



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:33 PM UTC

PDB ID : 7KBU / pdb_00007kbu
Title : Structure of Hevin FS-EC
Authors : Machius, M.; Fan, S.; Rudenko, G.
Deposited on : 2020-10-03
Resolution : 2.27 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

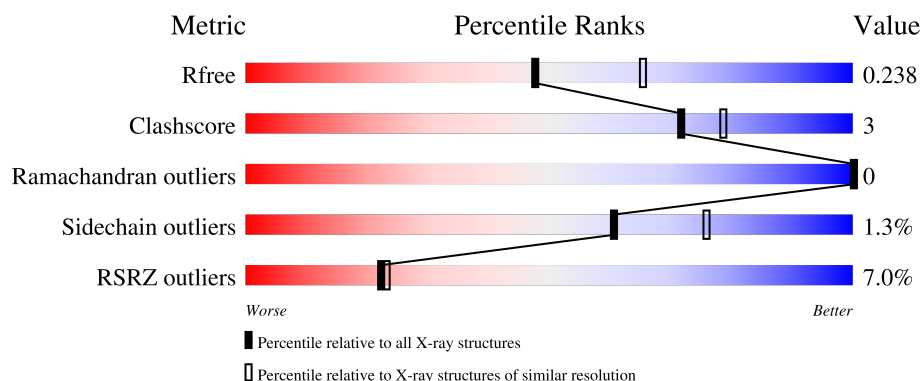
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	244	5% 83% 7% 9%
1	B	244	7% 69% 9% 21%
2	C	2	100%
2	D	2	100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6939 atoms, of which 3307 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 Proliferation-inducing protein 33.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	221	Total	C	H	N	O	S	0	1	0
			3538	1140	1736	311	331	20			
1	B	192	Total	C	H	N	O	S	0	4	0
			3105	1008	1517	272	290	18			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	664	PHE	-	expression tag	UNP Q8N4S1
A	665	ALA	-	expression tag	UNP Q8N4S1
A	666	SER	-	expression tag	UNP Q8N4S1
A	667	THR	-	expression tag	UNP Q8N4S1
A	668	SER	-	expression tag	UNP Q8N4S1
A	669	HIS	-	expression tag	UNP Q8N4S1
A	670	HIS	-	expression tag	UNP Q8N4S1
A	671	HIS	-	expression tag	UNP Q8N4S1
A	672	HIS	-	expression tag	UNP Q8N4S1
A	673	HIS	-	expression tag	UNP Q8N4S1
A	674	HIS	-	expression tag	UNP Q8N4S1
B	664	PHE	-	expression tag	UNP Q8N4S1
B	665	ALA	-	expression tag	UNP Q8N4S1
B	666	SER	-	expression tag	UNP Q8N4S1
B	667	THR	-	expression tag	UNP Q8N4S1
B	668	SER	-	expression tag	UNP Q8N4S1
B	669	HIS	-	expression tag	UNP Q8N4S1
B	670	HIS	-	expression tag	UNP Q8N4S1
B	671	HIS	-	expression tag	UNP Q8N4S1
B	672	HIS	-	expression tag	UNP Q8N4S1
B	673	HIS	-	expression tag	UNP Q8N4S1
B	674	HIS	-	expression tag	UNP Q8N4S1

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

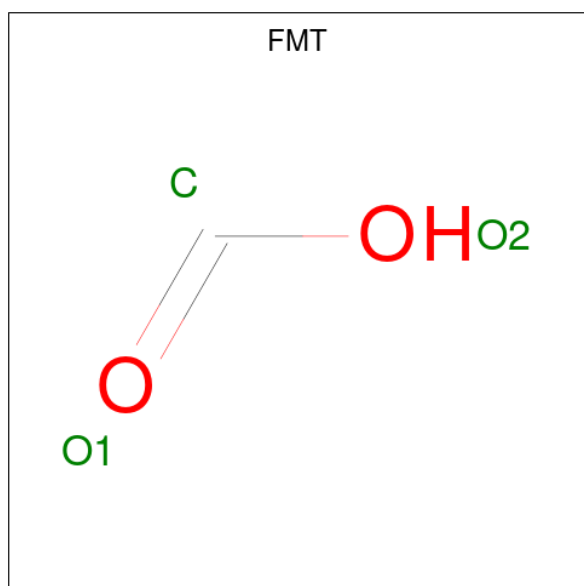


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	2	Total 53	C 16	H 25	N 2	O 10	0	0	0
2	D	2	Total 53	C 16	H 25	N 2	O 10	0	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		
3	B	4	Total	Ca	0	0
			4	4		

- Molecule 4 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



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

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

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Cl	0	0
			3	3		
5	B	1	Total	Cl	0	0
			1	1		

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

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

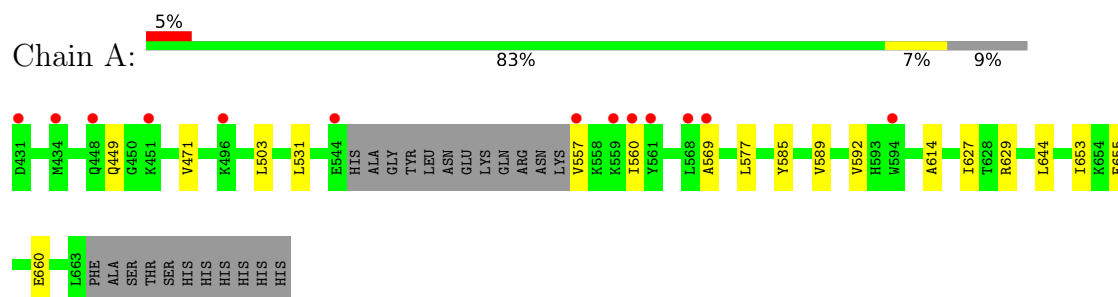
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	82	Total	O	0	1
			83	83		
7	B	79	Total	O	0	1
			80	80		

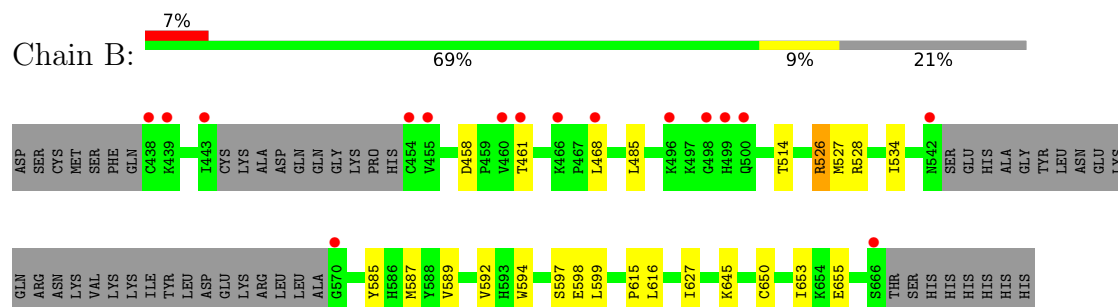
3 Residue-property plots [i](#)

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.

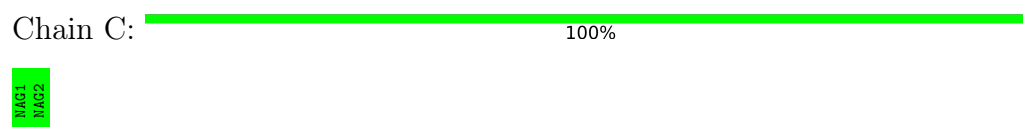
- Molecule 1: Proliferation-inducing protein 33



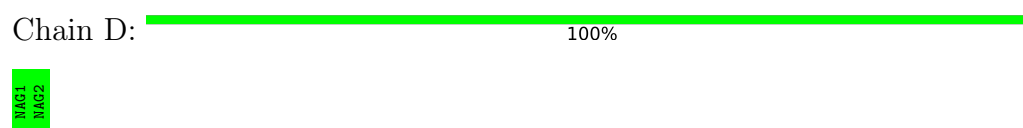
- Molecule 1: Proliferation-inducing protein 33



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



- Molecule 2: 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	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.66Å 132.29Å 149.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.00 – 2.27 33.00 – 2.27	Depositor EDS
% Data completeness (in resolution range)	97.1 (33.00-2.27) 97.0 (33.00-2.27)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.27Å)	Xtriage
Refinement program	PHENIX (1.19rc7_4070: ???)	Depositor
R, R_{free}	0.186 , 0.238 0.189 , 0.238	Depositor DCC
R_{free} test set	1298 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6939	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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: NA, FMT, CL, NAG, CA

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	0.43	1/1848 (0.1%)	0.54	0/2496
1	B	0.41	1/1639 (0.1%)	0.52	0/2216
All	All	0.42	2/3487 (0.1%)	0.53	0/4712

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	614	ALA	C-O	-6.57	1.18	1.24
1	B	615	PRO	C-O	-5.03	1.17	1.24

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)	H(added)	Clashes	Symm-Clashes
1	A	1802	1736	1735	11	0
1	B	1588	1517	1506	12	0
2	C	28	25	25	0	0
2	D	28	25	25	0	0
3	A	2	0	0	0	0
3	B	4	0	0	0	0
4	A	3	1	1	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	9	3	3	0	0
5	A	3	0	0	0	0
5	B	1	0	0	0	0
6	B	1	0	0	0	0
7	A	83	0	0	0	0
7	B	80	0	0	1	0
All	All	3632	3307	3295	22	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 3.

All (22) 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:458:ASP:O	1:B:461:THR:HG22	2.04	0.58
1:A:531:LEU:HD11	1:A:577:LEU:HD23	1.86	0.57
1:B:526[A]:ARG:HG2	7:B:828:HOH:O	2.04	0.56
1:B:585:TYR:HA	1:B:589:VAL:HB	1.90	0.54
1:B:527:MET:HE2	1:B:587:MET:HG2	1.92	0.52
1:B:485:LEU:C	1:B:485:LEU:HD23	2.36	0.51
1:B:594:TRP:CZ2	1:B:598:GLU:HG3	2.47	0.49
1:A:644:LEU:HD23	1:A:660:GLU:HG2	1.93	0.49
1:A:569:ALA:HB3	1:B:468:LEU:HD12	1.95	0.48
1:A:531:LEU:CD1	1:A:577:LEU:HD23	2.43	0.47
1:A:585:TYR:HA	1:A:589:VAL:HB	1.97	0.46
1:A:655:GLU:H	1:A:655:GLU:CD	2.25	0.44
1:B:592:VAL:HG11	1:B:653:ILE:HD12	2.00	0.43
1:A:627:ILE:HG21	1:A:629:ARG:NH2	2.35	0.42
1:A:471:VAL:HB	1:A:503:LEU:CD1	2.48	0.42
1:A:592:VAL:HG11	1:A:653:ILE:HD12	2.02	0.42
1:A:449:GLN:N	1:A:449:GLN:CD	2.77	0.41
1:B:655[A]:GLU:H	1:B:655[A]:GLU:CD	2.29	0.41
1:B:599:LEU:HD11	1:B:616:LEU:HD22	2.02	0.41
1:B:645:LYS:HE2	1:B:645:LYS:HB2	1.89	0.41
1:A:557:VAL:N	1:A:560:ILE:HG12	2.37	0.40
1:B:514:THR:HA	1:B:627:ILE:O	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	218/244 (89%)	213 (98%)	5 (2%)	0	100	100
1	B	190/244 (78%)	184 (97%)	6 (3%)	0	100	100
All	All	408/488 (84%)	397 (97%)	11 (3%)	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	204/224 (91%)	204 (100%)	0	100	100
1	B	180/224 (80%)	174 (97%)	6 (3%)	33	47
All	All	384/448 (86%)	378 (98%)	6 (2%)	61	71

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	526[A]	ARG
1	B	526[B]	ARG
1	B	528	ARG
1	B	534	ILE
1	B	597	SER
1	B	650	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	484	HIS
1	A	533	ASN
1	A	537	GLN
1	A	572	HIS
1	A	661	ASN

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	$\# Z > 2$
2	NAG	C	1	2,1	14,14,15	0.24	0	17,19,21	0.51	0
2	NAG	C	2	2	14,14,15	0.29	0	17,19,21	0.46	0
2	NAG	D	1	2,1	14,14,15	0.28	0	17,19,21	0.49	0
2	NAG	D	2	2	14,14,15	0.30	0	17,19,21	0.50	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
2	NAG	C	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	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.

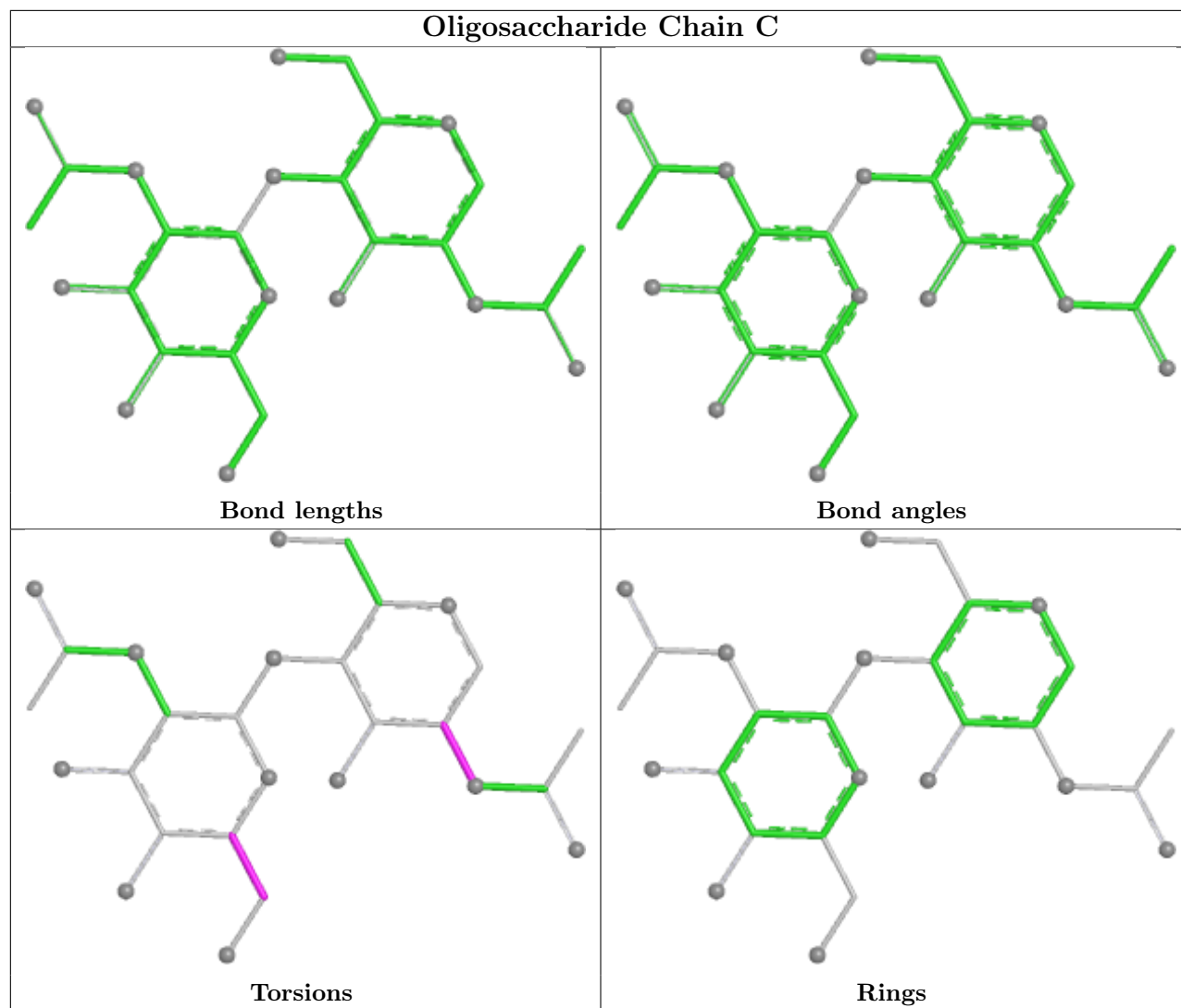
All (4) torsion outliers are listed below:

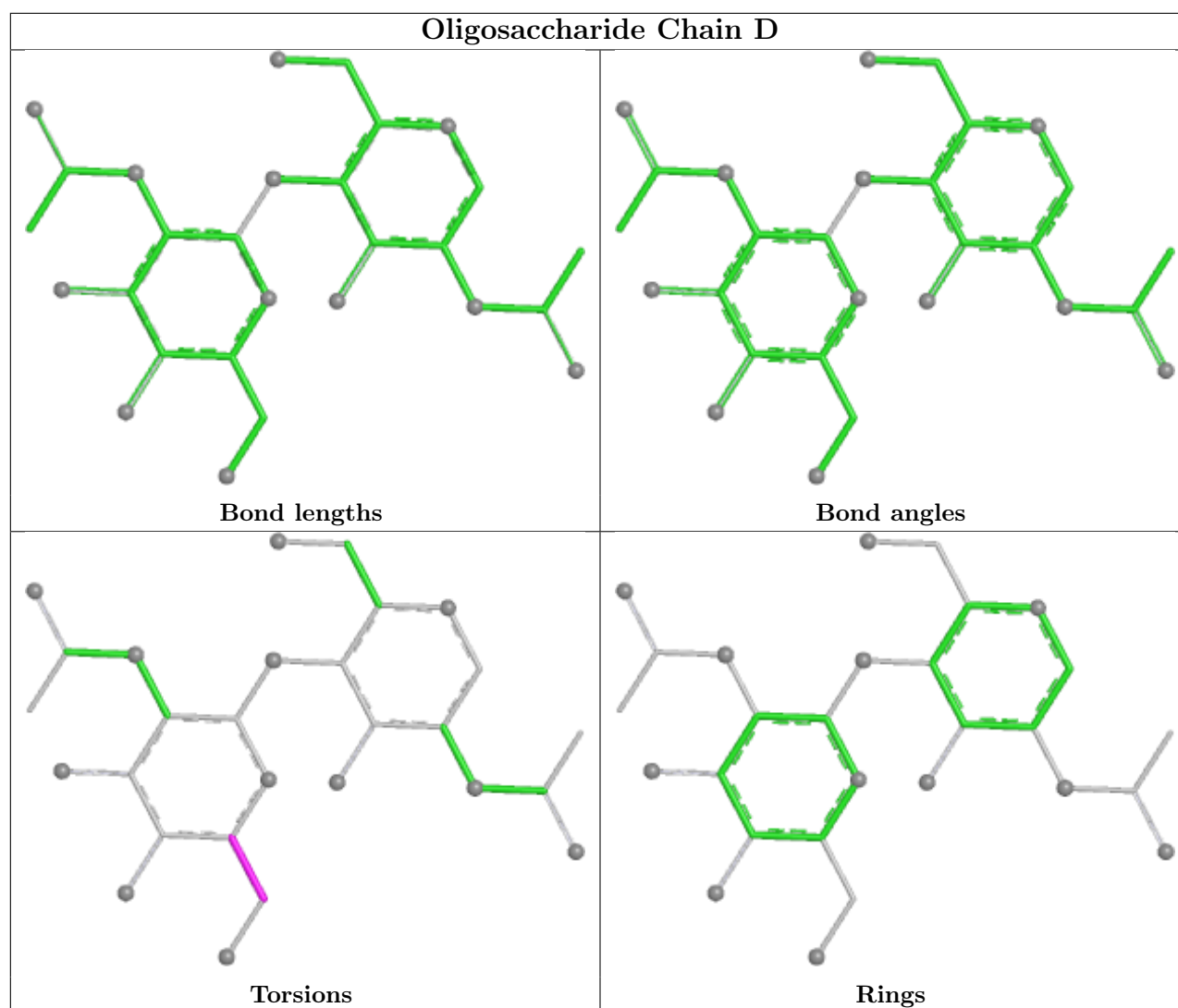
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	C	1	NAG	C1-C2-N2-C7

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](#)

Of 15 ligands modelled in this entry, 11 are monoatomic - leaving 4 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	$\# Z > 2$
4	FMT	B	705	-	2,2,2	0.58	0	1,1,1	0.30	0
4	FMT	B	706	6	2,2,2	0.72	0	1,1,1	0.39	0
4	FMT	A	703	-	2,2,2	0.74	0	1,1,1	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	FMT	B	707	-	2,2,2	0.64	0	1,1,1	0.35	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	221/244 (90%)	0.16	13 (5%) 28 29	11, 39, 82, 120	1 (0%)
1	B	192/244 (78%)	0.24	16 (8%) 17 18	14, 42, 91, 114	3 (1%)
All	All	413/488 (84%)	0.20	29 (7%) 22 23	11, 41, 89, 120	4 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	569	ALA	4.8
1	B	443	ILE	4.3
1	A	561	TYR	4.0
1	B	570	GLY	4.0
1	B	499	HIS	3.8
1	B	666	SER	3.7
1	A	559	LYS	3.7
1	B	496	LYS	3.6
1	A	594	TRP	3.1
1	B	454	CYS	3.0
1	A	448	GLN	3.0
1	B	542	ASN	2.9
1	A	557	VAL	2.9
1	B	500	GLN	2.8
1	B	460	VAL	2.6
1	B	439	LYS	2.6
1	B	438	CYS	2.5
1	A	560	ILE	2.5
1	B	468	LEU	2.4
1	A	431	ASP	2.4
1	B	455	VAL	2.3
1	A	451	LYS	2.3
1	A	568	LEU	2.2
1	A	496	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	498	GLY	2.2
1	B	466	LYS	2.1
1	A	544	GLU	2.1
1	B	461	THR	2.1
1	A	434	MET	2.0

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](#)

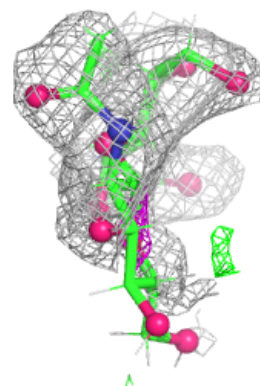
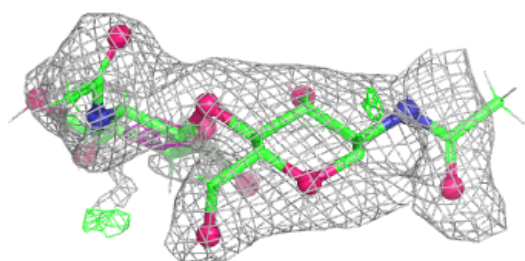
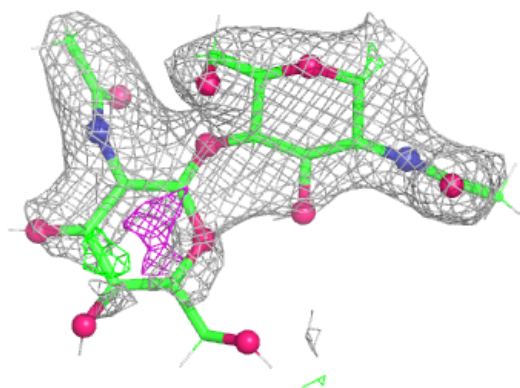
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	C	2	14/15	0.78	0.17	41,75,94,95	0
2	NAG	D	1	14/15	0.87	0.10	34,46,55,66	0
2	NAG	C	1	14/15	0.89	0.11	44,62,72,83	0
2	NAG	D	2	14/15	0.89	0.11	35,52,71,80	0

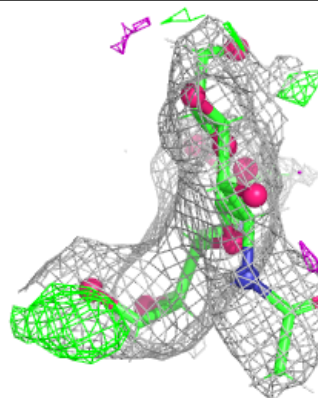
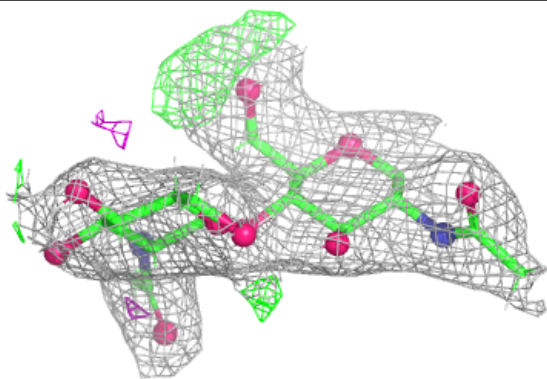
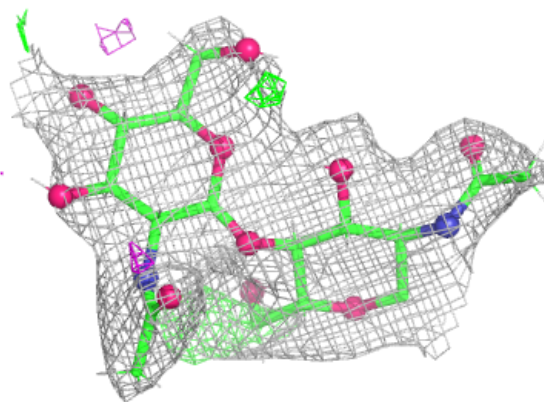
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

**Electron density around Chain D:**

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



6.4 Ligands

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
4	FMT	B	707	3/3	0.73	0.23	38,50,54,65	0
3	CA	B	703	1/1	0.86	0.09	52,52,52,52	0
4	FMT	A	703	3/3	0.87	0.16	35,46,53,55	0
5	CL	A	704	1/1	0.90	0.14	55,55,55,55	0
4	FMT	B	706	3/3	0.95	0.09	25,30,36,39	0
5	CL	A	706	1/1	0.96	0.10	58,58,58,58	0
5	CL	B	709	1/1	0.96	0.17	50,50,50,50	0
4	FMT	B	705	3/3	0.97	0.07	28,30,39,47	0
3	CA	B	701	1/1	0.97	0.05	41,41,41,41	0
3	CA	B	702	1/1	0.97	0.05	43,43,43,43	0
6	NA	B	708	1/1	0.97	0.06	29,29,29,29	0
5	CL	A	705	1/1	0.98	0.04	31,31,31,31	0
3	CA	A	701	1/1	0.98	0.04	33,33,33,33	0
3	CA	B	704	1/1	0.99	0.02	17,17,17,17	0
3	CA	A	702	1/1	0.99	0.02	26,26,26,26	0

6.5 Other polymers

There are no such residues in this entry.