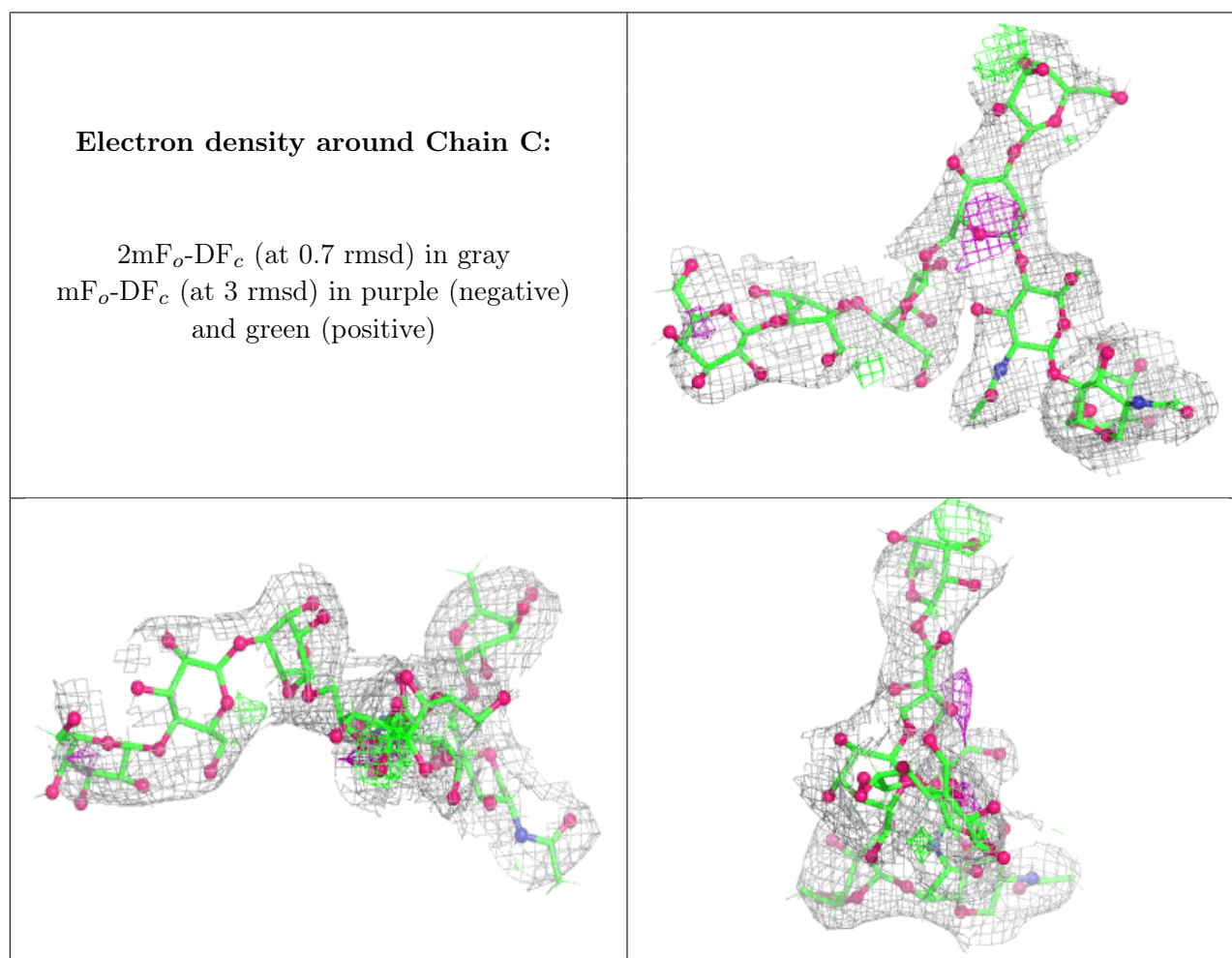
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SGN	D	1	1/20	-0.62	0.41	100,100,100,100	1
2	MAN	C	7	11/12	0.48	0.18	123,134,159,161	22
2	GAL	C	6	11/12	0.66	0.12	131,145,167,175	0
3	IDS	D	2	16/17	0.66	0.11	105,111,135,138	22
3	SGN	D	9	19/20	0.70	0.11	101,112,132,137	28
3	IDS	D	4	16/17	0.71	0.18	99,107,132,134	22
3	IDS	D	6	16/17	0.74	0.16	99,108,123,131	22

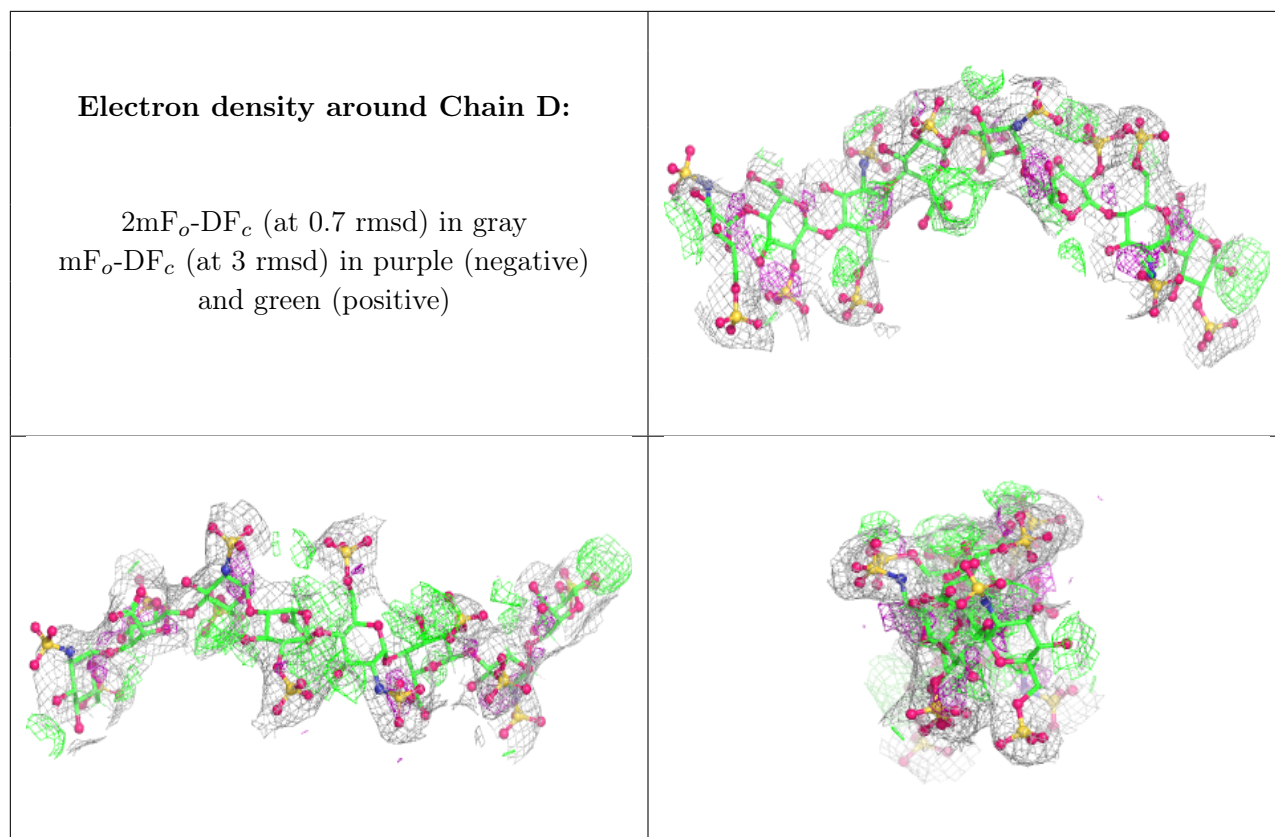
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IDS	D	8	16/17	0.75	0.10	102,109,132,138	22
2	BMA	C	3	11/12	0.79	0.14	117,132,152,159	0
2	MAN	C	4	11/12	0.79	0.09	112,134,155,168	0
3	SGN	D	3	19/20	0.80	0.11	99,112,137,140	28
2	MAN	C	5	11/12	0.81	0.09	118,131,154,158	0
3	SGN	D	7	19/20	0.83	0.12	99,106,129,134	28
3	SGN	D	5	19/20	0.87	0.12	99,103,125,132	28
2	NAG	C	1	14/15	0.88	0.09	100,112,127,135	0
2	FUC	C	8	10/11	0.89	0.07	98,114,129,138	0
2	NAG	C	2	14/15	0.91	0.09	104,119,141,145	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, 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	EDO	B	402	4/4	0.66	0.22	100,121,133,141	0
4	NAG	B	401	14/15	0.68	0.09	117,137,163,165	0

6.5 Other polymers [i](#)

There are no such residues in this entry.