



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:05 AM UTC

PDB ID : 4RDA / pdb_00004rda
Title : X-RAY STRUCTURE OF THE AMYLOID PRECURSOR PROTEIN-LIKE PROTEIN 1 (APLP1) E2 DOMAIN IN COMPLEX WITH A HEPARIN DO-DECASACCHARIDE
Authors : Dahms, S.O.; Than, M.E.
Deposited on : 2014-09-18
Resolution : 2.50 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

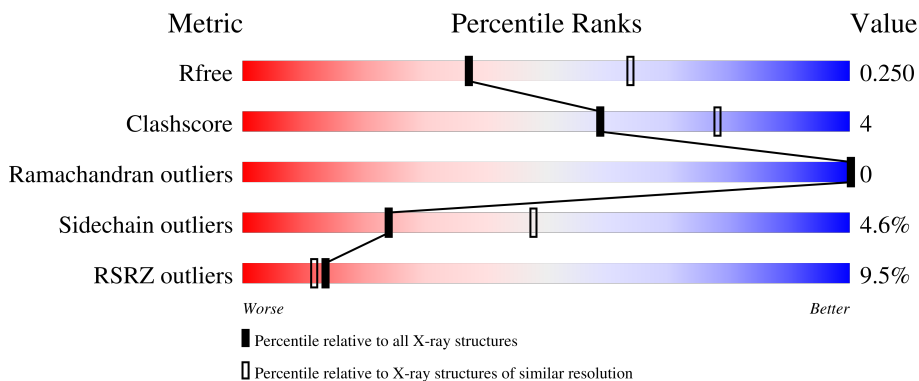
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


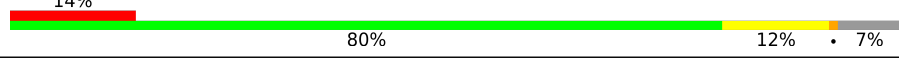
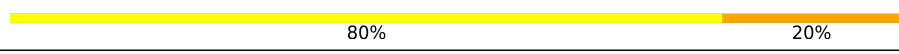

The reported resolution of this entry is 2.50 Å.

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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	210	 4% 81% 14% ..
1	B	210	 14% 80% 12% • 7%
2	C	5	 80% 20%
3	D	6	 83% 17%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 3554 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.

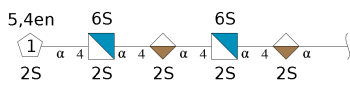
- Molecule 1 is a protein called Amyloid-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	203	Total 1673	C 1031	N 324	O 312	S 6	67	1	0
1	B	196	Total 1620	C 999	N 315	O 300	S 6	88	1	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	286	GLU	-	cloning artifact	UNP P51693
A	287	ALA	-	cloning artifact	UNP P51693
A	288	GLU	-	cloning artifact	UNP P51693
A	289	PHE	-	cloning artifact	UNP P51693
B	286	GLU	-	cloning artifact	UNP P51693
B	287	ALA	-	cloning artifact	UNP P51693
B	288	GLU	-	cloning artifact	UNP P51693
B	289	PHE	-	cloning artifact	UNP P51693

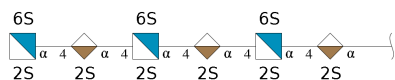
- Molecule 2 is an oligosaccharide called 4-deoxy-2-O-sulfo-alpha-L-threo-hex-4-enopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	5	Total 86	C 30	N 2	O 47	S 7	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)-al

pha-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	N	O	S			
3	D	6	106	36	3	58	9	19	0	0

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0

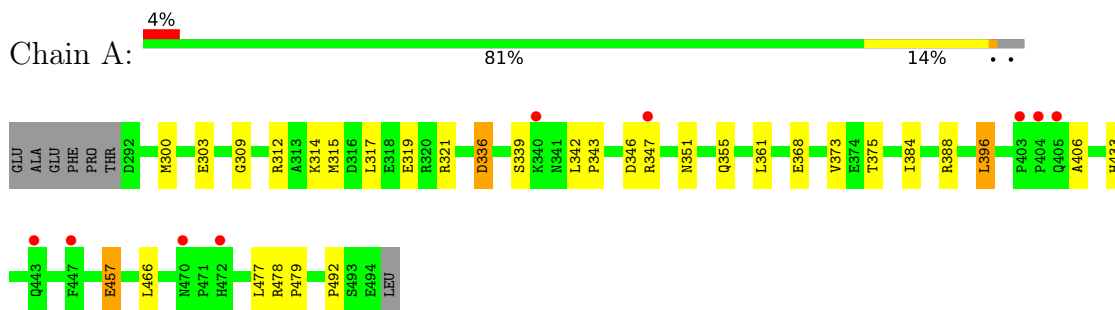
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	45	45	45	0	0
5	B	23	23	23	0	0

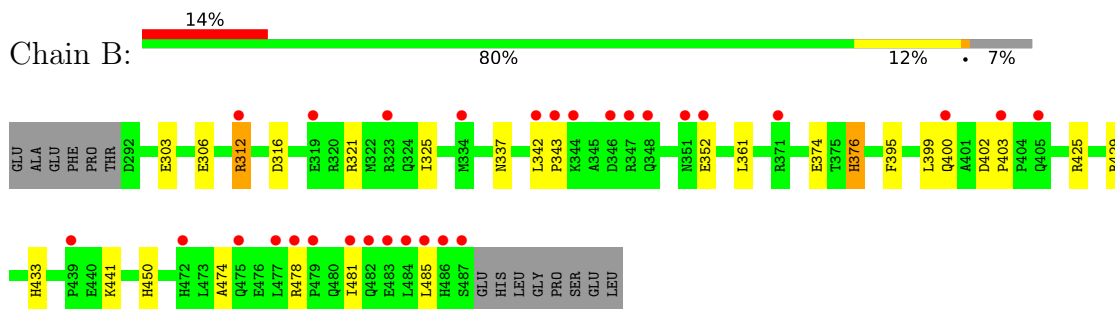
3 Residue-property plots

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.

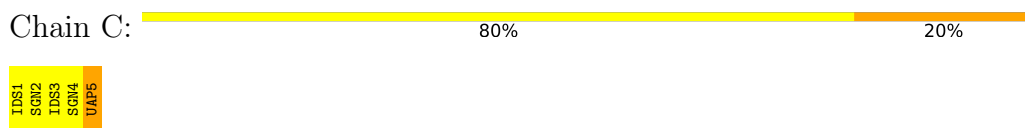
- Molecule 1: Amyloid-like protein 1



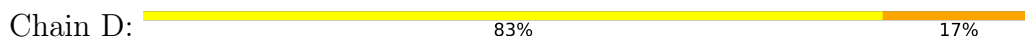
- Molecule 1: Amyloid-like protein 1



- Molecule 2: 4-deoxy-2-O-sulfo-alpha-L-threo-hex-4-enopyranuronic 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



- 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



IDS1
SGM2
IDS3
SGM4
IDS5
SGM6

4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	91.97Å 91.97Å 208.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.98 – 2.50 45.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.3 (45.98-2.50) 99.3 (45.98-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.51Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.216 , 0.245 0.227 , 0.250	Depositor DCC
R_{free} test set	1803 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	53.6	Xtrriage
Anisotropy	0.480	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3554	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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: IDS, SGN, ZN, UAP

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	0.53	0/1701	0.83	0/2292
1	B	0.57	2/1646 (0.1%)	0.82	4/2217 (0.2%)
All	All	0.55	2/3347 (0.1%)	0.82	4/4509 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	376	HIS	ND1-CE1	5.56	1.38	1.32
1	B	450	HIS	ND1-CE1	5.50	1.38	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	450	HIS	CB-CG-CD2	-6.57	122.65	131.20
1	B	376	HIS	CB-CG-CD2	-6.51	122.73	131.20
1	B	376	HIS	CB-CG-ND1	5.68	131.22	122.70
1	B	450	HIS	CB-CG-ND1	5.68	131.21	122.70

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	1673	0	1648	16	0
1	B	1620	0	1603	11	0
2	C	86	0	29	4	0
3	D	106	0	40	1	0
4	A	1	0	0	0	0
5	A	45	0	0	0	0
5	B	23	0	0	0	0
All	All	3554	0	3320	28	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 4.

All (28) 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)
2:C:5:UAP:O2S	3:D:6:SGN:H62	1.68	0.90
1:B:306:GLU:OE2	1:B:376:HIS:HD2	1.75	0.69
1:B:425:ARG:HH11	1:B:429:ARG:HH22	1.39	0.68
1:A:396:LEU:HD11	1:A:466:LEU:HD13	1.84	0.59
1:B:425:ARG:NH1	1:B:429:ARG:HH22	2.01	0.56
1:A:342:LEU:HD22	1:A:343:PRO:HD2	1.88	0.56
1:A:384:ILE:O	1:A:388:ARG:HG2	2.07	0.54
1:A:351:ASN:O	1:A:355:GLN:HG3	2.09	0.52
1:A:321:ARG:HH21	1:A:368:GLU:CD	2.17	0.51
1:A:315:MET:O	1:A:319:GLU:HG2	2.10	0.51
1:A:336:ASP:OD1	1:A:347[A]:ARG:NH2	2.28	0.50
1:B:342:LEU:HB3	1:B:343:PRO:HD2	1.95	0.49
1:A:478:ARG:HB3	1:A:479:PRO:HD3	1.96	0.47
1:B:395:PHE:O	1:B:399:LEU:HB2	2.14	0.47
1:A:339:SER:HB3	1:A:342:LEU:HD12	1.97	0.47
1:A:300:MET:SD	1:A:309:GLY:HA3	2.56	0.46
1:A:342:LEU:HD13	1:A:346:ASP:HB3	1.98	0.46
1:A:457:GLU:HG2	1:A:492:PRO:HB2	1.98	0.45
1:A:314:LYS:NZ	2:C:5:UAP:O1S	2.48	0.45
1:A:406:ALA:HB1	1:A:477:LEU:HD21	1.99	0.45
1:B:402:ASP:HA	1:B:403:PRO:HA	1.77	0.44
1:B:474:ALA:O	1:B:478:ARG:HB2	2.20	0.41
1:B:312:ARG:NH2	1:B:316:ASP:OD1	2.50	0.41
1:A:433:HIS:NE2	2:C:5:UAP:O6B	2.30	0.41
1:B:321:ARG:O	1:B:325:ILE:HG13	2.21	0.41
1:B:481:ILE:O	1:B:485:LEU:N	2.39	0.41
1:B:433:HIS:NE2	2:C:5:UAP:O3S	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:LEU:O	1:A:321:ARG:HG2	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	Allowed	Outliers	Percentiles	
1	A	202/210 (96%)	200 (99%)	2 (1%)	0	100	100
1	B	195/210 (93%)	193 (99%)	2 (1%)	0	100	100
All	All	397/420 (94%)	393 (99%)	4 (1%)	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	177/182 (97%)	169 (96%)	8 (4%)	24	49
1	B	171/182 (94%)	163 (95%)	8 (5%)	23	47
All	All	348/364 (96%)	332 (95%)	16 (5%)	24	48

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	GLU
1	A	312	ARG
1	A	336	ASP
1	A	361	LEU
1	A	373	VAL
1	A	375	THR
1	A	396	LEU
1	A	457	GLU
1	B	303	GLU
1	B	312	ARG
1	B	337	ASN
1	B	352	GLU
1	B	361	LEU
1	B	374	GLU
1	B	400	GLN
1	B	441	LYS

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	480	GLN
1	B	376	HIS
1	B	430	HIS
1	B	450	HIS
1	B	454	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](#)

11 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	IDS	C	1	2	17,17,17	1.13	1 (5%)	22,26,26	0.64	0
2	SGN	C	2	2	19,19,20	2.13	4 (21%)	23,29,31	1.52	4 (17%)
2	IDS	C	3	2	16,16,17	1.08	1 (6%)	16,24,26	0.94	1 (6%)
2	SGN	C	4	2	19,19,20	2.02	4 (21%)	23,29,31	1.40	3 (13%)
2	UAP	C	5	2	15,15,16	1.80	5 (33%)	18,22,24	1.74	2 (11%)
3	IDS	D	1	3	17,17,17	1.15	2 (11%)	22,26,26	0.88	1 (4%)
3	SGN	D	2	3	19,19,20	2.24	4 (21%)	23,29,31	1.26	1 (4%)
3	IDS	D	3	3	16,16,17	1.07	1 (6%)	16,24,26	1.13	2 (12%)
3	SGN	D	4	3	19,19,20	2.24	5 (26%)	23,29,31	1.27	1 (4%)
3	IDS	D	5	3	16,16,17	1.07	1 (6%)	16,24,26	0.72	1 (6%)
3	SGN	D	6	3	19,19,20	2.15	4 (21%)	23,29,31	1.19	1 (4%)

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	IDS	C	1	2	-	0/9/29/29	0/1/1/1
2	SGN	C	2	2	-	1/11/28/31	0/1/1/1
2	IDS	C	3	2	-	3/9/26/29	0/1/1/1
2	SGN	C	4	2	-	1/11/28/31	0/1/1/1
2	UAP	C	5	2	-	3/9/22/25	0/1/1/1
3	IDS	D	1	3	-	0/9/29/29	0/1/1/1
3	SGN	D	2	3	-	4/11/28/31	0/1/1/1
3	IDS	D	3	3	-	0/9/26/29	0/1/1/1
3	SGN	D	4	3	-	3/11/28/31	0/1/1/1
3	IDS	D	5	3	-	3/9/26/29	0/1/1/1
3	SGN	D	6	3	-	6/11/28/31	0/1/1/1

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	2	SGN	O1S-S1	5.72	1.48	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	SGN	O2S-S1	5.68	1.48	1.42
3	D	2	SGN	O2S-S1	5.64	1.48	1.42
3	D	4	SGN	O2S-S1	5.50	1.48	1.42
2	C	2	SGN	O1S-S1	5.35	1.48	1.42
3	D	4	SGN	O1S-S1	5.27	1.48	1.42
3	D	6	SGN	O2S-S1	5.24	1.48	1.42
3	D	6	SGN	O1S-S1	5.23	1.48	1.42
2	C	4	SGN	O1S-S1	4.63	1.47	1.42
2	C	4	SGN	O2S-S1	4.40	1.47	1.42
3	D	6	SGN	S1-N2	4.17	1.64	1.59
3	D	4	SGN	S1-N2	4.04	1.64	1.59
2	C	4	SGN	S1-N2	3.87	1.64	1.59
3	D	2	SGN	S1-N2	3.80	1.64	1.59
2	C	5	UAP	O5-C5	3.43	1.41	1.37
2	C	5	UAP	O2-S	-3.34	1.47	1.57
2	C	4	SGN	O6-S2	-3.27	1.48	1.56
3	D	6	SGN	O6-S2	-3.20	1.48	1.56
2	C	3	IDS	O2-S	-3.19	1.47	1.57
2	C	2	SGN	S1-N2	3.14	1.63	1.59
3	D	4	SGN	O6-S2	-3.13	1.48	1.56
3	D	5	IDS	O2-S	-3.02	1.48	1.57
3	D	2	SGN	O6-S2	-3.00	1.48	1.56
2	C	1	IDS	O2-S	-2.93	1.48	1.57
2	C	2	SGN	O6-S2	-2.90	1.49	1.56
2	C	5	UAP	C1-C2	2.84	1.56	1.51
3	D	1	IDS	O2-S	-2.68	1.49	1.57
3	D	3	IDS	O2-S	-2.68	1.49	1.57
3	D	4	SGN	C1-C2	2.47	1.55	1.52
2	C	5	UAP	C3-C4	2.40	1.53	1.50
2	C	5	UAP	O6B-C6	-2.21	1.24	1.30
3	D	1	IDS	C1-C2	2.11	1.54	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5	UAP	O5-C5-C4	-5.40	119.98	124.94
3	D	2	SGN	O1S-S1-O2S	-4.86	109.55	120.36
3	D	6	SGN	O1S-S1-O2S	-4.83	109.62	120.36
2	C	4	SGN	O1S-S1-O2S	-4.73	109.84	120.36
3	D	4	SGN	O1S-S1-O2S	-4.65	110.02	120.36
2	C	2	SGN	O1S-S1-O2S	-4.49	110.37	120.36
2	C	2	SGN	C6-C5-C4	2.90	118.16	112.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	IDS	O2-C2-C3	2.80	110.86	106.95
2	C	3	IDS	O2-C2-C3	2.78	110.83	106.95
2	C	5	UAP	O6B-C6-C5	2.74	120.27	114.06
2	C	2	SGN	O6-C6-C5	2.64	112.28	107.57
2	C	4	SGN	O6-C6-C5	2.55	112.11	107.57
3	D	1	IDS	C4-C3-C2	2.53	115.41	109.68
3	D	3	IDS	C4-C3-C2	2.39	114.57	110.23
2	C	2	SGN	O6S-S2-O6	2.34	111.76	106.37
2	C	4	SGN	O6S-S2-O6	2.25	111.54	106.37
3	D	5	IDS	O2-C2-C3	2.06	109.83	106.95

There are no chirality outliers.

All (24) torsion outliers are listed below:

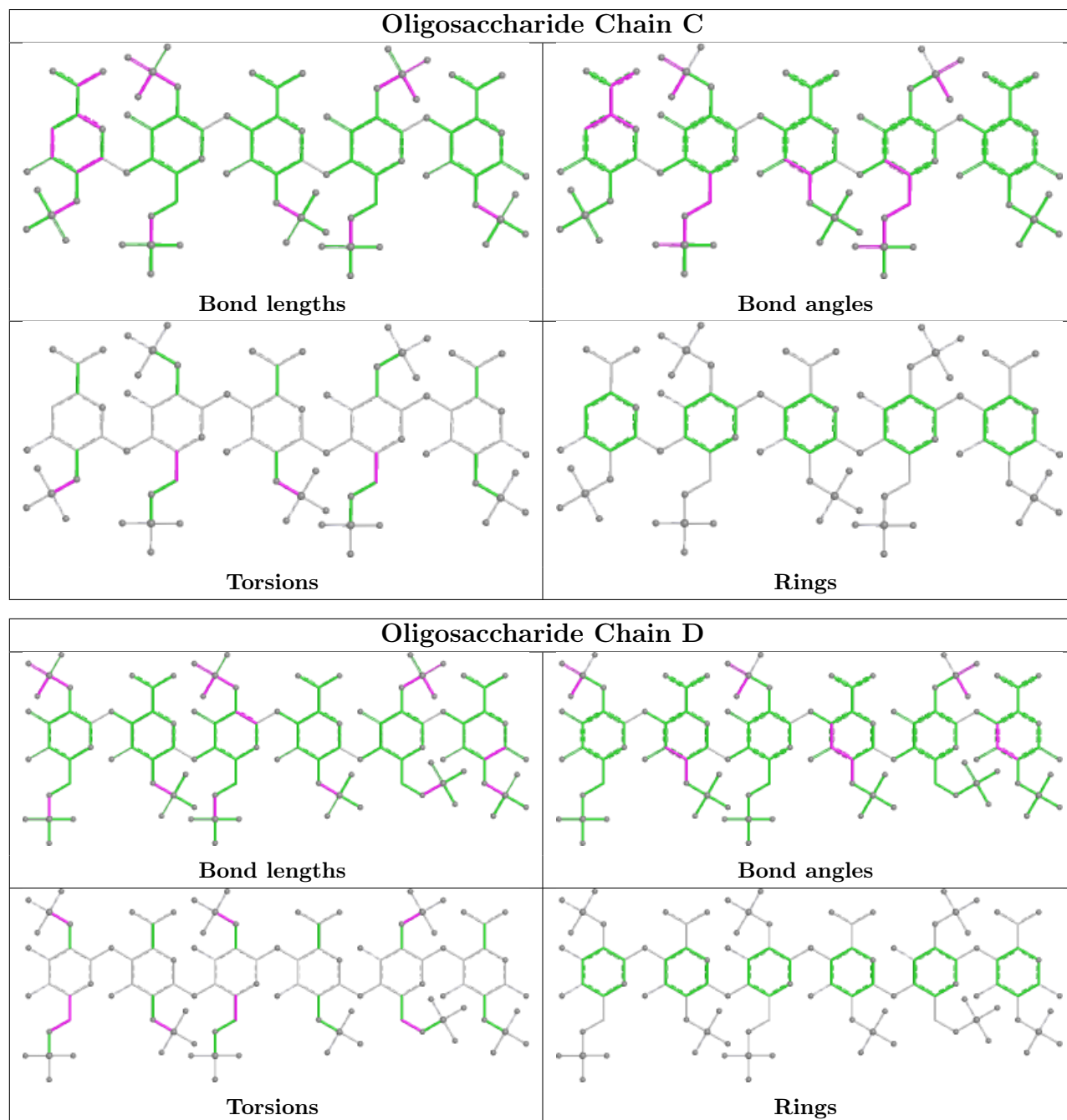
Mol	Chain	Res	Type	Atoms
2	C	2	SGN	O5-C5-C6-O6
2	C	3	IDS	C2-O2-S-O2S
2	C	3	IDS	C2-O2-S-O3S
2	C	4	SGN	O5-C5-C6-O6
3	D	2	SGN	C2-N2-S1-O1S
3	D	2	SGN	C2-N2-S1-O2S
3	D	2	SGN	C2-N2-S1-O3S
3	D	4	SGN	C4-C5-C6-O6
3	D	4	SGN	O5-C5-C6-O6
3	D	6	SGN	C4-C5-C6-O6
3	D	6	SGN	O5-C5-C6-O6
3	D	6	SGN	C2-N2-S1-O2S
3	D	6	SGN	C2-N2-S1-O3S
2	C	3	IDS	C2-O2-S-O1S
2	C	5	UAP	C2-O2-S-O2S
2	C	5	UAP	C2-O2-S-O3S
3	D	6	SGN	C2-N2-S1-O1S
2	C	5	UAP	C2-O2-S-O1S
3	D	5	IDS	C2-O2-S-O3S
3	D	2	SGN	C5-C6-O6-S2
3	D	6	SGN	C5-C6-O6-S2
3	D	5	IDS	C2-O2-S-O1S
3	D	5	IDS	C2-O2-S-O2S
3	D	4	SGN	C2-N2-S1-O2S

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	5	UAP	4	0
3	D	6	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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	203/210 (96%)	0.24	9 (4%) 39 34	27, 54, 84, 111	27 (13%)
1	B	196/210 (93%)	0.78	29 (14%) 5 4	26, 62, 109, 141	31 (15%)
All	All	399/420 (95%)	0.51	38 (9%) 14 12	26, 58, 101, 141	58 (14%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	487	SER	6.2
1	B	486	HIS	4.8
1	B	475	GLN	4.6
1	B	405	GLN	4.3
1	A	340	LYS	4.2
1	B	485	LEU	4.0
1	A	404	PRO	3.8
1	B	482	GLN	3.6
1	B	343	PRO	3.5
1	B	484	LEU	3.2
1	B	478	ARG	3.1
1	B	371[A]	ARG	3.1
1	B	348	GLN	3.1
1	B	400	GLN	3.0
1	B	403	PRO	3.0
1	B	481	ILE	2.9
1	B	477	LEU	2.9
1	A	470	ASN	2.9
1	A	347[A]	ARG	2.8
1	B	323	ARG	2.8
1	A	472	HIS	2.7
1	A	447	PHE	2.7
1	B	351	ASN	2.6
1	B	347	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	319	GLU	2.6
1	B	483	GLU	2.6
1	B	346	ASP	2.5
1	B	312	ARG	2.5
1	A	443	GLN	2.4
1	B	479	PRO	2.4
1	B	352	GLU	2.4
1	B	344	LYS	2.3
1	B	334	MET	2.3
1	B	342	LEU	2.2
1	B	439	PRO	2.2
1	A	405	GLN	2.2
1	B	472	HIS	2.1
1	A	403	PRO	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](#)

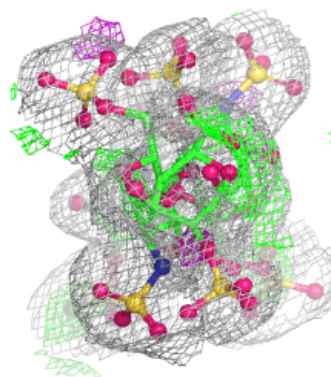
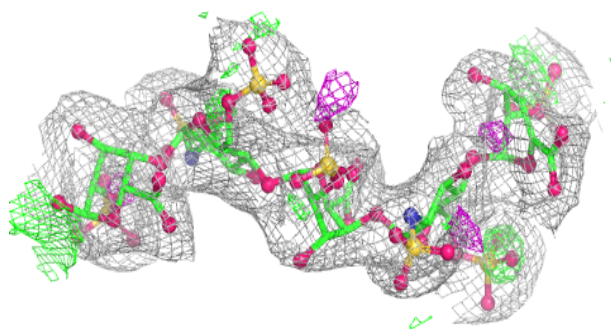
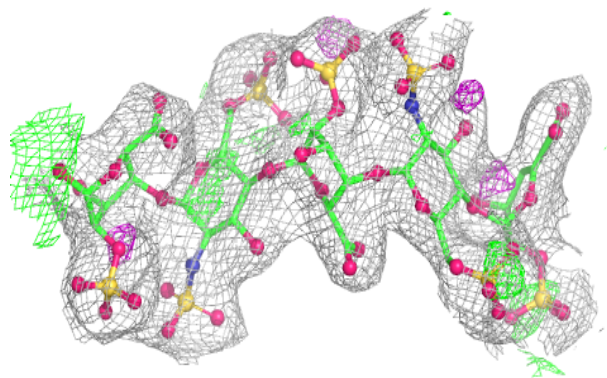
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	IDS	D	1	17/17	0.32	0.24	162,166,169,170	6
3	IDS	D	3	16/17	0.38	0.18	159,169,171,172	4
3	SGN	D	2	19/20	0.60	0.22	175,176,179,179	4
2	IDS	C	1	17/17	0.61	0.16	101,116,133,134	4
3	SGN	D	6	19/20	0.78	0.22	107,114,120,122	9
3	IDS	D	5	16/17	0.85	0.16	120,124,138,139	4
3	SGN	D	4	19/20	0.86	0.17	109,110,142,145	8
2	SGN	C	2	19/20	0.92	0.11	83,85,99,99	8
2	IDS	C	3	16/17	0.93	0.12	88,93,100,100	4
2	SGN	C	4	19/20	0.93	0.12	76,82,88,96	8
2	UAP	C	5	15/16	0.94	0.12	73,78,80,83	4

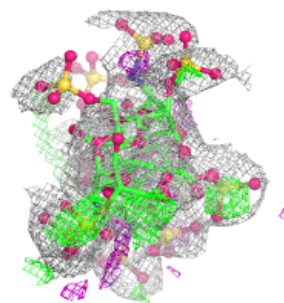
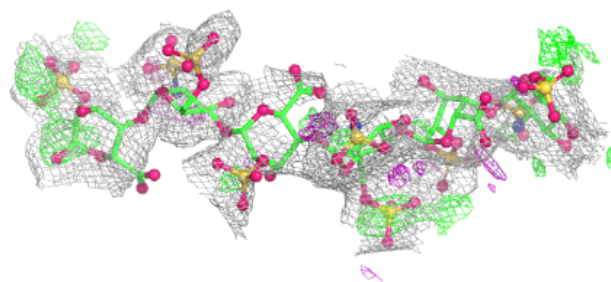
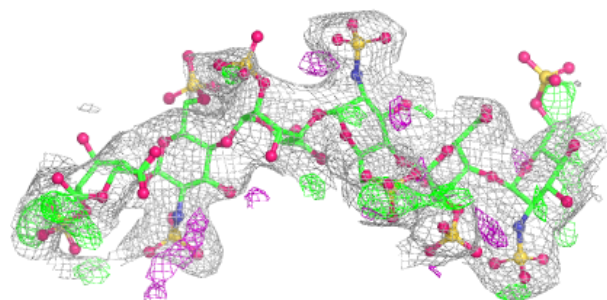
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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 [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
4	ZN	A	506	1/1	1.00	0.04	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.