



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:54 PM UTC

PDB ID : 2FBJ / pdb_00002fbj
Title : REFINED CRYSTAL STRUCTURE OF THE GALACTAN-BINDING IMMUNOGLOBULIN FAB J539 AT 1.95-ANGSTROMS RESOLUTION
Authors : Bhat, T.N.; Padlan, E.A.; Davies, D.R.
Deposited on : 1989-08-18
Resolution : 1.95 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)
Xtrriage (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

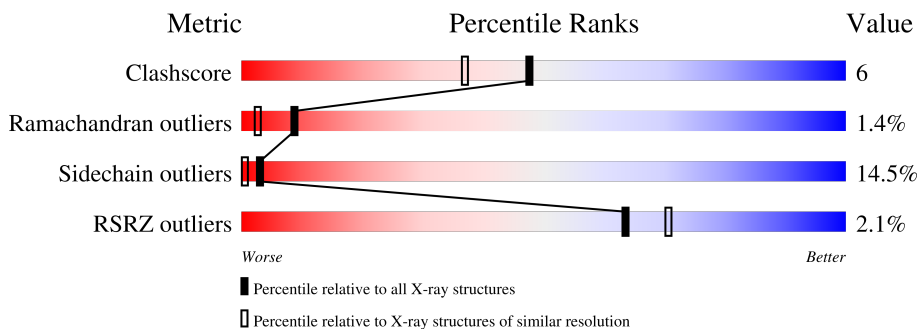
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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))
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	L	213	
2	H	220	
3	A	2	
4	B	3	

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
4	FUC	B	3	X	-	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3761 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 IGA-KAPPA J539 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	213	1636	1024	270	335	7	0	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	2	ILE	LEU	conflict	GB 437099
L	11	THR	MET	conflict	GB 437099
L	12	ALA	SER	conflict	GB 437099
L	15	LEU	PRO	conflict	GB 437099
L	?	-	ARG	deletion	GB 437099
L	?	-	PHE	deletion	GB 437099
L	41	THR	ALA	conflict	GB 437099
L	45	PRO	LEU	conflict	GB 437099
L	49	GLU	ASP	conflict	GB 437099
L	50	ILE	THR	conflict	GB 437099
L	55	SER	PRO	conflict	GB 437099
L	75	ASN	SER	conflict	GB 437099
L	76	THR	SER	conflict	GB 437099
L	84	ILE	SER	conflict	GB 437099
L	86	TYR	PHE	conflict	GB 437099
L	88	GLN	HIS	conflict	GB 437099
L	?	-	SER	deletion	GB 437099
L	91	THR	SER	conflict	GB 437099
L	95	ILE	-	insertion	GB 437099

- Molecule 2 is a protein called IGA-KAPPA J539 FAB (HEAVY CHAIN).

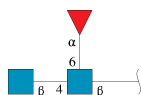
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	220	1683	1067	279	327	10	0	0	0

- Molecule 3 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
			Total	C	N	O			
3	A	2	28	16	2	10	0	0	0

- Molecule 4 is an oligosaccharide called 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	N	O			
4	B	3	38	22	2	14	0	0	0

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
5	H	1	1	1	0	0

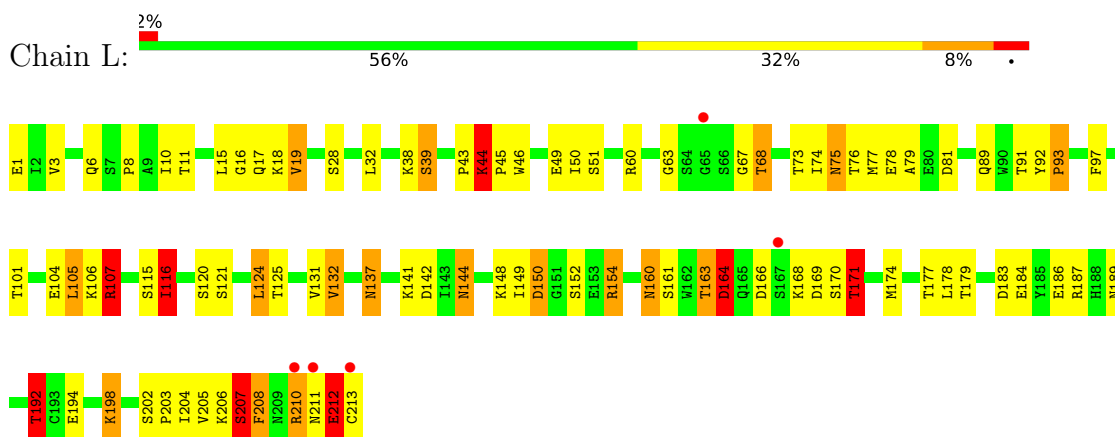
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	L	193	193	193	0	0
6	H	182	182	182	0	0

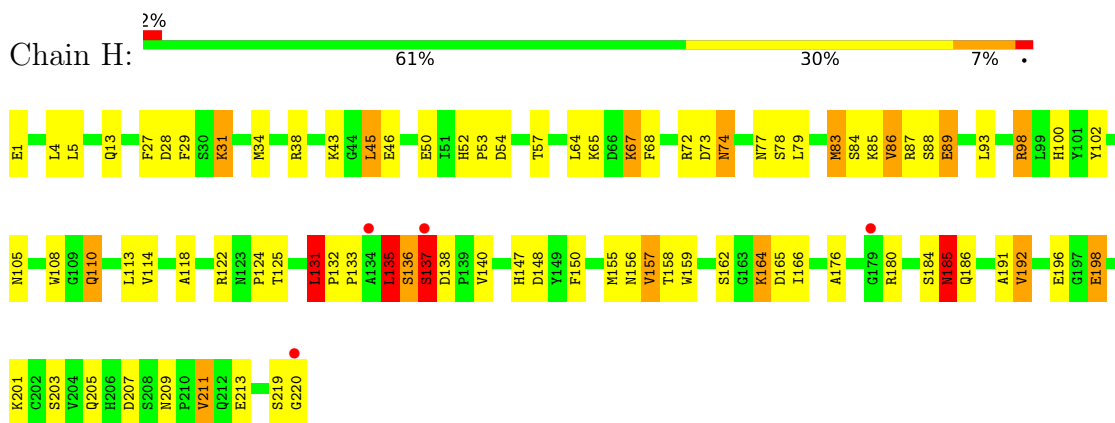
3 Residue-property plots [i](#)

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: IGA-KAPPA J539 FAB (LIGHT CHAIN)



- Molecule 2: IGA-KAPPA J539 FAB (HEAVY CHAIN)



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



MAG1
MAG2
FUC3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.02Å 74.29Å 131.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.95 65.67 – 1.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-1.95) 71.9 (65.67-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtrriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.194 , (Not available) 0.187 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtrriage
Anisotropy	0.427	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 69.3	EDS
L-test for twinning ¹	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3761	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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: ZN, NAG, FUC

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	L	0.95	0/1674	2.38	92/2277 (4.0%)
2	H	0.92	0/1728	2.31	93/2353 (4.0%)
All	All	0.93	0/3402	2.34	185/4630 (4.0%)

There are no bond length outliers.

All (185) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	163	THR	CA-C-N	16.11	146.23	120.94
1	L	163	THR	C-N-CA	16.11	146.23	120.94
1	L	210	ARG	CD-NE-CZ	14.41	144.57	124.40
2	H	88	SER	CA-C-N	13.49	139.71	120.28
2	H	88	SER	C-N-CA	13.49	139.71	120.28
1	L	164	ASP	CA-CB-CG	13.16	125.76	112.60
2	H	28	ASP	CA-CB-CG	12.57	125.17	112.60
1	L	107	ARG	CA-CB-CG	11.97	138.04	114.10
2	H	136	SER	CA-C-N	11.32	143.16	121.54
2	H	136	SER	C-N-CA	11.32	143.16	121.54
2	H	77	ASN	CA-CB-CG	10.49	123.09	112.60
1	L	137	ASN	CA-CB-CG	9.91	122.52	112.60
1	L	189	ASN	CA-CB-CG	9.88	122.48	112.60
1	L	212	GLU	CA-CB-CG	9.63	133.36	114.10
1	L	169	ASP	CA-CB-CG	9.43	122.03	112.60
1	L	208	PHE	CA-CB-CG	9.34	123.14	113.80
2	H	89	GLU	CB-CG-CD	9.04	127.97	112.60
1	L	78	GLU	CB-CG-CD	8.77	127.50	112.60
1	L	150	ASP	CA-CB-CG	8.71	121.31	112.60
1	L	68	THR	CA-CB-CG2	8.64	125.19	110.50
1	L	163	THR	CA-C-O	8.62	131.98	121.89
1	L	210	ARG	CA-CB-CG	8.53	131.16	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	49	GLU	CA-C-O	8.45	131.65	121.84
2	H	86	VAL	CB-CA-C	8.43	125.03	111.71
2	H	147	HIS	CA-CB-CG	8.20	122.00	113.80
2	H	198	GLU	CB-CG-CD	8.07	126.32	112.60
1	L	168	LYS	CA-C-N	8.01	136.43	122.09
1	L	168	LYS	C-N-CA	8.01	136.43	122.09
2	H	85	LYS	CA-C-N	8.00	132.37	120.69
2	H	85	LYS	C-N-CA	8.00	132.37	120.69
1	L	171	THR	N-CA-CB	-7.93	98.17	110.46
2	H	98	ARG	CA-CB-CG	7.90	129.89	114.10
1	L	163	THR	CA-CB-CG2	7.71	123.62	110.50
2	H	84	SER	N-CA-C	7.71	122.94	112.68
2	H	86	VAL	N-CA-CB	-7.58	100.05	110.05
2	H	147	HIS	N-CA-C	7.51	121.69	109.59
2	H	185	ASN	CB-CA-C	7.51	124.23	109.35
2	H	98	ARG	CD-NE-CZ	7.47	134.85	124.40
2	H	131	LEU	CA-CB-CG	7.42	142.29	116.30
2	H	110	GLN	CB-CG-CD	7.40	125.18	112.60
1	L	164	ASP	O-C-N	-7.39	114.14	122.86
1	L	1	GLU	CB-CG-CD	7.38	125.14	112.60
2	H	131	LEU	CB-CA-C	7.33	119.92	108.84
1	L	107	ARG	CD-NE-CZ	7.23	134.52	124.40
1	L	75	ASN	CA-CB-CG	-7.20	105.40	112.60
1	L	107	ARG	N-CA-CB	-7.16	99.91	111.22
2	H	158	THR	CA-CB-CG2	7.14	122.64	110.50
1	L	198	LYS	CA-CB-CG	6.92	127.93	114.10
1	L	38	LYS	CA-C-N	6.91	134.73	121.54
1	L	38	LYS	C-N-CA	6.91	134.73	121.54
1	L	121	SER	CA-C-N	6.88	129.38	120.44
1	L	121	SER	C-N-CA	6.88	129.38	120.44
1	L	187	ARG	CD-NE-CZ	6.84	133.97	124.40
2	H	74	ASN	N-CA-CB	6.83	122.03	110.49
2	H	192	VAL	CA-CB-CG1	6.83	122.00	110.40
2	H	89	GLU	CA-CB-CG	6.82	127.73	114.10
2	H	13	GLN	CB-CG-CD	6.81	124.18	112.60
2	H	137	SER	CA-C-N	6.76	138.31	121.80
2	H	137	SER	C-N-CA	6.76	138.31	121.80
1	L	60	ARG	CD-NE-CZ	6.76	133.86	124.40
2	H	156	ASN	CA-CB-CG	6.75	119.35	112.60
1	L	15	LEU	CB-CA-C	6.75	120.69	109.89
2	H	52	HIS	CA-CB-CG	6.71	120.52	113.80
2	H	31	LYS	CA-CB-CG	6.70	127.50	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	196	GLU	CB-CG-CD	6.67	123.94	112.60
2	H	122	ARG	CD-NE-CZ	6.66	133.72	124.40
2	H	118	ALA	CA-C-N	6.64	130.24	120.95
2	H	118	ALA	C-N-CA	6.64	130.24	120.95
2	H	27	PHE	CA-CB-CG	6.60	120.40	113.80
1	L	81	ASP	CA-CB-CG	6.57	119.17	112.60
1	L	125	THR	CA-CB-CG2	6.52	121.58	110.50
1	L	116	ILE	CB-CG1-CD1	6.51	127.48	113.80
1	L	44	LYS	CA-CB-CG	6.49	127.09	114.10
2	H	180	ARG	NE-CZ-NH1	6.44	127.94	121.50
2	H	54	ASP	CB-CA-C	6.41	122.13	111.23
2	H	205	GLN	CB-CG-CD	6.39	123.47	112.60
1	L	17	GLN	CA-CB-CG	6.38	126.85	114.10
1	L	97	PHE	CA-CB-CG	6.37	120.17	113.80
2	H	57	THR	O-C-N	6.34	130.62	123.27
2	H	86	VAL	CA-CB-CG1	6.33	121.15	110.40
2	H	125	THR	N-CA-CB	6.23	120.35	110.57
1	L	116	ILE	CB-CA-C	6.22	119.84	110.63
2	H	207	ASP	CA-CB-CG	6.21	118.81	112.60
2	H	1	GLU	CA-C-N	6.20	128.87	120.63
2	H	1	GLU	C-N-CA	6.20	128.87	120.63
1	L	68	THR	N-CA-CB	-6.19	102.76	111.00
1	L	152	SER	CA-C-O	6.17	128.13	121.16
1	L	179	THR	N-CA-CB	6.14	120.21	110.57
1	L	51	SER	N-CA-CB	-6.14	102.11	110.95
1	L	207	SER	CA-CB-OG	6.08	123.26	111.10
2	H	191	ALA	CA-C-N	6.08	130.08	120.47
2	H	191	ALA	C-N-CA	6.08	130.08	120.47
1	L	154	ARG	NE-CZ-NH1	6.03	127.53	121.50
2	H	68	PHE	CA-CB-CG	5.99	119.79	113.80
1	L	205	VAL	CA-CB-CG1	5.92	120.46	110.40
1	L	179	THR	CA-C-O	5.81	126.71	120.38
2	H	87	ARG	CA-CB-CG	5.81	125.71	114.10
2	H	132	PRO	O-C-N	5.80	123.98	121.31
1	L	19	VAL	CA-CB-CG2	5.78	120.22	110.40
1	L	101	THR	CA-CB-CG2	5.77	120.32	110.50
1	L	144	ASN	CA-CB-CG	5.77	118.37	112.60
2	H	29	PHE	CA-CB-CG	5.74	119.54	113.80
1	L	212	GLU	CB-CG-CD	5.73	122.34	112.60
2	H	38	ARG	NE-CZ-NH2	-5.72	114.05	119.20
1	L	163	THR	N-CA-C	-5.71	102.31	110.59
2	H	100	HIS	CB-CG-CD2	5.70	138.61	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	210	ARG	CB-CG-CD	5.68	124.37	111.30
1	L	3	VAL	CA-CB-CG1	5.68	120.05	110.40
1	L	192	THR	CA-CB-CG2	5.66	120.12	110.50
2	H	46	GLU	CA-C-O	5.64	126.22	120.24
1	L	131	VAL	CA-CB-CG2	5.63	119.98	110.40
2	H	73	ASP	CA-C-N	5.63	132.30	121.54
2	H	73	ASP	C-N-CA	5.63	132.30	121.54
2	H	150	PHE	CA-CB-CG	5.63	119.43	113.80
2	H	84	SER	CA-C-O	-5.63	112.25	120.13
2	H	28	ASP	CB-CA-C	5.60	120.82	111.30
2	H	136	SER	O-C-N	-5.59	116.45	122.88
2	H	88	SER	CA-C-O	5.57	126.44	120.20
2	H	64	LEU	CA-C-N	5.52	128.44	120.38
2	H	64	LEU	C-N-CA	5.52	128.44	120.38
2	H	54	ASP	CA-C-N	5.51	132.06	121.54
2	H	54	ASP	C-N-CA	5.51	132.06	121.54
2	H	73	ASP	CB-CA-C	5.51	121.38	110.42
1	L	183	ASP	CA-CB-CG	5.51	118.11	112.60
1	L	44	LYS	CA-C-N	5.50	126.36	119.98
1	L	44	LYS	C-N-CA	5.50	126.36	119.98
2	H	192	VAL	CB-CA-C	5.48	120.66	112.16
1	L	142	ASP	CA-CB-CG	5.47	118.07	112.60
1	L	189	ASN	CA-C-O	-5.46	113.39	119.67
1	L	204	ILE	N-CA-C	-5.45	100.04	107.99
1	L	160	ASN	CA-CB-CG	5.42	118.03	112.60
1	L	211	ASN	CA-CB-CG	5.42	118.02	112.60
1	L	93	PRO	N-CA-CB	-5.42	96.64	102.60
2	H	219	SER	CA-C-N	5.40	131.42	121.70
2	H	219	SER	C-N-CA	5.40	131.42	121.70
1	L	141	LYS	N-CA-C	5.40	117.92	111.71
2	H	50	GLU	CG-CD-OE2	-5.37	106.04	118.40
2	H	184	SER	CA-C-O	5.37	127.29	121.06
1	L	67	GLY	O-C-N	5.37	129.68	122.70
2	H	87	ARG	CD-NE-CZ	5.37	131.92	124.40
1	L	73	THR	CA-CB-CG2	5.36	119.61	110.50
1	L	124	LEU	CA-C-N	5.32	127.41	120.28
1	L	124	LEU	C-N-CA	5.32	127.41	120.28
1	L	171	THR	CB-CA-C	5.31	119.64	110.45
2	H	67	LYS	CA-CB-CG	5.31	124.72	114.10
1	L	184	GLU	CA-CB-CG	5.31	124.71	114.10
2	H	158	THR	CA-CB-OG1	-5.30	101.65	109.60
1	L	212	GLU	CA-C-N	5.28	131.21	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	212	GLU	C-N-CA	5.28	131.21	121.70
1	L	186	GLU	CB-CG-CD	5.28	121.58	112.60
1	L	124	LEU	CB-CA-C	5.27	119.54	110.79
1	L	74	ILE	N-CA-CB	5.26	118.48	111.64
2	H	166	ILE	CB-CA-C	5.25	118.62	110.96
1	L	104	GLU	CB-CG-CD	5.24	121.50	112.60
2	H	140	VAL	CA-CB-CG1	5.22	119.28	110.40
1	L	6	GLN	OE1-CD-NE2	5.22	127.82	122.60
1	L	132	VAL	CA-CB-CG1	5.22	119.27	110.40
1	L	184	GLU	CG-CD-OE1	5.21	130.39	118.40
2	H	157	VAL	CA-C-N	5.21	130.75	122.94
2	H	157	VAL	C-N-CA	5.21	130.75	122.94
2	H	105	ASN	OD1-CG-ND2	-5.20	117.40	122.60
2	H	108	TRP	CA-CB-CG	5.20	123.48	113.60
2	H	77	ASN	CB-CG-ND2	5.19	124.18	116.40
2	H	83	MET	N-CA-CB	5.19	118.69	110.55
2	H	198	GLU	CA-CB-CG	5.19	124.48	114.10
2	H	72	ARG	NE-CZ-NH2	5.17	123.85	119.20
1	L	68	THR	CA-CB-OG1	-5.15	101.87	109.60
1	L	91	THR	N-CA-CB	5.15	119.19	110.79
1	L	10	ILE	N-CA-CB	5.15	118.82	111.82
1	L	63	GLY	CA-C-O	5.15	126.05	121.57
2	H	157	VAL	CA-CB-CG2	5.13	119.13	110.40
2	H	186	GLN	CA-CB-CG	5.13	124.36	114.10
1	L	11	THR	CA-CB-CG2	5.12	119.21	110.50
2	H	53	PRO	CA-C-N	-5.12	115.54	123.17
2	H	53	PRO	C-N-CA	-5.12	115.54	123.17
2	H	74	ASN	OD1-CG-ND2	-5.11	117.49	122.60
1	L	166	ASP	CA-C-O	-5.11	115.10	120.92
1	L	50	ILE	CA-C-O	-5.09	114.42	120.78
2	H	209	ASN	OD1-CG-ND2	-5.08	117.52	122.60
1	L	204	ILE	N-CA-CB	5.07	117.14	111.21
2	H	102	TYR	CA-C-N	5.07	130.24	120.66
2	H	102	TYR	C-N-CA	5.07	130.24	120.66
1	L	212	GLU	CB-CA-C	5.04	120.44	110.42
1	L	169	ASP	CA-C-O	5.03	125.10	119.41
2	H	192	VAL	N-CA-CB	-5.01	102.08	110.65

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	L	1636	0	1579	25	0
2	H	1683	0	1626	13	0
3	A	28	0	23	1	0
4	B	38	0	33	2	0
5	H	1	0	0	0	0
6	H	182	0	0	3	3
6	L	193	0	0	7	4
All	All	3761	0	3261	37	4

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 6.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:18:LYS:HE2	6:L:372:HOH:O	0.90	1.07
2:H:220:GLY:HA3	6:H:398:HOH:O	1.61	1.01
1:L:194:GLU:OE2	6:L:382:HOH:O	1.96	0.84
1:L:150:ASP:OD1	6:L:404:HOH:O	1.96	0.82
1:L:192:THR:HB	1:L:207:SER:HB2	1.65	0.78
1:L:16:GLY:HA2	1:L:76:THR:HG23	1.66	0.78
2:H:83:MET:HE1	2:H:114:VAL:HG21	1.68	0.75
1:L:93:PRO:HG3	3:A:1:NAG:H3	1.72	0.70
2:H:203:SER:HB3	4:B:1:NAG:H81	1.75	0.68
1:L:137:ASN:HD22	1:L:171:THR:HG21	1.62	0.65
1:L:107:ARG:HG3	1:L:170:SER:HB2	1.79	0.64
1:L:79:ALA:HA	1:L:105:LEU:HD13	1.81	0.62
2:H:164:LYS:NZ	6:H:394:HOH:O	2.30	0.61
2:H:159:TRP:HE1	2:H:185:ASN:HD21	1.49	0.60
2:H:220:GLY:CA	6:H:398:HOH:O	2.33	0.60
2:H:124:PRO:HG3	2:H:155:MET:HE1	1.84	0.59
2:H:201:LYS:HE2	2:H:213:GLU:HB3	1.85	0.58
1:L:148:LYS:HB2	1:L:192:THR:HG23	1.87	0.57
2:H:131:LEU:HD12	2:H:135:LEU:HD23	1.88	0.55
1:L:149:ILE:HD11	1:L:178:LEU:HD21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:159:TRP:HE1	2:H:185:ASN:ND2	2.04	0.55
1:L:212:GLU:HG2	1:L:213:CYS:H	1.72	0.55
2:H:211:VAL:HG11	4:B:1:NAG:H82	1.88	0.54
1:L:132:VAL:HG22	1:L:177:THR:HG23	1.91	0.53
2:H:34:MET:HB3	2:H:79:LEU:HD22	1.92	0.51
1:L:8:PRO:HA	6:L:392:HOH:O	2.12	0.50
1:L:43:PRO:HG2	2:H:45:LEU:HD11	1.95	0.49
1:L:46:TRP:HH2	6:L:374:HOH:O	1.97	0.48
1:L:137:ASN:HD22	1:L:171:THR:CG2	2.27	0.46
1:L:77:MET:HG3	1:L:105:LEU:HD12	2.00	0.43
1:L:44:LYS:HA	1:L:45:PRO:HD3	1.85	0.43
1:L:116:ILE:HD12	1:L:208:PHE:CD1	2.54	0.43
1:L:202:SER:HA	1:L:203:PRO:HD3	1.83	0.42
1:L:164:ASP:HB2	6:L:379:HOH:O	2.19	0.42
1:L:92:TYR:HA	1:L:93:PRO:HA	1.94	0.41
1:L:160:ASN:HB3	1:L:174:MET:HE3	2.04	0.40
1:L:154:ARG:HD2	6:L:255:HOH:O	2.21	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:406:HOH:O	6:H:402:HOH:O[3_545]	1.37	0.83
6:L:404:HOH:O	6:L:405:HOH:O[4_545]	1.42	0.78
6:L:400:HOH:O	6:H:404:HOH:O[3_545]	1.69	0.51
6:L:401:HOH:O	6:H:403:HOH:O[3_545]	2.09	0.11

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	L	211/213 (99%)	202 (96%)	8 (4%)	1 (0%)	24 16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	218/220 (99%)	202 (93%)	11 (5%)	5 (2%)	5	1
All	All	429/433 (99%)	404 (94%)	19 (4%)	6 (1%)	9	3

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	39	SER
2	H	74	ASN
2	H	137	SER
2	H	176	ALA
2	H	135	LEU
2	H	138	ASP

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	L	186/186 (100%)	160 (86%)	26 (14%)	3	0
2	H	186/186 (100%)	158 (85%)	28 (15%)	3	0
All	All	372/372 (100%)	318 (86%)	54 (14%)	3	0

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	19	VAL
1	L	28	SER
1	L	32	LEU
1	L	39	SER
1	L	44	LYS
1	L	68	THR
1	L	75	ASN
1	L	89	GLN
1	L	105	LEU
1	L	106	LYS

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Mol	Chain	Res	Type
1	L	107	ARG
1	L	115	SER
1	L	116	ILE
1	L	120	SER
1	L	124	LEU
1	L	144	ASN
1	L	161	SER
1	L	163	THR
1	L	164	ASP
1	L	171	THR
1	L	192	THR
1	L	198	LYS
1	L	206	LYS
1	L	207	SER
1	L	210	ARG
1	L	212	GLU
2	H	4	LEU
2	H	5	LEU
2	H	31	LYS
2	H	43	LYS
2	H	45	LEU
2	H	65	LYS
2	H	67	LYS
2	H	78	SER
2	H	86	VAL
2	H	89	GLU
2	H	93	LEU
2	H	98	ARG
2	H	110	GLN
2	H	113	LEU
2	H	131	LEU
2	H	133	PRO
2	H	135	LEU
2	H	136	SER
2	H	137	SER
2	H	148	ASP
2	H	157	VAL
2	H	162	SER
2	H	164	LYS
2	H	165	ASP
2	H	185	ASN
2	H	192	VAL

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Mol	Chain	Res	Type
2	H	198	GLU
2	H	211	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	36	GLN
1	L	137	ASN
1	L	156	ASN
1	L	209	ASN
2	H	105	ASN
2	H	110	GLN
2	H	147	HIS
2	H	185	ASN
2	H	212	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](#)

5 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	$\# Z > 2$
3	NAG	A	1	3,2	14,14,15	0.95	0	17,19,21	5.05	9 (52%)
3	NAG	A	2	3	14,14,15	0.97	0	17,19,21	5.53	6 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1	2,4	14,14,15	0.98	0	17,19,21	3.83	7 (41%)
4	NAG	B	2	4	14,14,15	0.93	0	17,19,21	5.75	7 (41%)
4	FUC	B	3	4	10,10,11	0.87	0	14,14,16	1.25	1 (7%)

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	NAG	A	1	3,2	-	4/6/23/26	0/1/1/1
3	NAG	A	2	3	-	6/6/23/26	0/1/1/1
4	NAG	B	1	2,4	-	4/6/23/26	0/1/1/1
4	NAG	B	2	4	-	5/6/23/26	0/1/1/1
4	FUC	B	3	4	2/2/4/5	-	0/1/1/1

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	NAG	C2-N2-C7	18.16	147.24	122.90
3	A	1	NAG	C2-N2-C7	17.96	146.97	122.90
4	B	2	NAG	C2-N2-C7	17.53	146.39	122.90
4	B	2	NAG	C1-O5-C5	14.33	131.38	112.19
4	B	1	NAG	C1-O5-C5	11.35	127.40	112.19
3	A	2	NAG	C1-O5-C5	10.99	126.92	112.19
4	B	1	NAG	C4-C3-C2	-8.15	99.07	111.02
3	A	1	NAG	C1-O5-C5	7.76	122.59	112.19
3	A	2	NAG	C4-C3-C2	-4.87	103.88	111.02
4	B	2	NAG	C4-C3-C2	-4.62	104.24	111.02
3	A	2	NAG	O5-C5-C6	4.08	115.61	107.66
4	B	3	FUC	C1-O5-C5	3.42	121.04	112.97
4	B	1	NAG	O4-C4-C3	3.40	118.38	110.38
4	B	1	NAG	O5-C1-C2	-3.36	106.10	111.29
3	A	1	NAG	C4-C3-C2	-3.36	106.10	111.02
3	A	2	NAG	O4-C4-C3	3.15	117.81	110.38
3	A	1	NAG	C6-C5-C4	-3.12	105.36	113.02
4	B	2	NAG	O4-C4-C3	2.72	116.79	110.38
4	B	1	NAG	O3-C3-C4	2.68	116.69	110.38
4	B	1	NAG	C3-C4-C5	-2.65	105.43	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	NAG	O4-C4-C5	-2.43	103.34	109.32
4	B	2	NAG	C3-C4-C5	-2.39	105.89	110.23
3	A	1	NAG	O7-C7-C8	-2.31	117.93	122.05
3	A	1	NAG	O5-C1-C2	-2.29	107.74	111.29
4	B	2	NAG	O5-C5-C6	2.18	111.91	107.66
4	B	2	NAG	O3-C3-C4	2.10	115.33	110.38
3	A	1	NAG	O4-C4-C3	2.07	115.27	110.38
3	A	1	NAG	O5-C5-C6	2.07	111.69	107.66
3	A	1	NAG	C1-C2-N2	2.06	113.68	110.43
4	B	1	NAG	O7-C7-N2	2.02	125.55	121.98

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	3	FUC	C5
4	B	3	FUC	C1

All (19) torsion outliers are listed below:

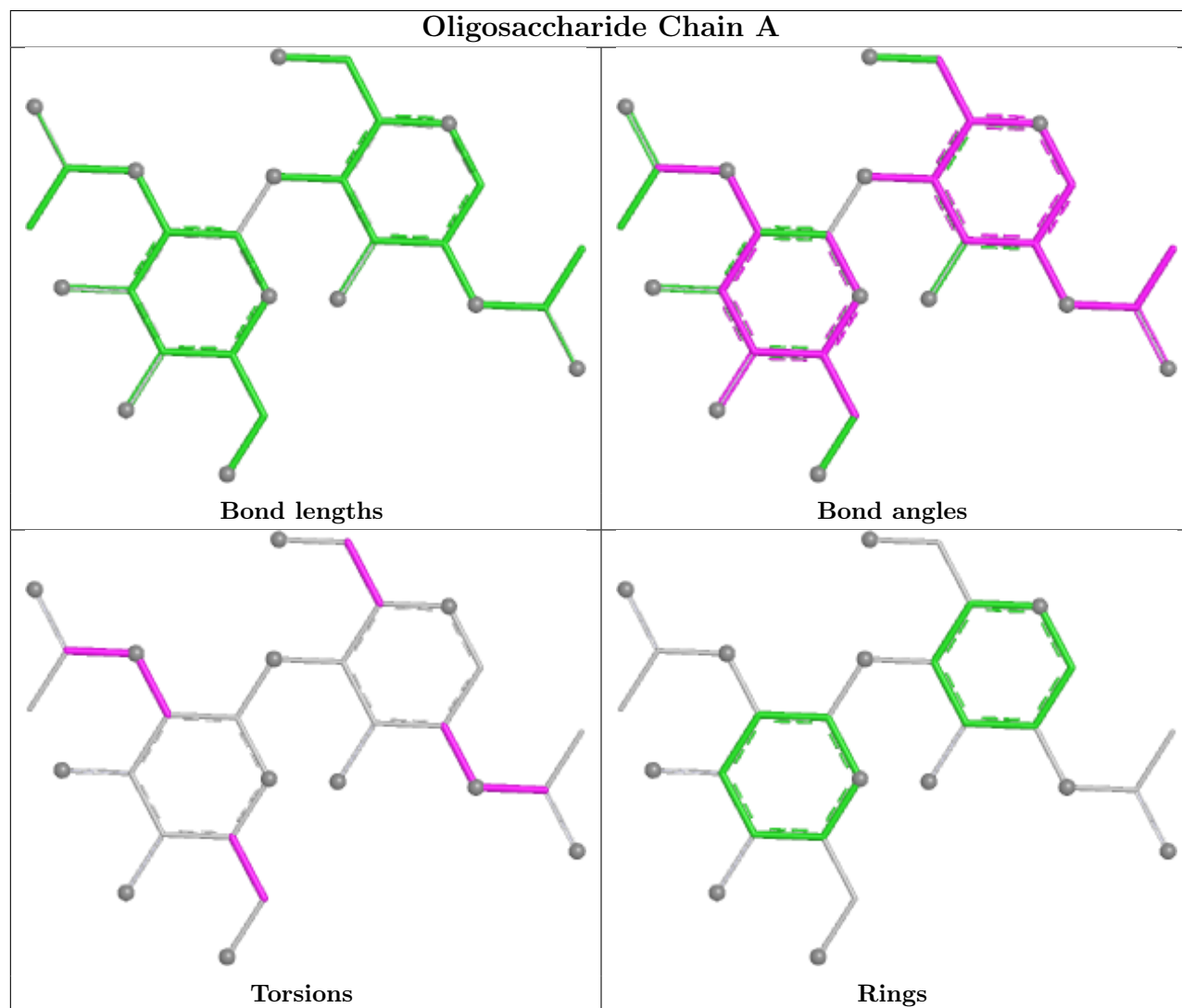
Mol	Chain	Res	Type	Atoms
3	A	2	NAG	C8-C7-N2-C2
3	A	2	NAG	O7-C7-N2-C2
4	B	1	NAG	C8-C7-N2-C2
4	B	1	NAG	O7-C7-N2-C2
4	B	2	NAG	C8-C7-N2-C2
4	B	2	NAG	O7-C7-N2-C2
3	A	1	NAG	O5-C5-C6-O6
4	B	1	NAG	O5-C5-C6-O6
4	B	1	NAG	C4-C5-C6-O6
3	A	1	NAG	O7-C7-N2-C2
3	A	1	NAG	C4-C5-C6-O6
3	A	2	NAG	C4-C5-C6-O6
4	B	2	NAG	C4-C5-C6-O6
4	B	2	NAG	C3-C2-N2-C7
3	A	2	NAG	O5-C5-C6-O6
3	A	1	NAG	C3-C2-N2-C7
4	B	2	NAG	O5-C5-C6-O6
3	A	2	NAG	C1-C2-N2-C7
3	A	2	NAG	C3-C2-N2-C7

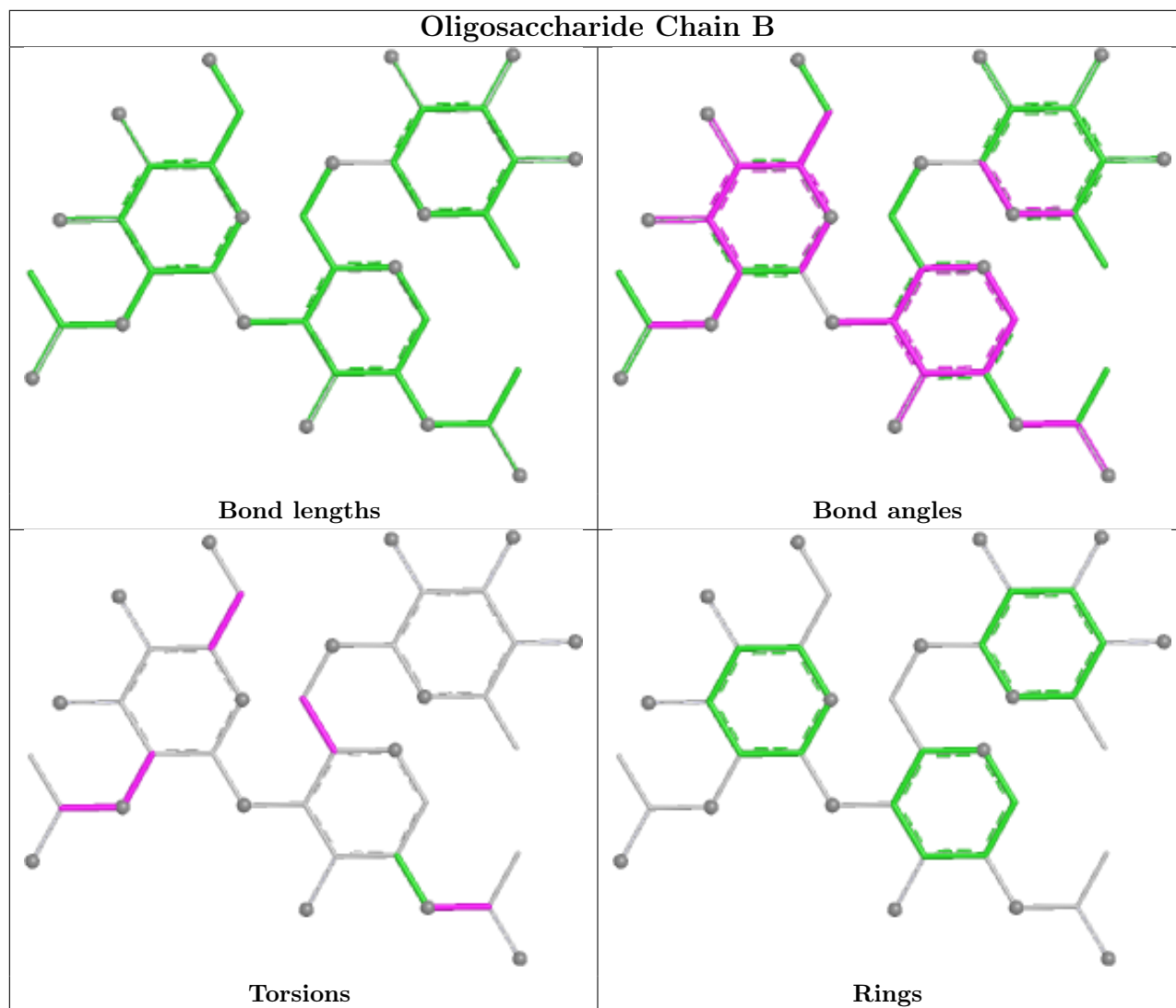
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1	NAG	2	0
3	A	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

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

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	L	213/213 (100%)	-0.28	5 (2%) 61 68	13, 25, 44, 73	0
2	H	220/220 (100%)	-0.23	4 (1%) 67 75	13, 24, 48, 55	0
All	All	433/433 (100%)	-0.26	9 (2%) 63 70	13, 24, 46, 73	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	213	CYS	4.1
1	L	65	GLY	2.7
1	L	211	ASN	2.4
2	H	179	GLY	2.3
2	H	134	ALA	2.2
1	L	167	SER	2.2
2	H	220	GLY	2.1
1	L	210	ARG	2.1
2	H	137	SER	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.

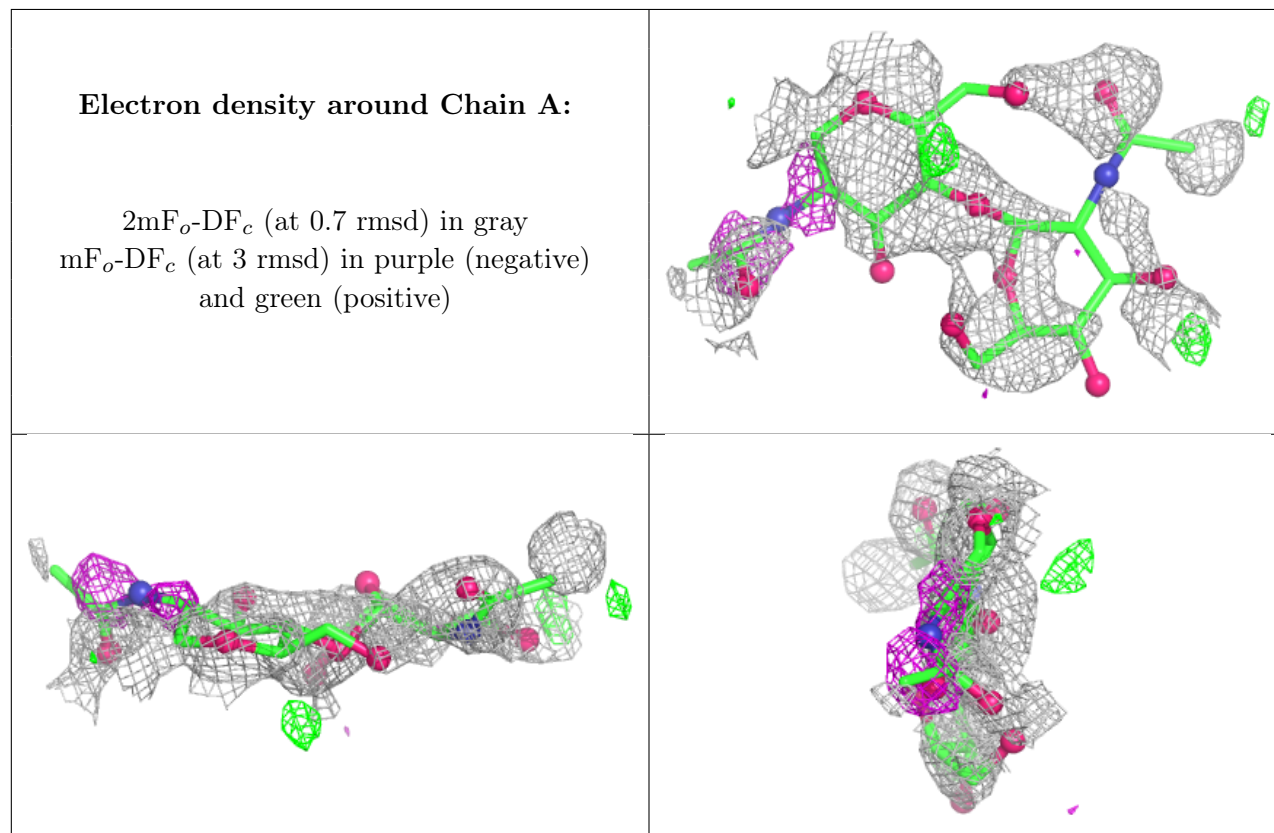
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	A	1	14/15	-	-	42,51,52,56	0

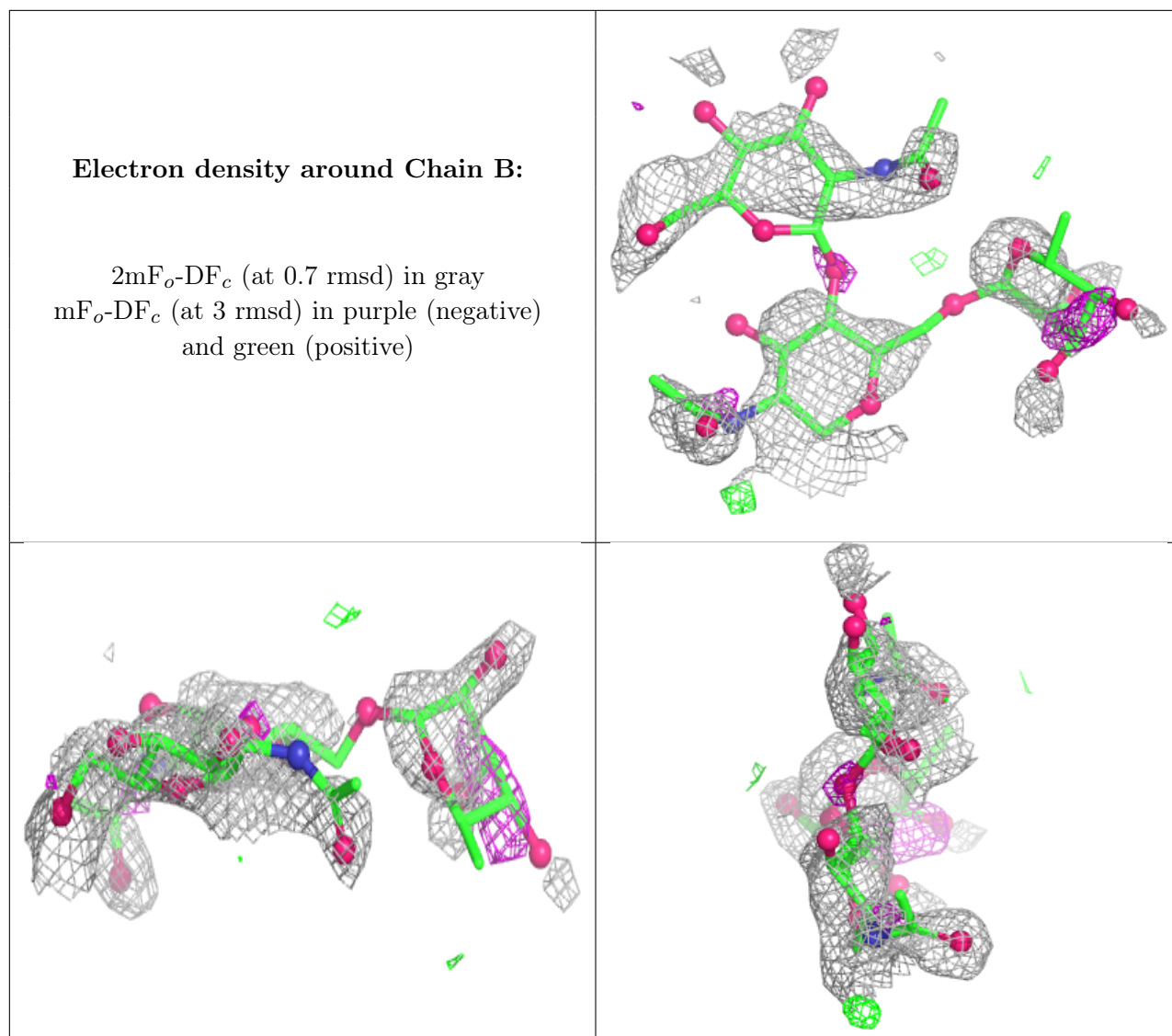
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	A	2	14/15	-	-	60,62,63,64	0
4	NAG	B	1	14/15	-	-	56,59,64,65	0
4	NAG	B	2	14/15	-	-	65,66,68,68	0
4	FUC	B	3	10/11	-	-	65,65,66,67	0

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(\AA^2)	Q<0.9
5	ZN	H	226	1/1	0.98	0.02	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.