



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:28 PM UTC

PDB ID : 1H3T / pdb_00001h3t
Title : Crystal structure of the human igg1 fc-fragment, glycoform (mn2f)2
Authors : Krapp, S.; Mimura, Y.; Jefferis, R.; Huber, R.; Sondermann, P.
Deposited on : 2002-09-19
Resolution : 2.40 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

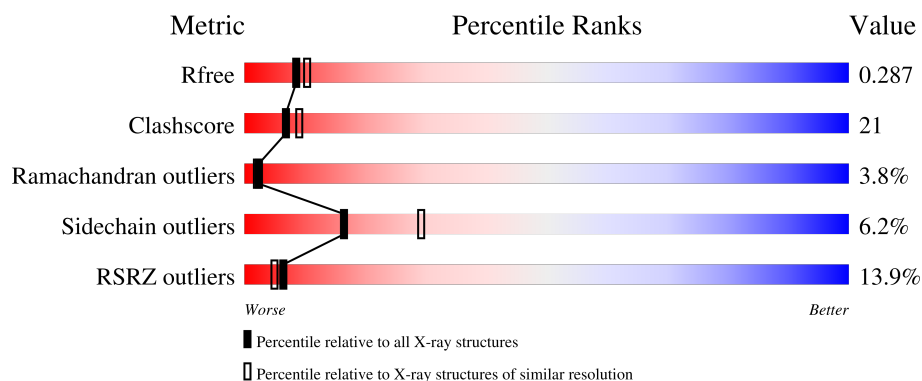
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	223	5% 56% 31% 6% 7%
1	B	223	21% 60% 24% 6% 9%
2	C	4	50% 50%

2 Entry composition [i](#)

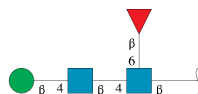
There are 4 unique types of molecules in this entry. The entry contains 3240 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 IG GAMMA-1 CHAIN C REGION.

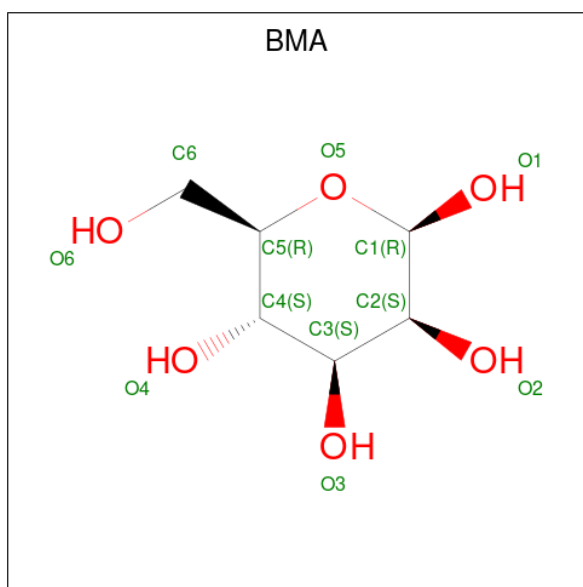
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	1
			1597	1016	270	304	7			
1	B	202	Total	C	N	O	S	0	0	5
			1490	954	253	276	7			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 3 is beta-D-mannopyranose (CCD ID: BMA) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			12	6	6		

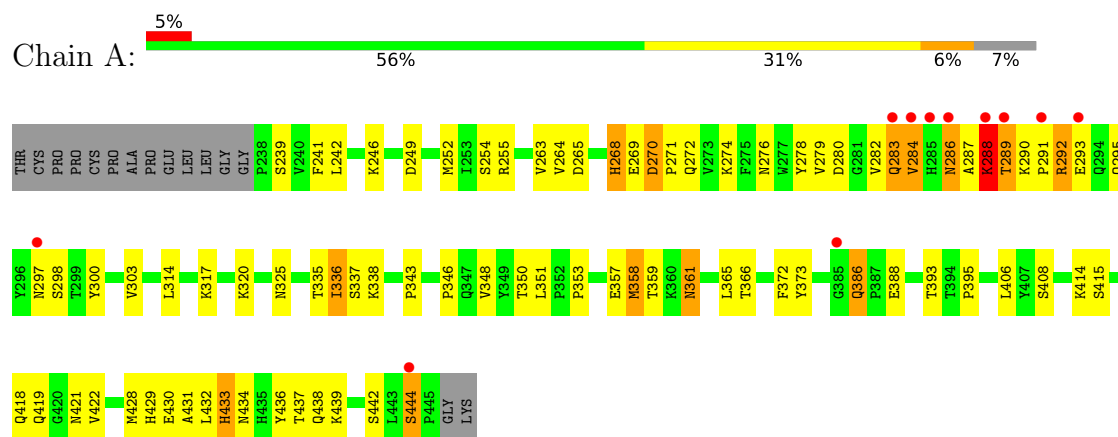
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total	O	0	0
			58	58		
4	B	34	Total	O	0	0
			34	34		

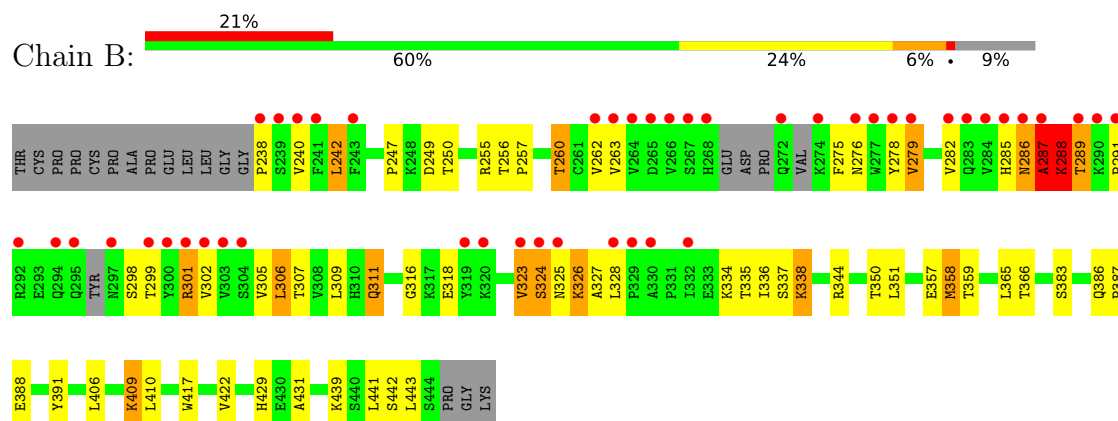
3 Residue-property plots

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: IG GAMMA-1 CHAIN C REGION



• Molecule 1: IG GAMMA-1 CHAIN C REGION



• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta a-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.57Å 80.78Å 139.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 50.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.1 (50.00-2.40) 93.9 (50.00-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.41Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.280 , 0.309 0.255 , 0.287	Depositor DCC
R_{free} test set	1041 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	43.5	Xtriage
Anisotropy	0.297	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	3240	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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: FUL, 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	0.52	1/1641 (0.1%)	1.03	10/2232 (0.4%)
1	B	0.49	1/1516 (0.1%)	1.03	6/2028 (0.3%)
All	All	0.51	2/3157 (0.1%)	1.03	16/4260 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	444	SER	C-N	-5.45	1.25	1.34
1	B	443	LEU	C-N	-5.28	1.25	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	288	LYS	N-CA-C	-10.49	88.46	110.80
1	B	287	ALA	N-CA-C	9.03	130.04	110.80
1	A	284	VAL	N-CA-C	-6.50	102.93	111.05
1	B	289	THR	N-CA-C	6.11	119.17	109.65
1	A	290	LYS	CA-C-N	5.99	127.32	119.84
1	A	290	LYS	C-N-CA	5.99	127.32	119.84
1	A	286	ASN	N-CA-C	5.91	118.79	110.23
1	A	386	GLN	CA-C-N	5.81	126.69	120.13
1	A	386	GLN	C-N-CA	5.81	126.69	120.13
1	B	286	ASN	CA-C-N	5.72	132.46	121.54
1	B	286	ASN	C-N-CA	5.72	132.46	121.54
1	B	327	ALA	N-CA-C	-5.51	105.17	112.94
1	A	348	VAL	N-CA-C	5.50	115.51	107.37
1	A	434	ASN	N-CA-C	-5.40	104.15	111.55
1	A	388	GLU	N-CA-C	-5.39	101.18	109.76
1	A	395	PRO	N-CA-C	-5.07	104.52	110.70

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	1597	0	1483	65	0
1	B	1490	0	1361	60	0
2	C	49	0	43	6	0
3	B	12	0	12	0	0
4	A	58	0	0	2	0
4	B	34	0	0	1	0
All	All	3240	0	2899	129	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 21.

All (129) 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:350:THR:HB	1:B:441:LEU:HG	1.42	1.00
1:B:323:VAL:HG12	1:B:324:SER:H	1.32	0.94
1:B:287:ALA:HB1	1:B:289:THR:H	1.33	0.91
1:B:298:SER:C	1:B:299:THR:CA	2.44	0.90
1:B:311:GLN:NE2	1:B:311:GLN:H	1.74	0.84
1:A:291:PRO:O	1:A:292:ARG:HG3	1.78	0.82
1:B:242:LEU:HD13	1:B:336:ILE:HG22	1.64	0.78
1:B:311:GLN:H	1:B:311:GLN:CD	1.91	0.78
1:B:358:MET:HE1	1:B:417:TRP:NE1	1.99	0.78
1:B:358:MET:HE1	1:B:417:TRP:HE1	1.48	0.77
1:B:350:THR:HG23	1:B:439:LYS:HG3	1.65	0.77
1:B:276:ASN:N	1:B:276:ASN:C	2.44	0.75
1:B:328:LEU:CG	1:B:328:LEU:CA	2.68	0.71
1:B:350:THR:CB	1:B:441:LEU:HG	2.19	0.70
1:A:278:TYR:CE2	1:A:284:VAL:HA	2.28	0.68
1:A:282:VAL:O	1:A:283:GLN:HB3	1.93	0.68
1:B:429:HIS:CD2	1:B:431:ALA:H	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:PRO:HA	1:A:303:VAL:O	1.94	0.66
1:A:429:HIS:CD2	1:A:431:ALA:H	2.14	0.65
1:B:262:VAL:HG13	1:B:301:ARG:HE	1.61	0.65
1:B:429:HIS:HD2	1:B:431:ALA:H	1.44	0.65
1:A:295:GLN:HB2	1:A:300:TYR:CE1	2.32	0.64
1:B:249:ASP:OD1	1:B:255:ARG:HD3	1.98	0.63
1:A:291:PRO:C	1:A:292:ARG:HG3	2.24	0.62
1:A:429:HIS:HD2	1:A:431:ALA:H	1.48	0.61
1:B:263:VAL:O	1:B:301:ARG:HA	2.00	0.61
1:B:311:GLN:NE2	1:B:311:GLN:N	2.47	0.61
1:A:280:ASP:OD2	1:A:317:LYS:HD3	2.00	0.60
1:A:422:VAL:HG22	1:A:442:SER:OG	2.01	0.60
1:B:249:ASP:HA	1:B:255:ARG:CD	2.31	0.59
1:A:414:LYS:O	1:A:418:GLN:HG3	2.02	0.59
1:B:309:LEU:HB3	1:B:311:GLN:NE2	2.17	0.59
1:A:268:HIS:CE1	1:A:295:GLN:HE21	2.20	0.59
1:B:287:ALA:HB1	1:B:289:THR:N	2.14	0.57
1:A:353:PRO:HG2	1:A:358:MET:CE	2.35	0.56
1:B:249:ASP:O	1:B:257:PRO:HG3	2.05	0.56
1:A:288:LYS:O	1:A:289:THR:O	2.24	0.56
1:B:350:THR:HB	1:B:441:LEU:CG	2.25	0.56
1:B:365:LEU:HD12	1:B:410:LEU:HD23	1.88	0.56
1:A:274:LYS:HE3	1:A:276:ASN:HD21	1.71	0.56
4:A:2034:HOH:O	1:B:409:LYS:HE2	2.05	0.55
1:A:353:PRO:HG2	1:A:358:MET:HE2	1.89	0.55
1:B:350:THR:CG2	1:B:439:LYS:HG3	2.36	0.55
1:B:240:VAL:HG21	1:B:323:VAL:HG21	1.89	0.55
1:A:314:LEU:HD22	1:A:430:GLU:HG3	1.89	0.54
2:C:2:NAG:H82	2:C:4:FUL:C1	2.37	0.54
1:A:283:GLN:CD	1:A:287:ALA:HB2	2.32	0.54
1:A:438:GLN:O	1:A:439:LYS:HD3	2.08	0.53
1:A:272:GLN:O	1:A:325:ASN:ND2	2.39	0.53
1:A:320:LYS:HB2	1:A:335:THR:HG22	1.90	0.53
1:A:274:LYS:HE3	1:A:276:ASN:ND2	2.24	0.53
1:A:268:HIS:HE1	1:A:295:GLN:HG3	1.74	0.52
1:B:406:LEU:HD12	1:B:406:LEU:C	2.34	0.52
1:A:346:PRO:HB3	1:A:372:PHE:HB3	1.92	0.52
1:A:415:SER:O	1:A:419:GLN:HG3	2.10	0.52
4:A:2031:HOH:O	1:B:351:LEU:HD22	2.09	0.52
1:B:249:ASP:C	1:B:257:PRO:HG3	2.35	0.51
1:B:336:ILE:HG12	1:B:337:SER:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LYS:HE3	1:A:288:LYS:H	1.76	0.51
1:A:350:THR:O	1:A:351:LEU:HD23	2.11	0.51
1:A:249:ASP:OD1	1:A:255:ARG:HD3	2.11	0.50
1:B:323:VAL:HG12	1:B:324:SER:N	2.12	0.50
1:A:436:TYR:CD1	1:A:437:THR:N	2.79	0.50
1:B:250:THR:HG22	1:B:257:PRO:HB3	1.93	0.50
1:B:287:ALA:O	1:B:288:LYS:HG2	2.11	0.49
1:A:351:LEU:HB2	1:A:366:THR:HB	1.94	0.49
1:B:238:PRO:HG2	1:B:328:LEU:CD1	2.41	0.49
1:A:282:VAL:O	1:A:283:GLN:CB	2.61	0.49
2:C:1:NAG:O3	2:C:1:NAG:C7	2.61	0.49
1:A:241:PHE:CE2	2:C:3:BMA:H3	2.48	0.49
1:B:260:THR:HG23	1:B:305:VAL:HG22	1.95	0.49
1:A:283:GLN:O	1:A:283:GLN:HG2	2.13	0.48
1:A:288:LYS:N	1:A:288:LYS:HD3	2.27	0.48
1:A:288:LYS:H	1:A:288:LYS:CE	2.26	0.48
1:B:249:ASP:HA	1:B:255:ARG:HD3	1.95	0.48
1:A:252:MET:SD	1:A:428:MET:HE1	2.53	0.48
2:C:1:NAG:H61	2:C:2:NAG:H82	1.95	0.48
1:B:350:THR:HG23	1:B:439:LYS:CG	2.38	0.48
1:A:386:GLN:CA	1:A:386:GLN:CD	2.87	0.48
1:B:351:LEU:HB2	1:B:366:THR:HB	1.96	0.48
1:A:353:PRO:HD3	1:A:365:LEU:HD23	1.95	0.48
1:A:436:TYR:CD1	1:A:436:TYR:C	2.92	0.48
1:B:325:ASN:ND2	1:B:326:LYS:H	2.12	0.48
1:A:283:GLN:CD	1:A:287:ALA:CB	2.87	0.47
1:B:383:SER:HB2	1:B:388:GLU:OE1	2.14	0.47
1:B:422:VAL:HG22	1:B:442:SER:HB3	1.96	0.47
1:B:309:LEU:HB3	1:B:311:GLN:HE22	1.78	0.47
1:A:353:PRO:HD3	1:A:365:LEU:CD2	2.43	0.47
1:B:316:GLY:HA2	4:B:2006:HOH:O	2.15	0.47
1:A:246:LYS:HB2	1:A:249:ASP:OD2	2.14	0.47
1:B:278:TYR:O	1:B:282:VAL:O	2.33	0.47
1:B:279:VAL:HA	1:B:318:GLU:O	2.15	0.47
1:A:406:LEU:C	1:A:406:LEU:HD12	2.40	0.47
1:B:357:GLU:C	1:B:359:THR:H	2.23	0.46
1:A:239:SER:HB2	1:A:264:VAL:CG2	2.45	0.46
1:A:297:ASN:OD1	1:A:298:SER:N	2.39	0.46
1:A:422:VAL:HA	1:A:442:SER:OG	2.15	0.46
1:B:338:LYS:NZ	1:B:338:LYS:HB3	2.30	0.46
1:A:270:ASP:OD2	1:A:270:ASP:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:GLU:C	1:A:271:PRO:HD3	2.41	0.45
1:B:344:ARG:CD	1:B:344:ARG:NH1	2.80	0.45
1:A:338:LYS:HZ2	1:A:430:GLU:CD	2.25	0.44
1:A:288:LYS:H	1:A:288:LYS:CD	2.30	0.44
1:A:278:TYR:HA	1:A:282:VAL:O	2.17	0.44
1:A:361:ASN:HD22	1:A:361:ASN:HA	1.61	0.44
1:A:421:ASN:N	1:A:421:ASN:HD22	2.16	0.44
1:B:275:PHE:CE1	1:B:302:VAL:O	2.70	0.44
1:A:357:GLU:C	1:A:359:THR:H	2.26	0.43
1:B:278:TYR:CD1	1:B:278:TYR:N	2.86	0.43
1:A:343:PRO:HA	1:A:373:TYR:O	2.18	0.43
1:A:432:LEU:O	1:A:433:HIS:C	2.61	0.43
1:A:239:SER:HB2	1:A:264:VAL:HG22	2.01	0.43
1:B:388:GLU:HB3	1:B:410:LEU:HD11	1.99	0.43
1:A:358:MET:HE3	1:A:358:MET:HB2	1.86	0.43
1:A:320:LYS:CB	1:A:335:THR:HG22	2.49	0.43
1:A:278:TYR:CD1	1:A:278:TYR:N	2.88	0.42
1:A:265:ASP:OD2	2:C:1:NAG:O7	2.37	0.42
1:B:306:LEU:HD12	1:B:307:THR:N	2.35	0.42
1:B:391:TYR:C	1:B:391:TYR:CD2	2.97	0.42
1:B:326:LYS:HE3	1:B:326:LYS:HB2	1.93	0.41
1:A:239:SER:O	1:A:263:VAL:HA	2.21	0.41
2:C:1:NAG:H61	2:C:2:NAG:C7	2.51	0.41
1:B:240:VAL:O	1:B:334:LYS:HE3	2.21	0.41
1:A:393:THR:HA	1:A:408:SER:HA	2.03	0.40
1:B:386:GLN:HA	1:B:387:PRO:HD3	1.81	0.40
1:A:279:VAL:O	1:A:280:ASP:HB2	2.21	0.40
1:A:336:ILE:HG13	1:A:337:SER:H	1.86	0.40
1:B:242:LEU:HD23	1:B:242:LEU:HA	1.84	0.40
1:B:256:THR:HA	1:B:257:PRO:HD3	1.95	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	206/223 (92%)	186 (90%)	13 (6%)	7 (3%)	3	2
1	B	185/223 (83%)	165 (89%)	12 (6%)	8 (4%)	2	1
All	All	391/446 (88%)	351 (90%)	25 (6%)	15 (4%)	2	2

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	288	LYS
1	A	289	THR
1	A	433	HIS
1	A	444	SER
1	B	286	ASN
1	B	287	ALA
1	B	288	LYS
1	A	283	GLN
1	B	279	VAL
1	B	301	ARG
1	B	324	SER
1	B	358	MET
1	A	292	ARG
1	A	293	GLU
1	B	323	VAL

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	171/206 (83%)	162 (95%)	9 (5%)	20	36
1	B	153/206 (74%)	142 (93%)	11 (7%)	13	23
All	All	324/412 (79%)	304 (94%)	20 (6%)	16	29

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	242	LEU
1	A	254	SER
1	A	268	HIS
1	A	270	ASP
1	A	286	ASN
1	A	288	LYS
1	A	336	ILE
1	A	358	MET
1	A	361	ASN
1	B	242	LEU
1	B	247	PRO
1	B	260	THR
1	B	285	HIS
1	B	291	PRO
1	B	306	LEU
1	B	311	GLN
1	B	326	LYS
1	B	335	THR
1	B	338	LYS
1	B	409	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	276	ASN
1	A	294	GLN
1	A	295	GLN
1	A	311	GLN
1	A	361	ASN
1	A	384	ASN
1	A	390	ASN
1	A	419	GLN
1	A	421	ASN
1	A	429	HIS
1	A	434	ASN
1	B	311	GLN
1	B	325	ASN
1	B	390	ASN
1	B	418	GLN
1	B	429	HIS
1	B	434	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	1,2	14,14,15	0.51	0	17,19,21	0.85	1 (5%)
2	NAG	C	2	2	14,14,15	0.52	0	17,19,21	0.83	1 (5%)
2	BMA	C	3	2	11,11,12	0.48	0	15,15,17	0.35	0
2	FUL	C	4	2	10,10,11	0.68	0	14,14,16	0.47	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	1,2	-	3/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	FUL	C	4	2	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C2-N2-C7	-2.39	119.69	122.90
2	C	1	NAG	C2-N2-C7	-2.10	120.08	122.90

There are no chirality outliers.

All (5) torsion outliers are listed below:

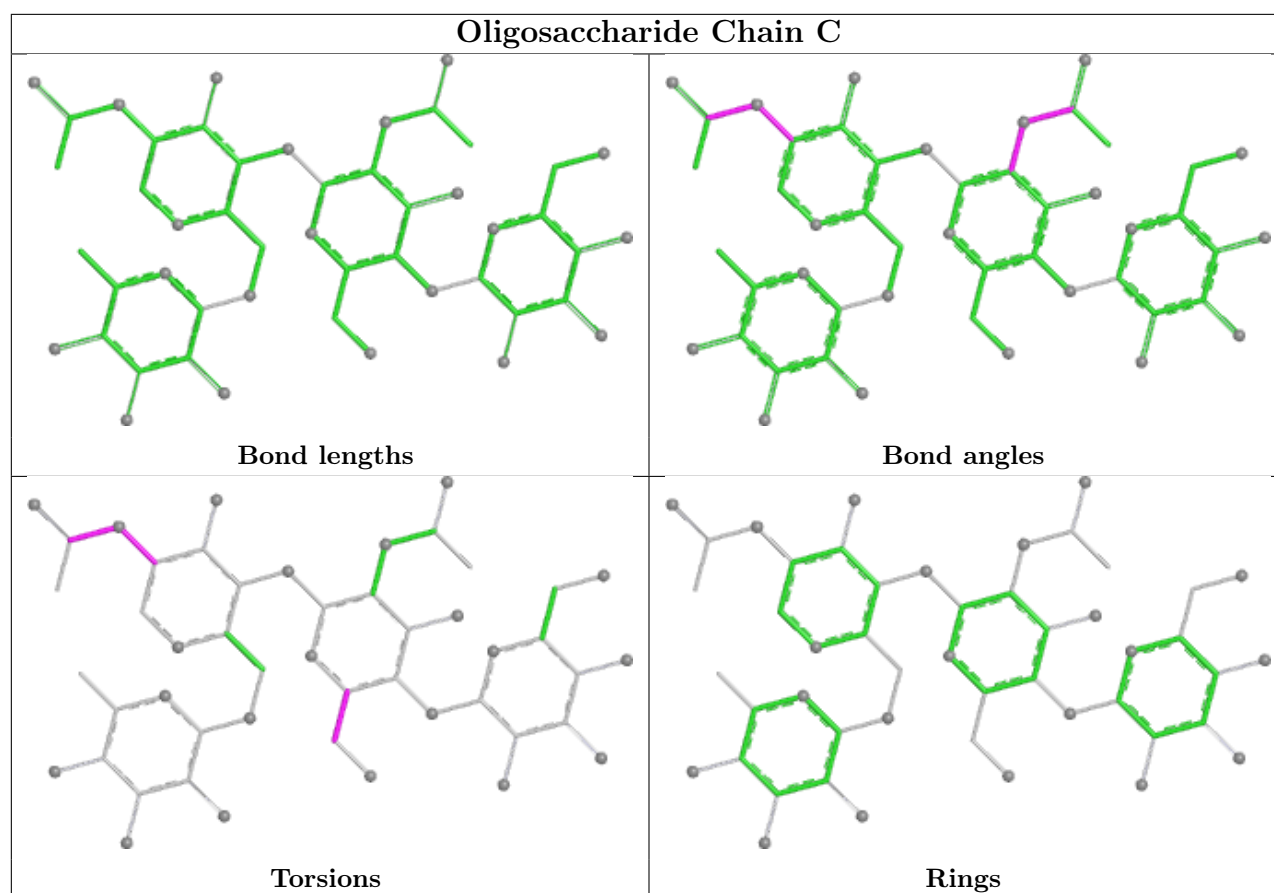
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C3-C2-N2-C7
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
2	C	2	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3	BMA	1	0
2	C	2	NAG	3	0
2	C	1	NAG	4	0
2	C	4	FUL	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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	BMA	B	1447	-	12,12,12	0.42	0	17,17,17	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	B	1447	-	-	0/2/22/22	0/1/1/1

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	208/223 (93%)	0.17	11 (5%) 32 28	15, 33, 57, 68	0
1	B	202/223 (90%)	0.89	46 (22%) 2 1	16, 43, 98, 107	0
All	All	410/446 (91%)	0.52	57 (13%) 6 5	15, 37, 92, 107	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	283	GLN	14.4
1	B	299	THR	8.7
1	B	272	GLN	7.7
1	A	285	HIS	7.1
1	B	291	PRO	5.3
1	B	300	TYR	5.2
1	B	295	GLN	5.0
1	B	324	SER	4.9
1	B	268	HIS	4.7
1	B	264	VAL	4.4
1	A	284	VAL	4.3
1	B	323	VAL	4.3
1	B	286	ASN	4.1
1	A	286	ASN	3.9
1	B	285	HIS	3.9
1	B	266	VAL	3.8
1	B	284	VAL	3.8
1	B	278	TYR	3.7
1	B	267	SER	3.7
1	B	263	VAL	3.5
1	A	297	ASN	3.5
1	B	319	TYR	3.4
1	B	297	ASN	3.3
1	B	287	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	240	VAL	3.2
1	B	238	PRO	3.1
1	B	289	THR	3.1
1	B	328	LEU	3.1
1	B	274	LYS	2.9
1	B	290	LYS	2.9
1	B	239	SER	2.8
1	B	265	ASP	2.8
1	B	320	LYS	2.8
1	B	277	TRP	2.7
1	B	304	SER	2.7
1	B	262	VAL	2.7
1	B	279	VAL	2.7
1	B	329	PRO	2.6
1	B	301	ARG	2.6
1	B	332	ILE	2.5
1	B	294	GLN	2.5
1	B	330	ALA	2.5
1	B	292	ARG	2.4
1	B	243	PHE	2.3
1	A	293	GLU	2.3
1	A	283	GLN	2.3
1	B	325	ASN	2.2
1	A	385	GLY	2.2
1	B	276	ASN	2.2
1	B	241	PHE	2.2
1	B	282	VAL	2.2
1	B	302	VAL	2.2
1	A	289	THR	2.2
1	A	444	SER	2.2
1	A	291	PRO	2.1
1	A	288	LYS	2.1
1	B	303	VAL	2.0

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

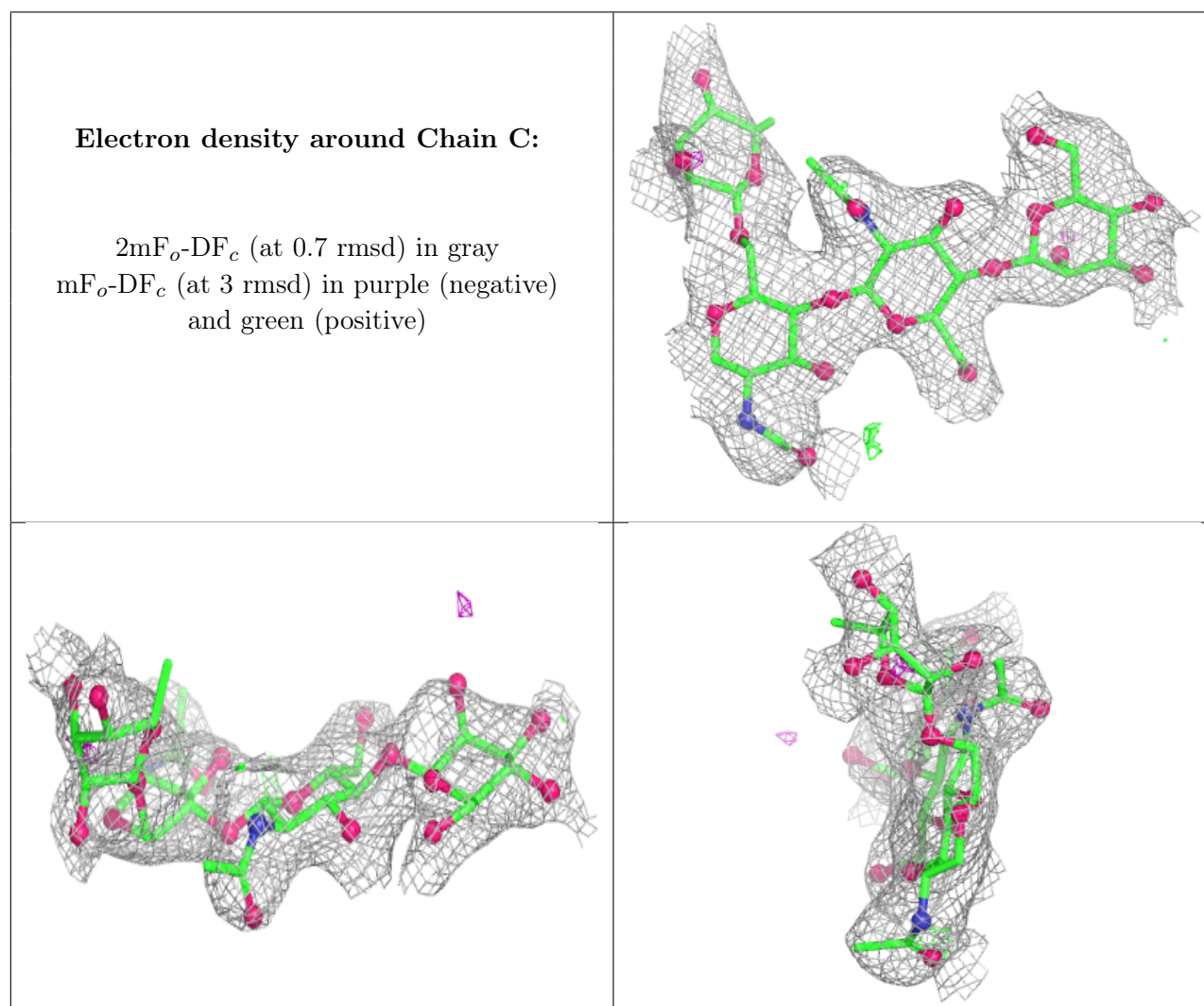
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [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
2	FUL	C	4	10/11	0.66	0.17	68,70,71,72	0
2	BMA	C	3	11/12	0.73	0.12	59,62,63,64	0
2	NAG	C	1	14/15	0.80	0.14	58,60,64,66	0
2	NAG	C	2	14/15	0.84	0.10	56,61,62,63	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

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
3	BMA	B	1447	12/12	0.48	0.18	95,95,96,96	0

6.5 Other polymers

There are no such residues in this entry.