



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:26 PM UTC

PDB ID : 2B4C / pdb_00002b4c
Title : Crystal structure of HIV-1 JR-FL gp120 core protein containing the third variable region (V3) complexed with CD4 and the X5 antibody
Authors : Huang, C.; Tang, M.; Zhang, M.Y.; Majeed, S.; Montabana, E.; Stanfield, R.L.; Dimitrov, D.S.; Korber, B.; Sodroski, J.; Wilson, I.A.; Wyatt, R.; Kwong, P.D.
Deposited on : 2005-09-23
Resolution : 3.30 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

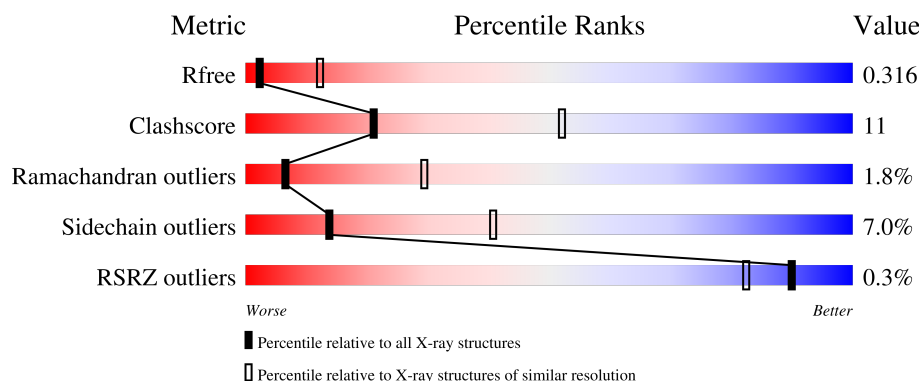
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

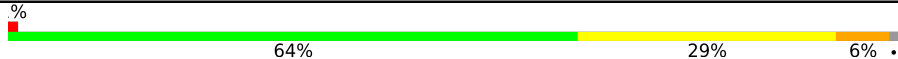
The reported resolution of this entry is 3.30 Å.

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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	G	344	
2	C	181	
3	L	215	
4	H	235	

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Mol	Chain	Length	Quality of chain
5	A	2	 100%

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
5	NAG	A	1	X	-	-	-
6	NAG	G	832	X	-	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7543 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 envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	339	Total	C	N	O	S	0	4	0
			2681	1674	477	509	21			

- Molecule 2 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	175	Total	C	N	O	S	0	0	0
			1363	851	239	269	4			

- Molecule 3 is a protein called anti-HIV-1 gp120 immunoglobulin X5 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	215	Total	C	N	O	S	0	0	0
			1636	1018	280	333	5			

- Molecule 4 is a protein called anti-HIV-1 gp120 immunoglobulin X5 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	233	Total	C	N	O	S	0	0	0
			1742	1098	290	346	8			

- Molecule 5 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



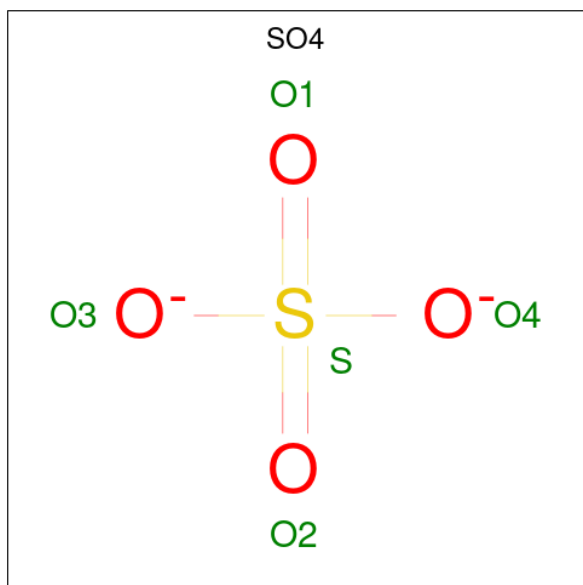
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	A	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



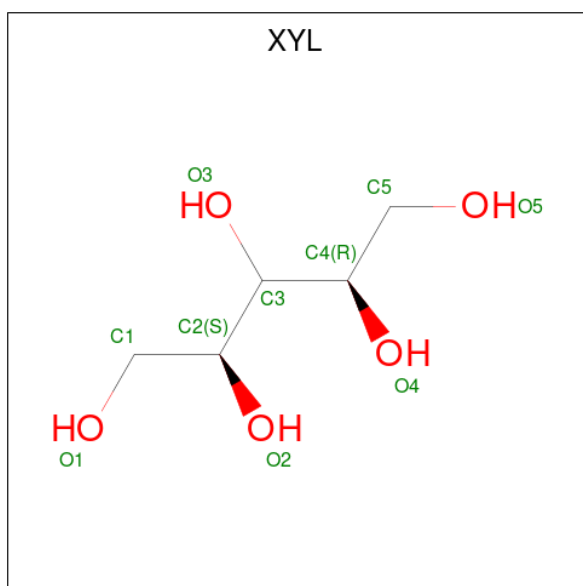
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	G	1	Total	C	N	O	0	0
			14	8	1	5		
6	G	1	Total	C	N	O	0	0
			14	8	1	5		
6	G	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	G	1	Total O S 5 4 1	0	0
7	L	1	Total O S 5 4 1	0	0
7	H	1	Total O S 5 4 1	0	0
7	H	1	Total O S 5 4 1	0	0
7	H	1	Total O S 5 4 1	0	0

- Molecule 8 is Xylitol (CCD ID: XYL) (formula: $C_5H_{12}O_5$).

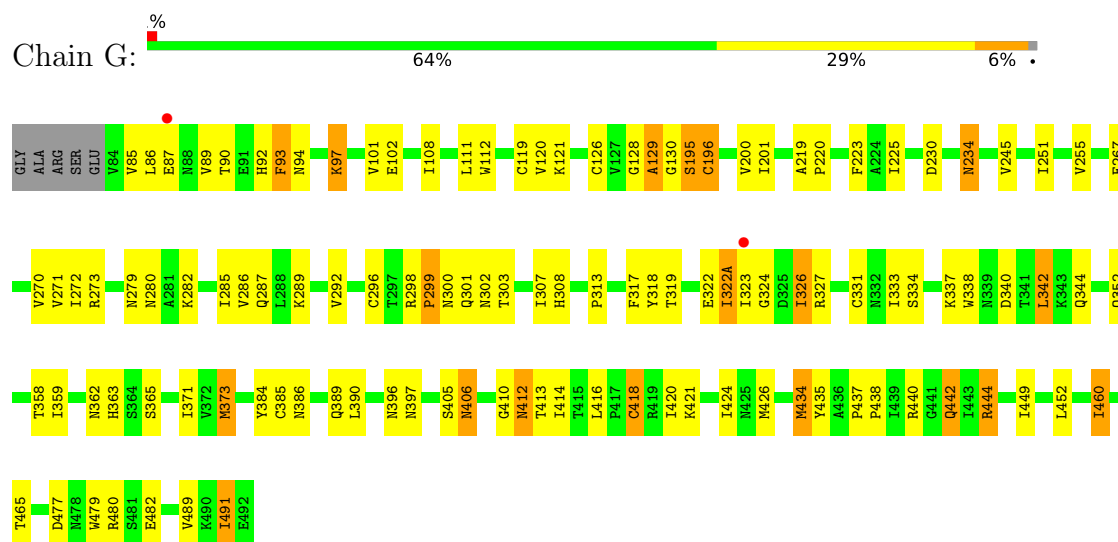


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	H	1	Total C O 10 5 5	0	0
8	H	1	Total C O 10 5 5	0	0
8	H	1	Total C O 10 5 5	0	0

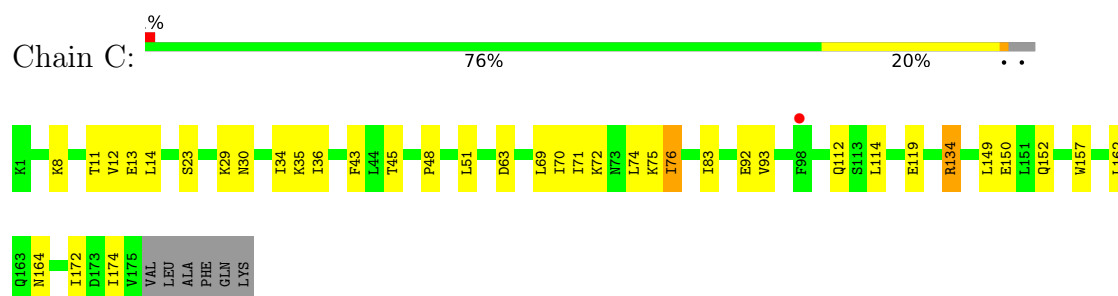
3 Residue-property plots

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.

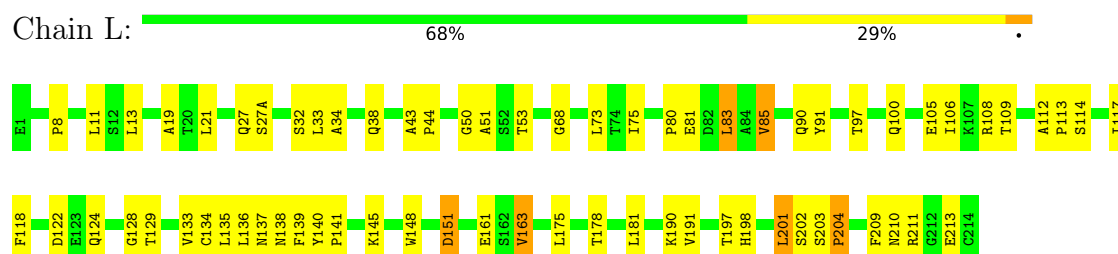
- Molecule 1: envelope glycoprotein



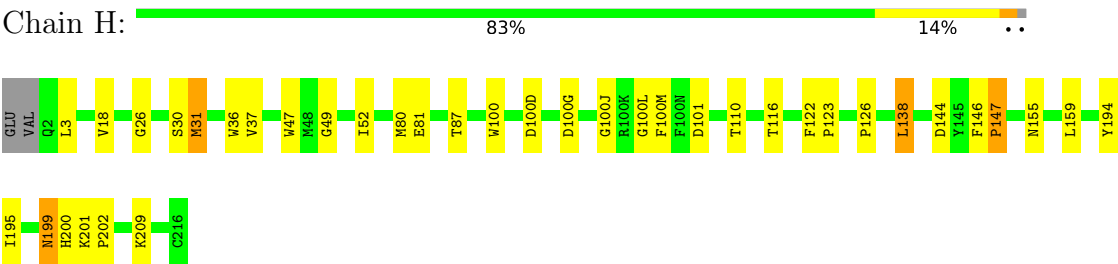
- Molecule 2: T-cell surface glycoprotein CD4



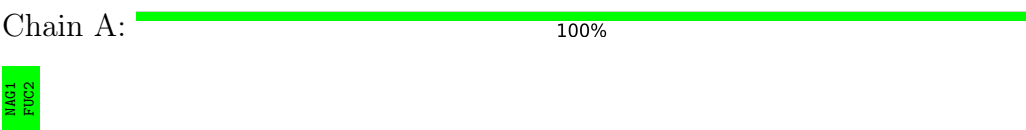
- Molecule 3: anti-HIV-1 gp120 immunoglobulin X5 light chain



- Molecule 4: anti-HIV-1 gp120 immunoglobulin X5 heavy chain



- Molecule 5: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 6 2 2	Depositor
Cell constants a, b, c, α , β , γ	225.99Å 225.99Å 97.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.30 20.00 – 3.31	Depositor EDS
% Data completeness (in resolution range)	86.2 (20.00-3.30) 85.7 (20.00-3.31)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 3.29Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.319 , 0.349 0.285 , 0.316	Depositor DCC
R_{free} test set	1928 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å ²)	134.8	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 57.2	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	0.91	EDS
Total number of atoms	7543	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% 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: FUC, NAG, SO4, XYL

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	G	0.41	1/2734 (0.0%)	0.83	0/3701
2	C	0.31	0/1382	0.80	1/1863 (0.1%)
3	L	0.32	0/1669	0.80	2/2264 (0.1%)
4	H	0.32	0/1788	0.85	2/2432 (0.1%)
All	All	0.35	1/7573 (0.0%)	0.82	5/10260 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	87	GLU	C-N	-12.24	1.17	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	100	TRP	N-CA-C	6.10	118.01	111.36
2	C	36	ILE	CB-CA-C	-5.56	106.98	111.71
3	L	118	PHE	CA-C-N	5.32	123.49	119.66
3	L	118	PHE	C-N-CA	5.32	123.49	119.66
4	H	30	SER	N-CA-C	5.31	117.50	111.02

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	G	2681	0	2629	84	0
2	C	1363	0	1389	29	0
3	L	1636	0	1591	38	0
4	H	1742	0	1662	23	0
5	A	24	0	22	0	0
6	G	42	0	39	0	0
7	G	5	0	0	0	0
7	H	15	0	0	0	0
7	L	5	0	0	0	0
8	H	30	0	36	0	0
All	All	7543	0	7368	164	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 11.

All (164) 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:G:326:ILE:H	1:G:326:ILE:HD13	1.35	0.92
4:H:126:PRO:HG3	4:H:138:LEU:HB3	1.52	0.91
1:G:371:ILE:HD13	2:C:45:THR:HG22	1.53	0.90
2:C:76:ILE:HD12	2:C:76:ILE:H	1.35	0.90
3:L:198:HIS:HB3	3:L:201:LEU:HB3	1.66	0.78
1:G:300:ASN:HD21	1:G:302:ASN:ND2	1.84	0.76
3:L:163:VAL:HG22	3:L:175:LEU:HD13	1.70	0.74
1:G:358:THR:HG23	1:G:396:ASN:HB3	1.70	0.73
1:G:371:ILE:HD11	2:C:43:PHE:HB3	1.71	0.72
1:G:85:VAL:C	1:G:86:LEU:HD12	2.15	0.71
1:G:251:ILE:HD12	1:G:482:GLU:HB3	1.72	0.71
1:G:491:ILE:O	1:G:491:ILE:HG23	1.93	0.68
3:L:90:GLN:HE21	3:L:97:THR:H	1.42	0.68
2:C:29:LYS:HB2	2:C:83:ILE:HD11	1.74	0.68
1:G:272:ILE:HD12	1:G:272:ILE:O	1.93	0.68
1:G:460:ILE:HD13	1:G:460:ILE:O	1.94	0.68
1:G:327:ARG:HH22	4:H:100(G):ASP:HB2	1.59	0.67
1:G:94:ASN:HD22	1:G:97:LYS:H	1.44	0.66
4:H:37:VAL:HG12	4:H:47:TRP:HA	1.78	0.66
1:G:327:ARG:NH2	4:H:100(G):ASP:HB2	2.10	0.66
1:G:300:ASN:HB3	1:G:442:GLN:CB	2.26	0.65
3:L:80:PRO:HA	3:L:106:ILE:HD13	1.77	0.65
3:L:135:LEU:HD23	3:L:136:LEU:N	2.11	0.65
1:G:279:ASN:HD22	1:G:282:LYS:HG2	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:51:LEU:HD23	2:C:71:ILE:HD12	1.79	0.64
1:G:120:VAL:HB	1:G:434:MET:HB3	1.81	0.63
3:L:108:ARG:HG2	3:L:109:THR:H	1.64	0.63
1:G:225:ILE:CD1	1:G:245:VAL:HG23	2.29	0.63
2:C:76:ILE:H	2:C:76:ILE:CD1	2.11	0.62
3:L:198:HIS:HB3	3:L:201:LEU:CB	2.28	0.62
1:G:300:ASN:HB3	1:G:442:GLN:HB2	1.81	0.61
2:C:83:ILE:HG22	2:C:92:GLU:HG2	1.83	0.60
2:C:76:ILE:HD12	2:C:76:ILE:N	2.12	0.60
1:G:371:ILE:HD13	2:C:45:THR:CG2	2.28	0.59
4:H:195:ILE:HD12	4:H:195:ILE:N	2.18	0.59
1:G:359:ILE:HD12	1:G:359:ILE:N	2.18	0.59
1:G:225:ILE:HD11	1:G:245:VAL:HG23	1.85	0.58
1:G:108:ILE:HD13	1:G:479:TRP:CE2	2.39	0.58
1:G:389:GLN:HE21	1:G:416:LEU:HD13	1.68	0.57
1:G:200:VAL:C	1:G:201:ILE:HD12	2.30	0.57
1:G:389:GLN:NE2	1:G:414:ILE:HG13	2.19	0.57
3:L:83:LEU:HD12	3:L:105:GLU:HA	1.89	0.55
1:G:94:ASN:ND2	1:G:97:LYS:H	2.04	0.55
2:C:74:LEU:HD13	2:C:75:LYS:N	2.22	0.55
1:G:334:SER:HB2	1:G:337:LYS:HB2	1.87	0.54
1:G:410:GLY:O	1:G:412:ASN:C	2.50	0.54
3:L:140:TYR:HB3	3:L:141:PRO:HD3	1.88	0.54
1:G:424:ILE:HD12	1:G:435:TYR:CD1	2.41	0.54
1:G:442:GLN:NE2	1:G:444:ARG:HH11	2.05	0.54
2:C:23:SER:HB3	2:C:63:ASP:HA	1.88	0.54
1:G:326:ILE:H	1:G:326:ILE:CD1	2.14	0.54
2:C:14:LEU:HB2	2:C:69:LEU:HB3	1.90	0.53
3:L:114:SER:OG	3:L:137:ASN:HB3	2.08	0.53
3:L:11:LEU:HG	3:L:13:LEU:HD13	1.91	0.53
4:H:37:VAL:HG23	4:H:37:VAL:O	2.08	0.53
3:L:134:CYS:HB2	3:L:148:TRP:CZ2	2.44	0.52
3:L:190:LYS:HA	3:L:211:ARG:HG2	1.91	0.52
1:G:121:LYS:HE2	1:G:426:MET:HE1	1.91	0.52
2:C:30:ASN:HD21	2:C:34:ILE:HB	1.75	0.52
3:L:151:ASP:HA	3:L:191:VAL:HB	1.92	0.52
2:C:8:LYS:HA	2:C:74:LEU:HD12	1.92	0.52
2:C:83:ILE:HD12	2:C:83:ILE:C	2.35	0.51
1:G:234:ASN:HD22	1:G:234:ASN:H	1.59	0.51
2:C:70:ILE:O	2:C:71:ILE:HD13	2.10	0.51
3:L:135:LEU:C	3:L:136:LEU:HD12	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:161:GLU:HB2	3:L:175:LEU:HD11	1.93	0.51
2:C:14:LEU:HD12	2:C:69:LEU:HD12	1.93	0.51
1:G:442:GLN:HE22	1:G:444:ARG:HH11	1.59	0.50
1:G:126:CYS:HA	1:G:196:CYS:HB3	1.93	0.50
3:L:19:ALA:HB3	3:L:75:ILE:HB	1.93	0.50
2:C:157:TRP:HB2	2:C:172:ILE:HG13	1.93	0.50
3:L:38:GLN:HB3	3:L:85:VAL:HG23	1.93	0.50
1:G:390:LEU:HG	1:G:416:LEU:HD11	1.93	0.50
1:G:85:VAL:HG22	1:G:86:LEU:N	2.27	0.49
4:H:47:TRP:CZ2	4:H:49:GLY:HA2	2.47	0.49
1:G:89:VAL:HG22	1:G:90:THR:N	2.27	0.49
1:G:128:GLY:O	1:G:129:ALA:C	2.55	0.49
1:G:405:SER:O	1:G:406:ASN:HB2	2.11	0.49
1:G:365:SER:HB3	2:C:48:PRO:HG3	1.93	0.49
4:H:87:THR:HG23	4:H:110:THR:HA	1.95	0.49
1:G:420:ILE:HD12	1:G:420:ILE:N	2.28	0.49
1:G:385:CYS:N	1:G:418:CYS:SG	2.85	0.48
3:L:32:SER:HB2	3:L:91:TYR:CE2	2.49	0.48
1:G:412:ASN:OD1	1:G:413:THR:HG23	2.13	0.48
3:L:145:LYS:HB2	3:L:197:THR:HB	1.95	0.48
4:H:194:TYR:C	4:H:195:ILE:HD12	2.38	0.48
1:G:317:PHE:HB3	1:G:318:TYR:CD1	2.49	0.47
1:G:322(A):ILE:HG13	1:G:322(A):ILE:O	2.14	0.47
1:G:442:GLN:HE22	1:G:444:ARG:NH1	2.11	0.47
2:C:157:TRP:CE2	2:C:174:ILE:HD12	2.49	0.47
1:G:421:LYS:HD3	4:H:100(D):ASP:CG	2.39	0.47
1:G:130:GLY:O	1:G:195:SER:C	2.57	0.47
1:G:319:THR:HG22	1:G:319:THR:O	2.14	0.47
1:G:201:ILE:HD12	1:G:201:ILE:N	2.29	0.47
2:C:114:LEU:HB2	2:C:149:LEU:HD11	1.96	0.47
1:G:129:ALA:O	1:G:130:GLY:C	2.58	0.47
1:G:219:ALA:HA	1:G:220:PRO:HD3	1.82	0.47
1:G:331:CYS:SG	1:G:385:CYS:SG	3.12	0.47
3:L:91:TYR:HB2	4:H:100(L):GLY:HA3	1.97	0.46
4:H:36:TRP:CE2	4:H:80:MET:HB2	2.50	0.46
1:G:108:ILE:HD13	1:G:479:TRP:CZ2	2.50	0.46
3:L:136:LEU:HD22	3:L:175:LEU:HD23	1.97	0.46
3:L:190:LYS:HG2	3:L:211:ARG:HE	1.80	0.46
3:L:190:LYS:HE2	3:L:211:ARG:HH21	1.81	0.46
1:G:307:ILE:HG22	1:G:308:HIS:N	2.30	0.46
3:L:33:LEU:HD13	3:L:34:ALA:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:86:LEU:HD12	1:G:86:LEU:N	2.32	0.45
3:L:21:LEU:HD12	3:L:73:LEU:HD23	1.99	0.45
4:H:155:ASN:HD22	4:H:159:LEU:HB2	1.82	0.45
4:H:201:LYS:N	4:H:202:PRO:CD	2.80	0.45
1:G:292:VAL:HB	1:G:449:ILE:HB	1.98	0.44
3:L:112:ALA:HA	3:L:113:PRO:HD3	1.81	0.44
1:G:101:VAL:HG11	1:G:480:ARG:HG3	1.99	0.44
4:H:199:ASN:HD22	4:H:200:HIS:N	2.14	0.44
1:G:285:ILE:HD12	1:G:285:ILE:N	2.33	0.44
2:C:134:ARG:H	2:C:134:ARG:HG2	1.72	0.44
4:H:200:HIS:CE1	4:H:202:PRO:HB2	2.52	0.44
1:G:322(A):ILE:O	1:G:324:GLY:N	2.51	0.44
4:H:52:ILE:HD11	4:H:100(J):GLY:N	2.33	0.43
1:G:307:ILE:HG23	1:G:317:PHE:O	2.17	0.43
3:L:8:PRO:HG3	3:L:11:LEU:HD13	2.00	0.43
3:L:117:ILE:HD13	3:L:209:PHE:HD2	1.84	0.43
3:L:133:VAL:HG22	3:L:178:THR:HG22	2.01	0.43
1:G:272:ILE:HG22	1:G:286:VAL:HG22	2.00	0.43
3:L:113:PRO:HB3	3:L:139:PHE:CD1	2.54	0.43
1:G:90:THR:HG23	1:G:90:THR:O	2.18	0.43
1:G:301:GLN:C	1:G:303:THR:H	2.27	0.43
1:G:338:TRP:O	1:G:342:LEU:HB2	2.19	0.43
2:C:74:LEU:HD13	2:C:74:LEU:C	2.44	0.43
3:L:32:SER:HB2	3:L:91:TYR:CZ	2.53	0.43
1:G:225:ILE:HD12	1:G:225:ILE:O	2.18	0.43
1:G:362:ASN:OD1	1:G:363:HIS:N	2.51	0.43
3:L:203:SER:HA	3:L:204:PRO:HD3	1.92	0.43
1:G:128:GLY:O	1:G:130:GLY:N	2.52	0.42
4:H:122:PHE:HA	4:H:123:PRO:HD3	1.80	0.42
1:G:296:CYS:HA	1:G:331:CYS:HA	2.01	0.42
2:C:93:VAL:O	2:C:93:VAL:HG13	2.20	0.42
3:L:124:GLN:HE21	3:L:124:GLN:HB3	1.67	0.42
1:G:326:ILE:HD13	1:G:326:ILE:N	2.17	0.41
1:G:477:ASP:HA	1:G:480:ARG:HB2	2.01	0.41
2:C:11:THR:HG22	2:C:72:LYS:HA	2.02	0.41
2:C:12:VAL:HG22	2:C:13:GLU:N	2.35	0.41
4:H:100(M):PHE:CD2	4:H:100(M):PHE:N	2.88	0.41
1:G:92:HIS:O	1:G:93:PHE:HD1	2.03	0.41
3:L:50:GLY:O	3:L:51:ALA:HB3	2.19	0.41
1:G:373:MET:HE3	1:G:384:TYR:HB3	2.02	0.41
2:C:157:TRP:CD1	2:C:174:ILE:HD12	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:101:ASP:OD2	4:H:101:ASP:N	2.49	0.41
1:G:358:THR:HB	1:G:465:THR:HG22	2.02	0.41
1:G:386:ASN:O	1:G:416:LEU:HD12	2.20	0.41
3:L:210:ASN:HB2	3:L:213:GLU:HG3	2.03	0.41
1:G:251:ILE:CD1	1:G:482:GLU:HB3	2.45	0.41
1:G:437:PRO:HA	1:G:438:PRO:HD3	1.96	0.41
3:L:43:ALA:HA	3:L:44:PRO:HD3	1.97	0.41
4:H:146:PHE:HA	4:H:147:PRO:HA	1.74	0.41
2:C:13:GLU:HG3	2:C:70:ILE:HG22	2.03	0.40
4:H:18:VAL:O	4:H:81:GLU:HA	2.21	0.40
1:G:120:VAL:HG11	4:H:31:MET:HE2	2.03	0.40
1:G:298:ARG:HA	1:G:299:PRO:HD3	1.97	0.40
1:G:220:PRO:HD2	1:G:223:PHE:HB2	2.03	0.40
1:G:280:ASN:HD22	2:C:35:LYS:HE2	1.87	0.40
3:L:108:ARG:HG2	3:L:109:THR:N	2.32	0.40
1:G:322:GLU:O	1:G:322(A):ILE:C	2.64	0.40
1:G:333:ILE:HD11	1:G:390:LEU:HD21	2.03	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	G	341/344 (99%)	290 (85%)	40 (12%)	11 (3%)	3	19
2	C	173/181 (96%)	158 (91%)	15 (9%)	0	100	100
3	L	213/215 (99%)	194 (91%)	14 (7%)	5 (2%)	5	25
4	H	231/235 (98%)	208 (90%)	21 (9%)	2 (1%)	14	43
All	All	958/975 (98%)	850 (89%)	90 (9%)	18 (2%)	6	28

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	129	ALA
1	G	299	PRO
1	G	323	ILE
1	G	412	ASN
3	L	202	SER
1	G	195	SER
1	G	322(A)	ILE
1	G	491	ILE
3	L	138	ASN
1	G	406	ASN
3	L	204	PRO
4	H	26	GLY
1	G	397	ASN
3	L	68	GLY
4	H	144	ASP
3	L	128	GLY
1	G	313[A]	PRO
1	G	313[B]	PRO

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	G	302/303 (100%)	272 (90%)	30 (10%)	7	27
2	C	159/164 (97%)	151 (95%)	8 (5%)	22	50
3	L	182/182 (100%)	169 (93%)	13 (7%)	13	40
4	H	192/194 (99%)	185 (96%)	7 (4%)	31	58
All	All	835/843 (99%)	777 (93%)	58 (7%)	14	41

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	93	PHE
1	G	97	LYS
1	G	102	GLU
1	G	111	LEU

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Mol	Chain	Res	Type
1	G	112	TRP
1	G	119	CYS
1	G	196	CYS
1	G	230	ASP
1	G	234	ASN
1	G	255	VAL
1	G	267	GLU
1	G	270	VAL
1	G	271	VAL
1	G	273	ARG
1	G	287	GLN
1	G	289	LYS
1	G	326	ILE
1	G	340	ASP
1	G	342	LEU
1	G	344	GLN
1	G	352	GLN
1	G	373	MET
1	G	418	CYS
1	G	434	MET
1	G	440	ARG
1	G	442	GLN
1	G	444	ARG
1	G	452	LEU
1	G	460	ILE
1	G	489	VAL
2	C	76	ILE
2	C	112	GLN
2	C	119	GLU
2	C	134	ARG
2	C	150	GLU
2	C	152	GLN
2	C	162	LEU
2	C	164	ASN
3	L	27	GLN
3	L	27(A)	SER
3	L	53	THR
3	L	81	GLU
3	L	83	LEU
3	L	85	VAL
3	L	100	GLN
3	L	122	ASP

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Mol	Chain	Res	Type
3	L	129	THR
3	L	151	ASP
3	L	163	VAL
3	L	181	LEU
3	L	201	LEU
4	H	3	LEU
4	H	31	MET
4	H	116	THR
4	H	138	LEU
4	H	147	PRO
4	H	199	ASN
4	H	209	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	94	ASN
1	G	105	GLN
1	G	229	ASN
1	G	234	ASN
1	G	241	ASN
1	G	279	ASN
1	G	295	ASN
1	G	302	ASN
1	G	328	GLN
1	G	352	GLN
1	G	386	ASN
1	G	389	GLN
1	G	392	ASN
1	G	397	ASN
1	G	407	ASN
1	G	442	GLN
2	C	89	GLN
2	C	94	GLN
2	C	112	GLN
2	C	163	GLN
3	L	37	GLN
3	L	89	GLN
3	L	90	GLN
3	L	124	GLN
3	L	138	ASN
4	H	19	GLN

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Mol	Chain	Res	Type
4	H	155	ASN
4	H	164	HIS
4	H	171	GLN
4	H	199	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 ⓘ

2 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	$\# Z > 2$
5	NAG	A	1	1,5	14,14,15	0.77	0	17,19,21	0.64	0
5	FUC	A	2	5	10,10,11	0.71	0	14,14,16	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
5	NAG	A	1	1,5	1/1/5/7	4/6/23/26	0/1/1/1
5	FUC	A	2	5	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1	NAG	C1

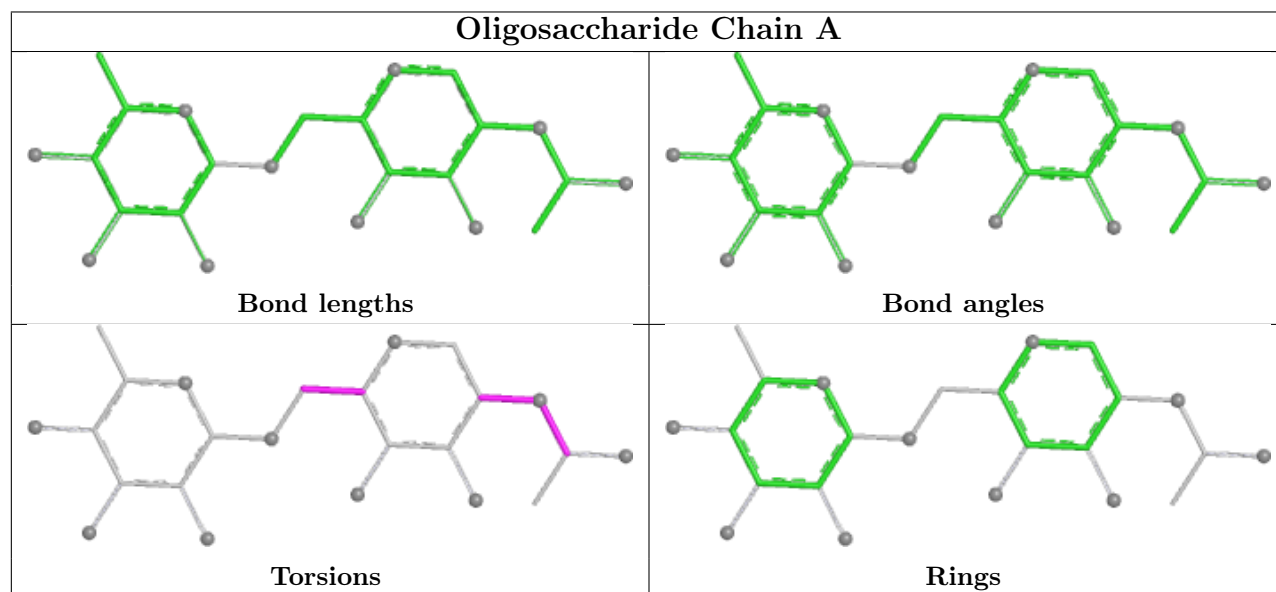
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1	NAG	C3-C2-N2-C7
5	A	1	NAG	C8-C7-N2-C2
5	A	1	NAG	O7-C7-N2-C2
5	A	1	NAG	O5-C5-C6-O6

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](#)

11 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SO4	H	222	-	4,4,4	0.23	0	6,6,6	0.07	0
7	SO4	H	221	-	4,4,4	0.40	0	6,6,6	0.06	0
6	NAG	G	832	1	14,14,15	0.59	0	17,19,21	0.79	1 (5%)
8	XYL	H	217	-	9,9,9	1.36	2 (22%)	11,11,11	0.90	0
7	SO4	L	215	-	4,4,4	0.40	0	6,6,6	0.07	0
7	SO4	H	220	-	4,4,4	0.40	0	6,6,6	0.07	0
7	SO4	G	5	-	4,4,4	0.24	0	6,6,6	0.07	0
6	NAG	G	762	1	14,14,15	0.58	0	17,19,21	0.69	1 (5%)
8	XYL	H	218	-	9,9,9	1.36	1 (11%)	11,11,11	0.89	0
8	XYL	H	219	-	9,9,9	1.37	2 (22%)	11,11,11	0.91	0
6	NAG	G	862	1	14,14,15	0.59	0	17,19,21	0.68	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
6	NAG	G	832	1	1/1/5/7	4/6/23/26	0/1/1/1
8	XYL	H	217	-	-	0/12/12/12	-
6	NAG	G	762	1	-	3/6/23/26	0/1/1/1
8	XYL	H	218	-	-	0/12/12/12	-
8	XYL	H	219	-	-	0/12/12/12	-
6	NAG	G	862	1	-	4/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	218	XYL	C4-C3	2.40	1.57	1.53
8	H	217	XYL	C4-C3	2.34	1.57	1.53
8	H	219	XYL	C4-C3	2.28	1.57	1.53
8	H	219	XYL	C2-C3	2.10	1.57	1.53
8	H	217	XYL	C2-C3	2.01	1.56	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	832	NAG	C2-N2-C7	-2.41	119.67	122.90
6	G	762	NAG	C2-N2-C7	-2.06	120.14	122.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	G	832	NAG	C1

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	762	NAG	C8-C7-N2-C2
6	G	762	NAG	O7-C7-N2-C2
6	G	832	NAG	C8-C7-N2-C2
6	G	832	NAG	O7-C7-N2-C2
6	G	862	NAG	C8-C7-N2-C2
6	G	862	NAG	O7-C7-N2-C2
6	G	832	NAG	O5-C5-C6-O6
6	G	832	NAG	C4-C5-C6-O6
6	G	862	NAG	O5-C5-C6-O6
6	G	862	NAG	C4-C5-C6-O6
6	G	762	NAG	O5-C5-C6-O6

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	G	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	87:GLU	C	88:ASN	N	1.17

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	G	339/344 (98%)	-0.27	2 (0%) 85 73	58, 121, 148, 160	4 (1%)
2	C	175/181 (96%)	-0.07	1 (0%) 85 73	100, 139, 161, 166	0
3	L	215/215 (100%)	-0.21	0 100 100	65, 111, 141, 154	0
4	H	233/235 (99%)	-0.41	0 100 100	48, 83, 121, 150	0
All	All	962/975 (98%)	-0.25	3 (0%) 90 82	48, 116, 154, 166	4 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	87	GLU	4.6
2	C	98	PHE	2.7
1	G	323	ILE	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

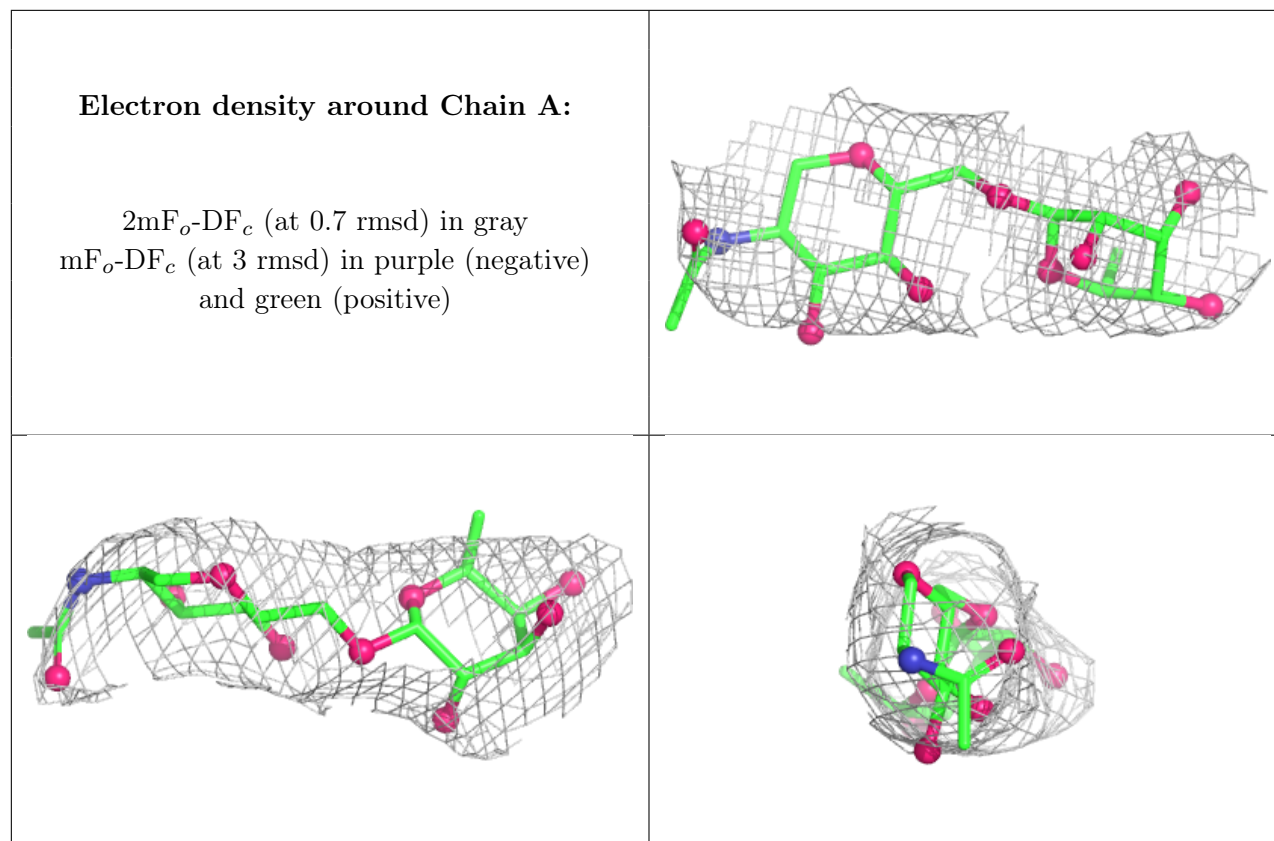
6.3 Carbohydrates [i](#)

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
5	NAG	A	1	14/15	-	-	138,139,140,141	0
5	FUC	A	2	10/11	-	-	141,142,143,143	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. 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($\text{\AA}^2$)	Q<0.9
8	XYL	H	217	10/10	0.30	0.12	145,150,150,150	0
8	XYL	H	219	10/10	0.36	0.13	153,155,156,157	0
7	SO4	H	221	5/5	0.52	0.09	189,189,190,190	0
7	SO4	H	222	5/5	0.69	0.08	143,143,143,143	5
7	SO4	L	215	5/5	0.70	0.06	186,187,187,187	0
7	SO4	H	220	5/5	0.70	0.07	161,161,161,161	0
8	XYL	H	218	10/10	0.77	0.11	134,136,137,137	0
6	NAG	G	862	14/15	0.78	0.07	135,138,140,140	0
6	NAG	G	832	14/15	0.79	0.10	141,144,147,147	0
7	SO4	G	5	5/5	0.83	0.13	163,163,164,164	5
6	NAG	G	762	14/15	0.85	0.08	105,108,110,110	0

6.5 Other polymers [i](#)

There are no such residues in this entry.