W O R L D W I D E
wwPDB
P R O T E I N D A T A B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 21, 2020 – 10:12 AM JST

PDB ID	:	7CZF
Title	:	Crystal structure of Kaposi Sarcoma associated herpesvirus (KSHV) gHgL in complex with the ligand binding domian (LBD) of EphA2
Authors	:	Su, C.; Wu, L.L.; Song, H.; Chai, Y.; Qi, J.X.; Yan, J.H.; Gao, G.F.
Deposited on	:	2020-09-08
Resolution	:	3.20 Å(reported)

The following versions of software and data (see references ⓘ) were used in the production of this report:

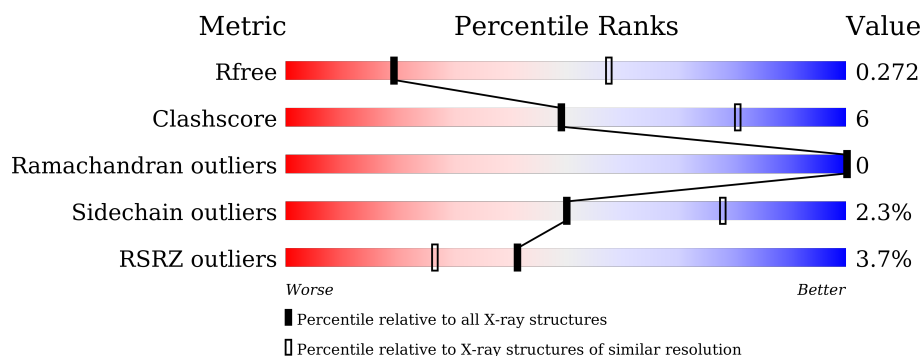|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

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 3.20 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	Percentile Ranks	Value
Rfree		0.272
Clashscore		6
Ramachandran outliers		0
Sidechain outliers		2.3%
RSRZ outliers		3.7%

Worse ────────────────────── Better

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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 <=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	185	4% / 74% 18% 8%
1	D	185	9% / 71% 14% 15%
2	B	677	3% / 79% 16% 5%
2	E	677	3% / 76% 18% 5%
3	C	157	% / 59% 13% • 27%
3	F	157	2% / 63% 10% 27%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	K	2	100%
4	L	2	100%
4	N	2	100%
4	a	2	100%
5	S	6	67% 33%
6	H	3	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
4	NAG	L	2	-	-	-	X
4	NAG	a	2	-	-	-	X
5	MAN	S	4	-	-	-	X
6	FUC	H	3	-	-	-	X

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 14901 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 Ephrin type-A receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	0	0
			1376	883	231	252	10			
1	D	158	Total	C	N	O	S	0	0	0
			1271	817	208	237	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207	HIS	-	expression tag	UNP P29317
A	208	HIS	-	expression tag	UNP P29317
A	209	HIS	-	expression tag	UNP P29317
A	210	HIS	-	expression tag	UNP P29317
A	211	HIS	-	expression tag	UNP P29317
A	212	HIS	-	expression tag	UNP P29317
D	207	HIS	-	expression tag	UNP P29317
D	208	HIS	-	expression tag	UNP P29317
D	209	HIS	-	expression tag	UNP P29317
D	210	HIS	-	expression tag	UNP P29317
D	211	HIS	-	expression tag	UNP P29317
D	212	HIS	-	expression tag	UNP P29317

- Molecule 2 is a protein called Envelope glycoprotein H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	644	Total	C	N	O	S	0	0	0
			5061	3237	851	945	28			
2	E	642	Total	C	N	O	S	0	0	0
			5049	3229	849	943	28			

- Molecule 3 is a protein called Envelope glycoprotein L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	114	Total 874	C 554	N 156	O 159	S 5	0	0	0
3	F	115	Total 882	C 562	N 157	O 158	S 5	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	17	ASP	-	expression tag	UNP Q76RG7
C	18	GLY	-	expression tag	UNP Q76RG7
C	19	ILE	-	expression tag	UNP Q76RG7
C	20	GLN	-	expression tag	UNP Q76RG7
C	168	HIS	-	expression tag	UNP Q76RG7
C	169	HIS	-	expression tag	UNP Q76RG7
C	170	HIS	-	expression tag	UNP Q76RG7
C	171	HIS	-	expression tag	UNP Q76RG7
C	172	HIS	-	expression tag	UNP Q76RG7
C	173	HIS	-	expression tag	UNP Q76RG7
F	17	ASP	-	expression tag	UNP Q76RG7
F	18	GLY	-	expression tag	UNP Q76RG7
F	19	ILE	-	expression tag	UNP Q76RG7
F	20	GLN	-	expression tag	UNP Q76RG7
F	168	HIS	-	expression tag	UNP Q76RG7
F	169	HIS	-	expression tag	UNP Q76RG7
F	170	HIS	-	expression tag	UNP Q76RG7
F	171	HIS	-	expression tag	UNP Q76RG7
F	172	HIS	-	expression tag	UNP Q76RG7
F	173	HIS	-	expression tag	UNP Q76RG7

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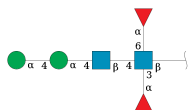

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	L	2	Total 28	C 16	N 2	O 10	0	0	0
4	a	2	Total 28	C 16	N 2	O 10	0	0	0
4	K	2	Total 28	C 16	N 2	O 10	0	0	0

Continued on next page...

W O R L D W I D E
PDB
PROTEIN DATA BANK

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	N	2	28	16	2	10	0	0	0

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-alpha-D-mannopyran ose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alp ha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.
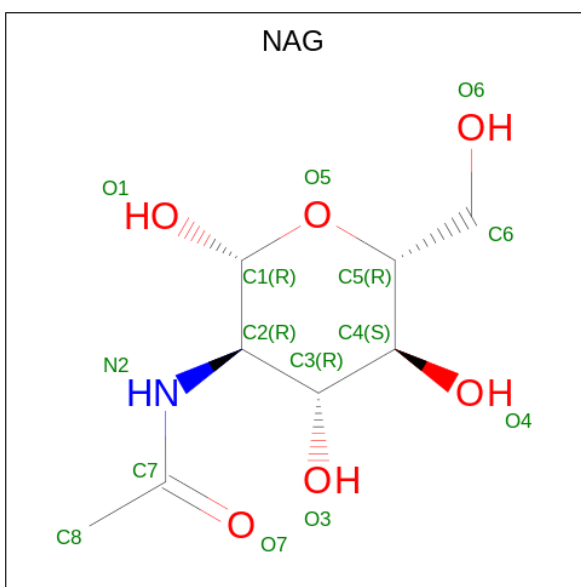

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	S	6	70	40	2	28	0	0	0

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[al pha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.
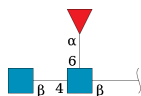
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
6	H	3	38	22	2	14	0	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

NAG

| Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	F	1	Total	C	N	O	0	0
			14	8	1	5		

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.
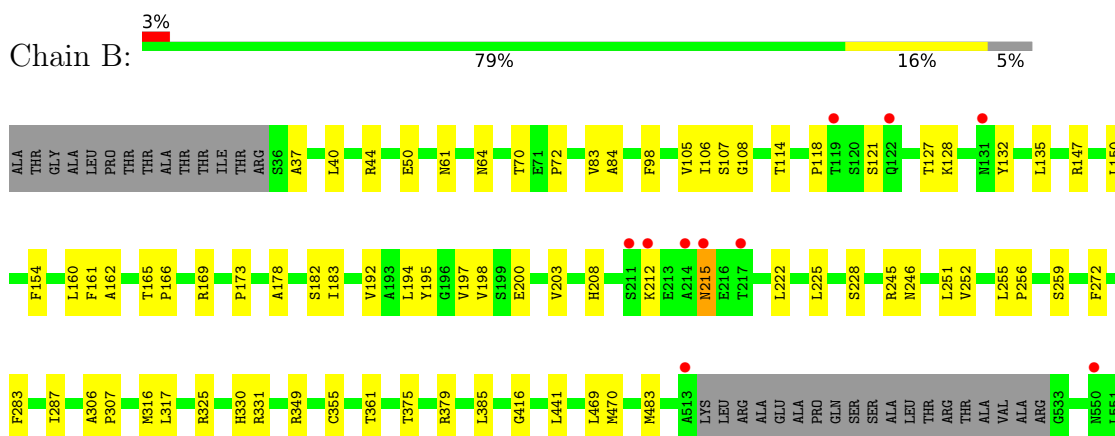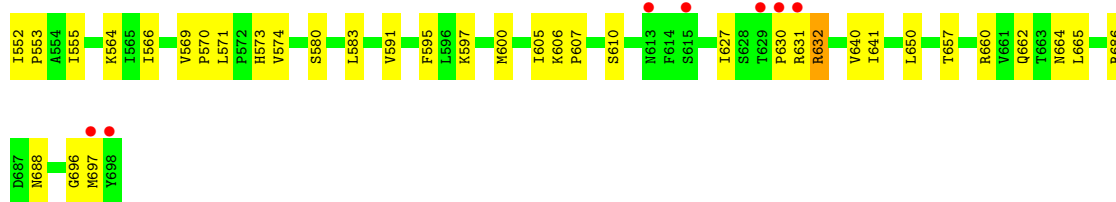
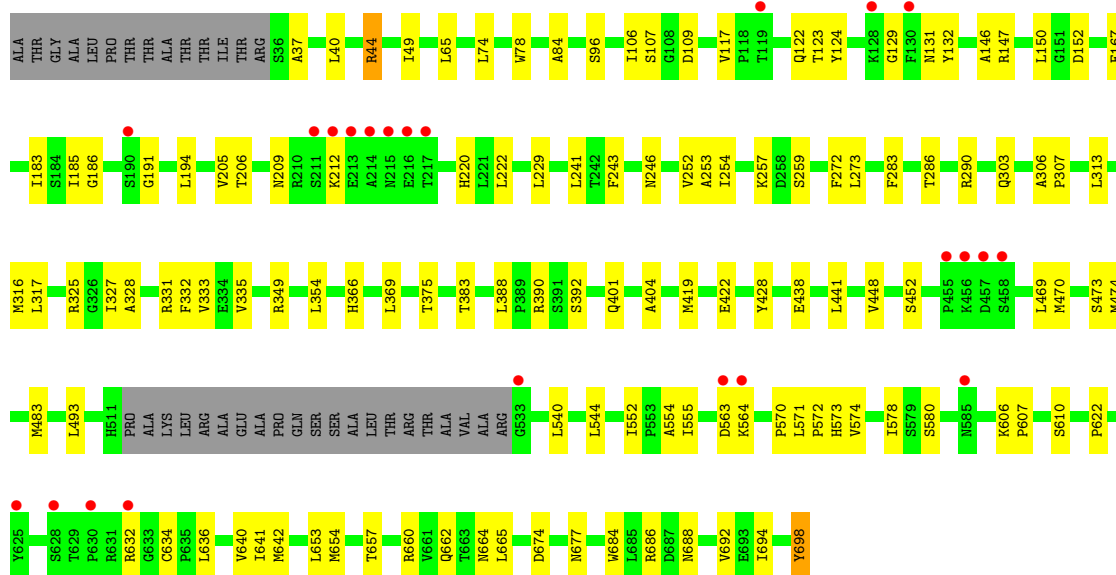• Molecule 1: Ephrin type-A receptor 2
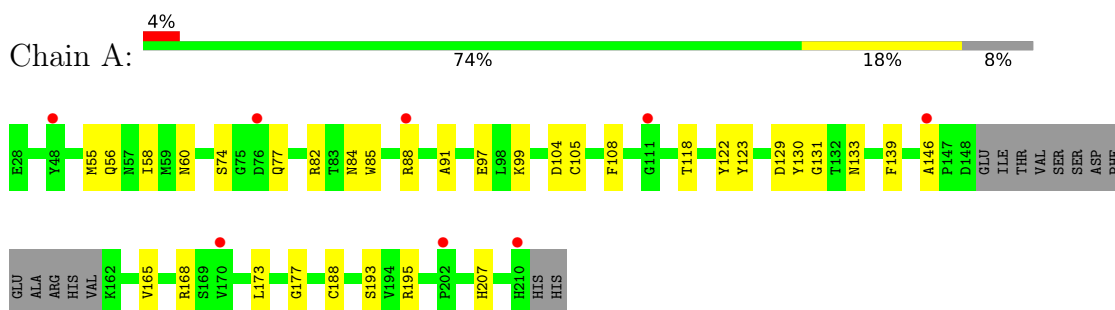
• Molecule 1: Ephrin type-A receptor 2
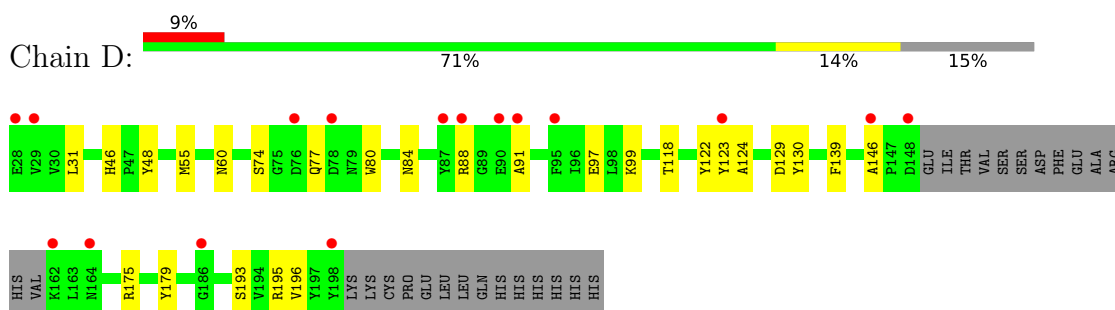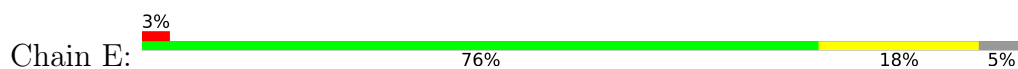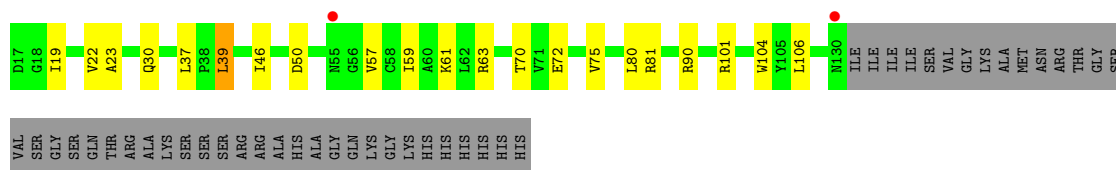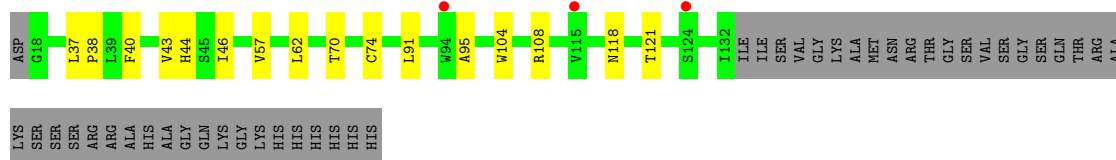

• Molecule 2: Envelope glycoprotein H

• Molecule 2: Envelope glycoprotein H

Chain E:

• Molecule 3: Envelope glycoprotein L

Chain C:

• Molecule 3: Envelope glycoprotein L

Chain F:

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

Chain L: 100%

NAG1
NAG2

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

Chain a: 100%

NAG1
NAG2

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

Chain K: 100%

NAG1
NAG2

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

Chain N: 100%

NAG1
NAG2

• Molecule 5: alpha-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S: 67%   33%

NAG1
NAG2
MAN3
MAN4
FUC5
FUC6

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

Chain H: 100%

NAG1
NAG2
FUC3

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	80.80Å 153.20Å 275.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.65 – 3.20 31.65 – 3.20	Depositor EDS
% Data completeness (in resolution range)	78.7 (31.65-3.20) 78.7 (31.65-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 3.18Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.239 , 0.272 0.239 , 0.272	Depositor DCC
R_{free} test set	2199 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å^2)	54.1	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 30.4	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	14901	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: FUC, NAG, MAN

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	0.24	0/1412	0.41	0/1911
1	D	0.24	0/1302	0.42	0/1763
2	B	0.24	0/5172	0.43	0/7033
2	E	0.24	0/5159	0.42	0/7014
3	C	0.24	0/893	0.45	0/1218
3	F	0.24	0/901	0.41	0/1229
All	All	0.24	0/14839	0.42	0/20168

There are no bond length outliers.

There are no bond angle outliers.

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	1376	0	1319	20	0
1	D	1271	0	1217	14	0
2	B	5061	0	5031	56	0
2	E	5049	0	5019	69	0
3	C	874	0	858	18	0
3	F	882	0	876	11	0
4	K	28	0	25	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	28	0	25	0	0
4	N	28	0	25	0	0
4	a	28	0	25	0	0
5	S	70	0	61	0	0
6	H	38	0	34	0	0
7	B	70	0	65	1	0
7	C	14	0	13	0	0
7	E	70	0	65	1	0
7	F	14	0	13	0	0
All	All	14901	0	14671	173	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 6.

The worst 5 of 173 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:E:674:ASP:O	2:E:677:ASN:ND2	2.22	0.73
2:B:627:ILE:HG13	2:B:696:GLY:HA3	1.70	0.72
2:B:105:VAL:HG22	2:B:245:ARG:HB3	1.73	0.70
2:B:606:LYS:HD2	2:B:610:SER:HB2	1.73	0.69
2:B:553:PRO:HB2	2:B:607:PRO:HB3	1.75	0.68

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	166/185 (90%)	166 (100%)	0	0	100	100
1	D	154/185 (83%)	154 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	640/677 (94%)	640 (100%)	0	0	100	100
2	E	638/677 (94%)	636 (100%)	2 (0%)	0	100	100
3	C	112/157 (71%)	112 (100%)	0	0	100	100
3	F	113/157 (72%)	113 (100%)	0	0	100	100
All	All	1823/2038 (90%)	1821 (100%)	2 (0%)	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	147/161 (91%)	143 (97%)	4 (3%)	44	75
1	D	135/161 (84%)	132 (98%)	3 (2%)	52	79
2	B	562/586 (96%)	547 (97%)	15 (3%)	44	75
2	E	561/586 (96%)	551 (98%)	10 (2%)	59	82
3	C	95/129 (74%)	93 (98%)	2 (2%)	53	79
3	F	96/129 (74%)	94 (98%)	2 (2%)	53	79
All	All	1596/1752 (91%)	1560 (98%)	36 (2%)	50	78

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	631	ARG
3	C	50	ASP
2	E	698	TYR
2	B	697	MET
1	D	48	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

17 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	$\#\|Z\| > 2$
6	NAG	H	1	2,6	14,14,15	0.28	0	17,19,21	0.44	0
6	NAG	H	2	6	14,14,15	0.21	0	17,19,21	0.39	0
6	FUC	H	3	6	10,10,11	0.79	0	14,14,16	0.94	0
4	NAG	K	1	2,4	14,14,15	0.24	0	17,19,21	0.46	0
4	NAG	K	2	4	14,14,15	0.20	0	17,19,21	0.40	0
4	NAG	L	1	2,4	14,14,15	0.27	0	17,19,21	0.49	0
4	NAG	L	2	4	14,14,15	0.32	0	17,19,21	0.48	0
4	NAG	N	1	2,4	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	N	2	4	14,14,15	0.30	0	17,19,21	0.37	0
5	NAG	S	1	2,5	14,14,15	0.20	0	17,19,21	0.40	0
5	NAG	S	2	5	14,14,15	0.21	0	17,19,21	0.43	0
5	MAN	S	3	5	11,11,12	0.70	0	15,15,17	1.00	2 (13%)
5	MAN	S	4	5	11,11,12	0.74	0	15,15,17	1.05	2 (13%)
5	FUC	S	5	5	10,10,11	0.78	0	14,14,16	0.80	0
5	FUC	S	6	5	10,10,11	0.76	0	14,14,16	0.82	0
4	NAG	a	1	2,4	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	a	2	4	14,14,15	0.22	0	17,19,21	0.40	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	H	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	H	2	6	-	0/6/23/26	0/1/1/1
6	FUC	H	3	6	-	-	0/1/1/1
4	NAG	K	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	L	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	L	2	4	-	4/6/23/26	0/1/1/1
4	NAG	N	1	2,4	-	1/6/23/26	0/1/1/1
4	NAG	N	2	4	-	3/6/23/26	0/1/1/1
5	NAG	S	1	2,5	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	0/6/23/26	0/1/1/1
5	MAN	S	3	5	-	2/2/19/22	0/1/1/1
5	MAN	S	4	5	-	2/2/19/22	0/1/1/1
5	FUC	S	5	5	-	-	0/1/1/1
5	FUC	S	6	5	-	-	0/1/1/1
4	NAG	a	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	a	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	S	3	MAN	C1-O5-C5	2.41	115.45	112.19
5	S	4	MAN	C1-O5-C5	2.37	115.40	112.19
5	S	3	MAN	O2-C2-C3	-2.23	105.67	110.14
5	S	4	MAN	O2-C2-C3	-2.21	105.71	110.14

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

| Mol	Chain	Res	Type	Atoms
4	L	2	NAG	O5-C5-C6-O6
5	S	1	NAG	O5-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6
4	L	2	NAG	C4-C5-C6-O6
5	S	1	NAG	C4-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.

Oligosaccharide Chain K

Oligosaccharide Chain L

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain H

Bond lengths   Bond angles

Torsions   Rings
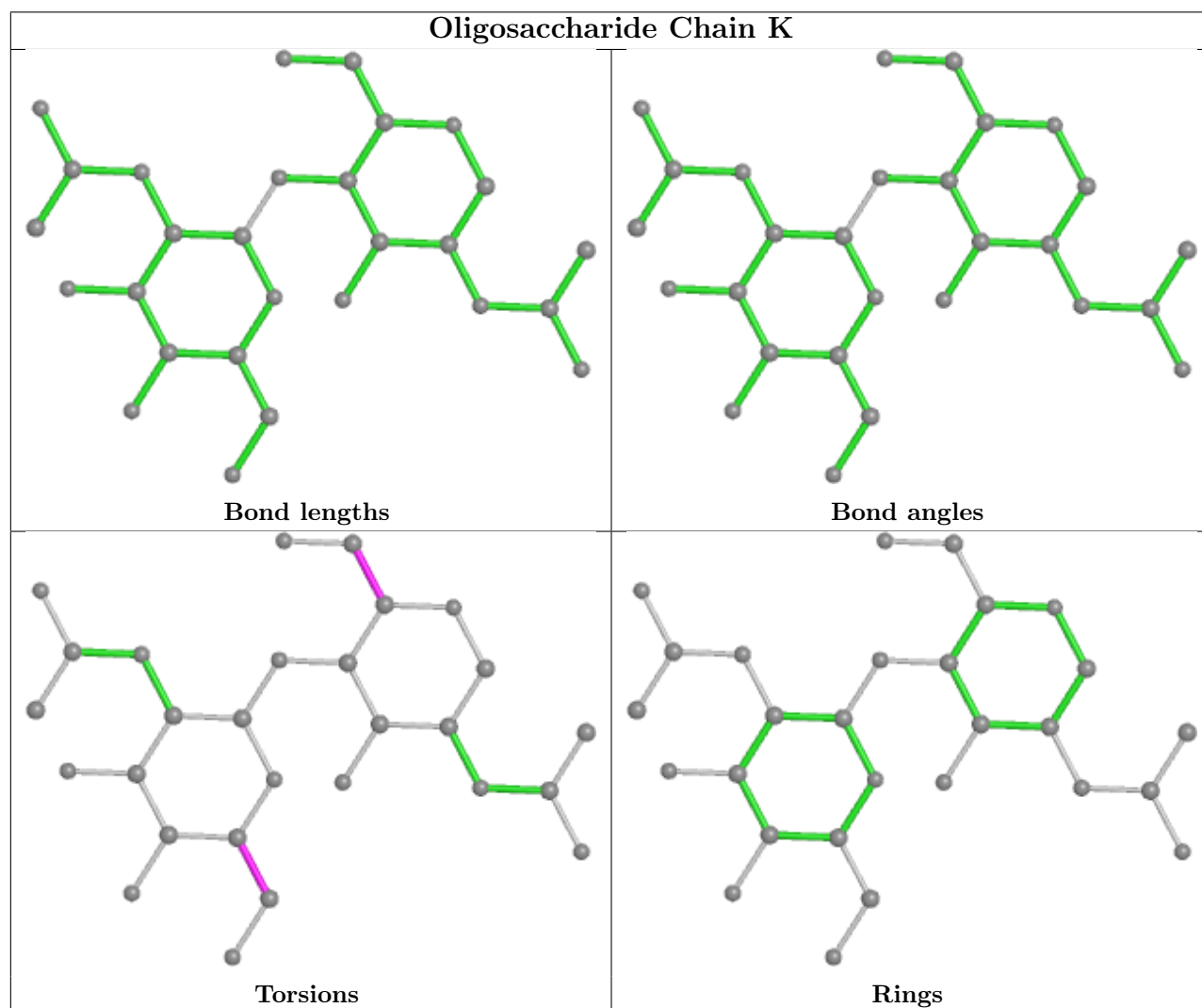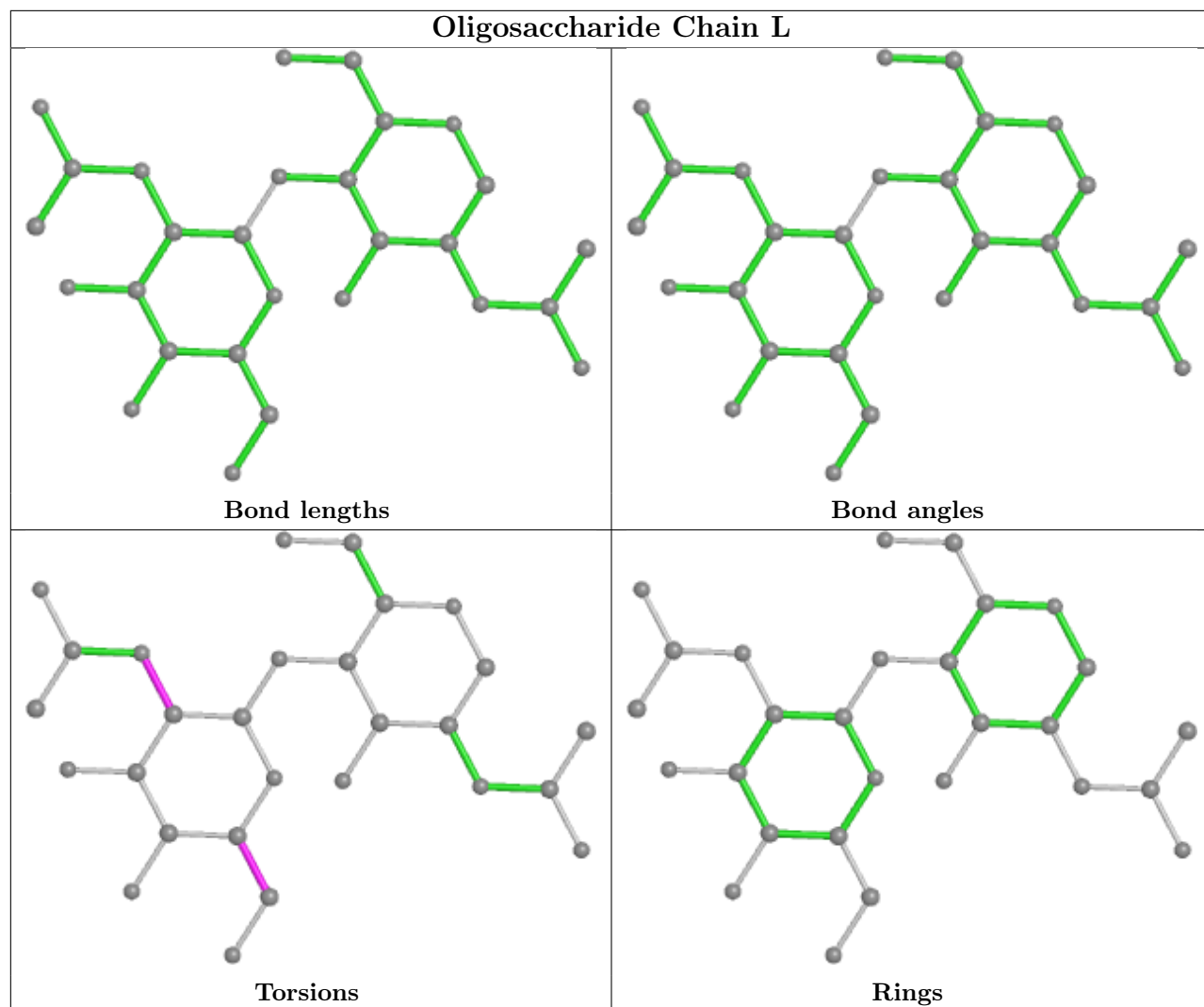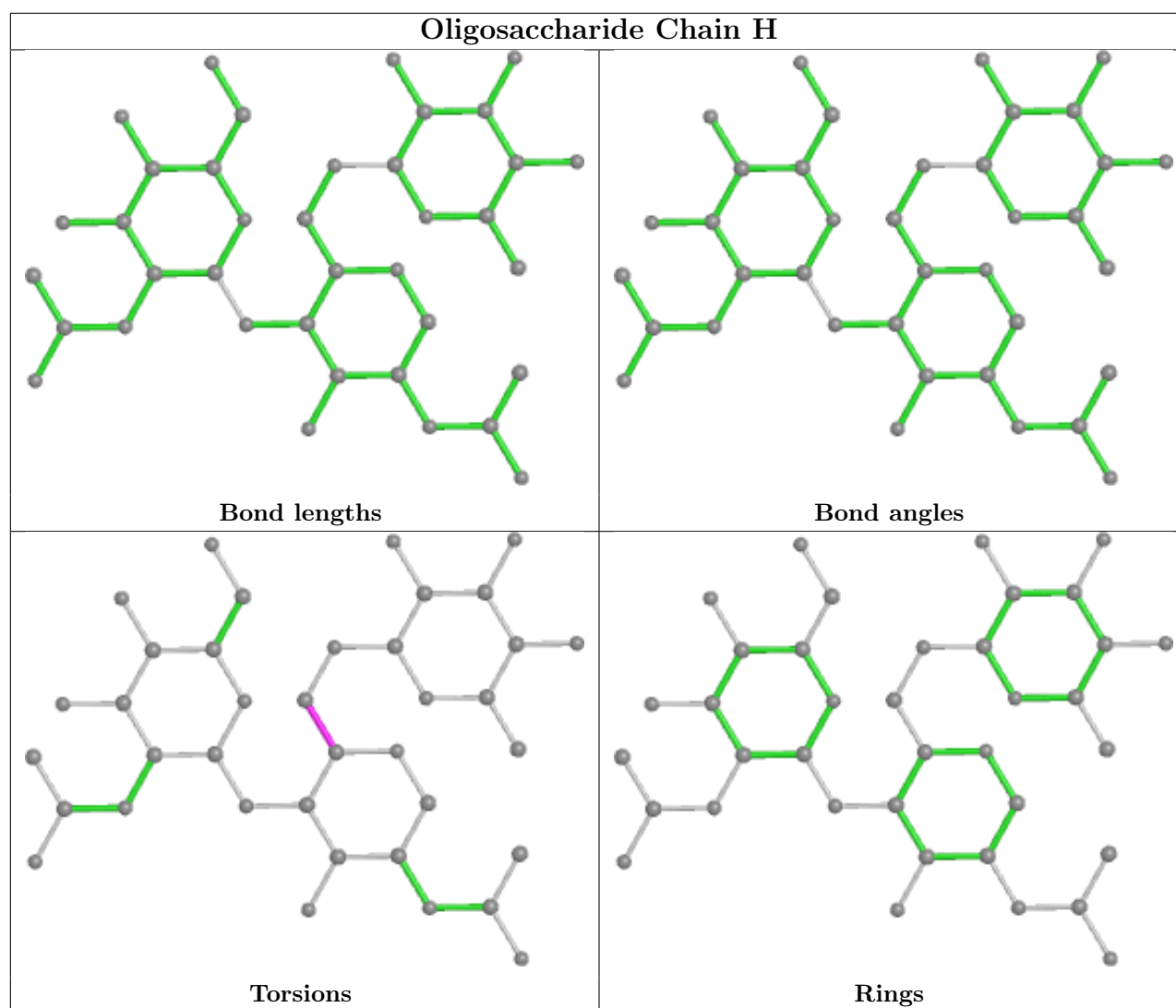
5.6 Ligand geometry ⓘ

12 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	NAG	E	705	2	14,14,15	0.22	0	17,19,21	0.33	0
7	NAG	B	701	2	14,14,15	0.22	0	17,19,21	0.42	0
7	NAG	E	701	2	14,14,15	0.24	0	17,19,21	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
7	NAG	B	705	2	14,14,15	0.23	0	17,19,21	0.45	0
7	NAG	B	702	2	14,14,15	0.26	0	17,19,21	0.42	0
7	NAG	F	201	3	14,14,15	0.26	0	17,19,21	0.43	0
7	NAG	E	703	2	14,14,15	0.23	0	17,19,21	0.42	0
7	NAG	E	704	2	14,14,15	0.23	0	17,19,21	0.41	0
7	NAG	C	201	3	14,14,15	0.27	0	17,19,21	0.32	0
7	NAG	B	704	2	14,14,15	0.22	0	17,19,21	0.43	0
7	NAG	B	703	2	14,14,15	0.22	0	17,19,21	0.41	0
7	NAG	E	702	2	14,14,15	0.20	0	17,19,21	0.40	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
7	NAG	E	705	2	-	0/6/23/26	0/1/1/1
7	NAG	B	701	2	-	1/6/23/26	0/1/1/1
7	NAG	E	701	2	-	0/6/23/26	0/1/1/1
7	NAG	B	705	2	-	0/6/23/26	0/1/1/1
7	NAG	B	702	2	-	0/6/23/26	0/1/1/1
7	NAG	F	201	3	-	0/6/23/26	0/1/1/1
7	NAG	E	703	2	-	2/6/23/26	0/1/1/1
7	NAG	E	704	2	-	2/6/23/26	0/1/1/1
7	NAG	C	201	3	-	2/6/23/26	0/1/1/1
7	NAG	B	704	2	-	2/6/23/26	0/1/1/1
7	NAG	B	703	2	-	1/6/23/26	0/1/1/1
7	NAG	E	702	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	201	NAG	C4-C5-C6-O6
7	C	201	NAG	O5-C5-C6-O6
7	E	703	NAG	O5-C5-C6-O6
7	E	703	NAG	C4-C5-C6-O6
7	B	704	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	702	NAG	1	0
7	E	702	NAG	1	0

5.7 Other polymers ⓘ

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 ⓘ

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(Å²)	Q<0.9
1	A	170/185 (91%)	0.47	8 (4%)	31	19	38, 95, 137, 167	0
1	D	158/185 (85%)	0.65	16 (10%)	7	4	50, 105, 149, 167	0
2	B	644/677 (95%)	-0.10	17 (2%)	56	40	14, 47, 110, 156	0
2	E	642/677 (94%)	-0.09	23 (3%)	42	27	10, 45, 112, 161	0
3	C	114/157 (72%)	0.01	2 (1%)	68	55	20, 63, 116, 137	0
3	F	115/157 (73%)	0.06	3 (2%)	56	40	29, 71, 117, 141	0
All	All	1843/2038 (90%)	0.03	69 (3%)	41	26	10, 57, 127, 167	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	698	TYR	6.3
2	E	212	LYS	5.5
2	B	212	LYS	5.4
2	B	513	ALA	4.2
2	E	215	ASN	4.2

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

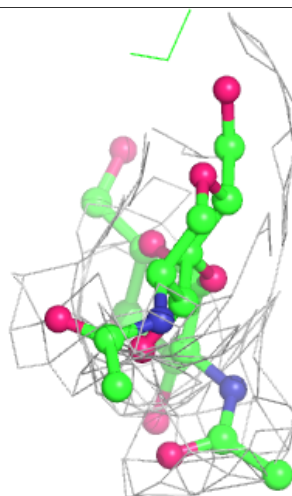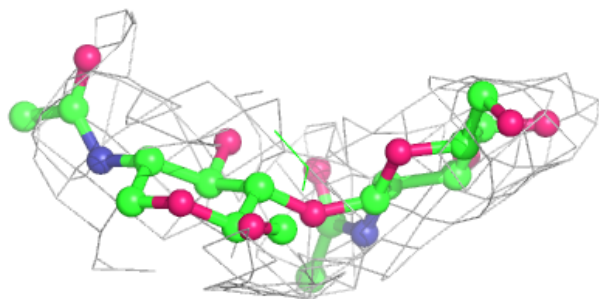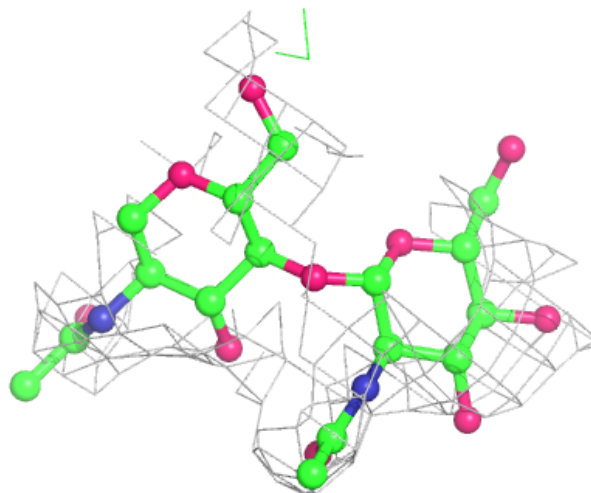There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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	MAN	S	4	11/12	0.60	0.80	159,171,178,183	0
4	NAG	L	2	14/15	0.62	0.54	152,164,171,176	0
6	NAG	H	2	14/15	0.69	0.38	98,113,121,123	0
4	NAG	a	2	14/15	0.73	0.43	99,125,141,143	0
4	NAG	N	2	14/15	0.73	0.39	144,158,167,175	0
4	NAG	K	2	14/15	0.74	0.37	104,124,135,146	0
6	FUC	H	3	10/11	0.76	0.55	134,143,148,152	0
4	NAG	L	1	14/15	0.78	0.31	121,138,154,157	0
6	NAG	H	1	14/15	0.79	0.27	100,118,126,129	0
5	NAG	S	2	14/15	0.79	0.26	93,114,121,129	0
5	FUC	S	5	10/11	0.80	0.43	137,142,152,157	0
5	MAN	S	3	11/12	0.81	0.52	115,123,132,134	0
5	FUC	S	6	10/11	0.82	0.50	94,110,121,129	0
4	NAG	K	1	14/15	0.83	0.20	71,93,102,106	0
5	NAG	S	1	14/15	0.87	0.20	107,122,124,126	0
4	NAG	N	1	14/15	0.89	0.39	77,87,102,110	0
4	NAG	a	1	14/15	0.89	0.27	64,82,87,91	0

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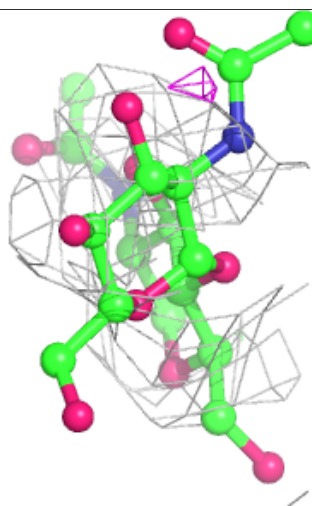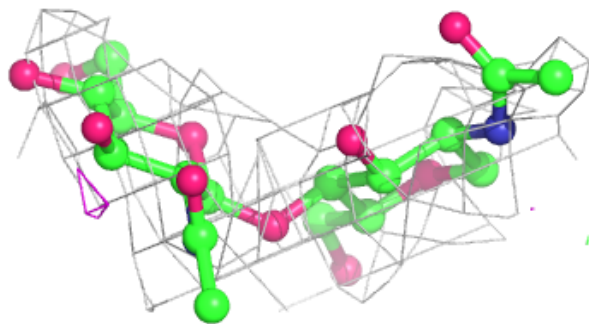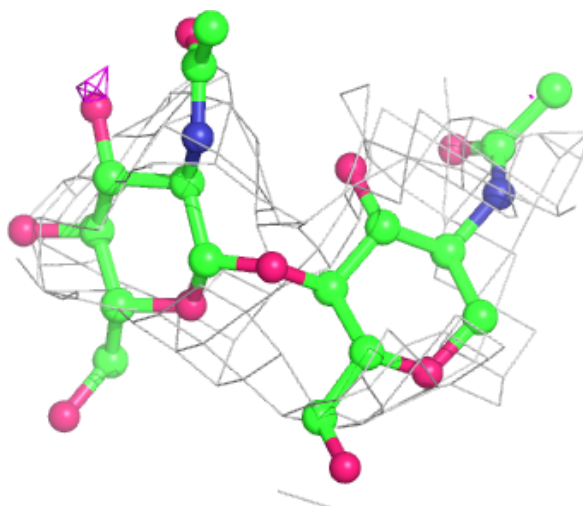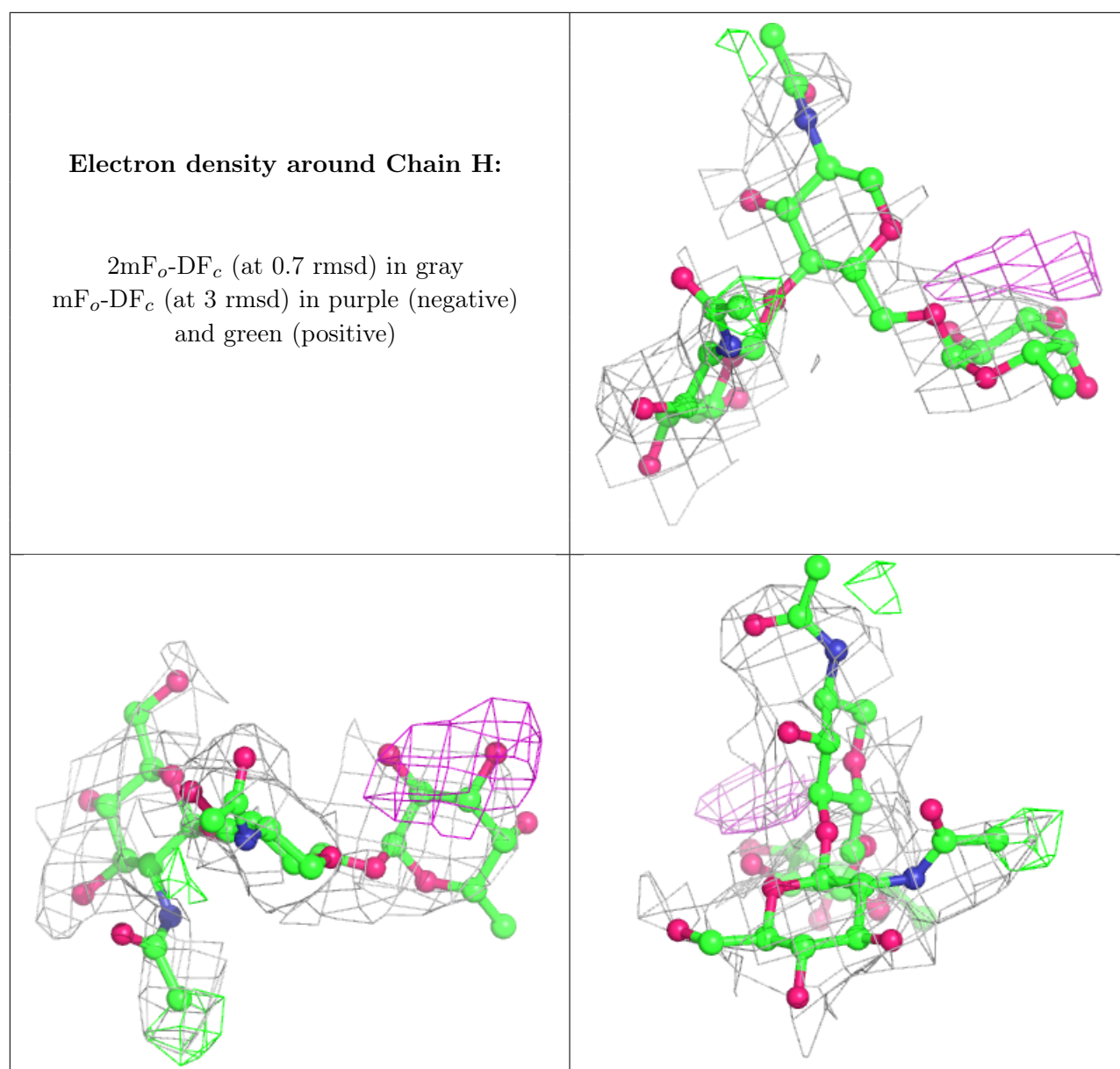
Electron density around Chain K:

$2mF_o$-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 L:

$2mF_o$-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 H:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (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
7	NAG	B	701	14/15	0.58	0.37	108,127,141,142	0
7	NAG	F	201	14/15	0.69	0.39	105,139,153,155	0
7	NAG	E	701	14/15	0.73	0.31	115,134,139,141	0
7	NAG	C	201	14/15	0.73	0.30	127,139,147,148	0
7	NAG	E	704	14/15	0.77	0.37	95,106,118,123	0

Continued on next page...

wwPDB X-ray Structure Validation Summary Report

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	NAG	E	705	14/15	0.79	0.32	71,81,101,104	0
7	NAG	B	705	14/15	0.80	0.39	96,112,124,127	0
7	NAG	B	702	14/15	0.83	0.32	68,77,81,86	0
7	NAG	B	703	14/15	0.83	0.25	62,65,71,83	0
7	NAG	E	702	14/15	0.83	0.37	90,98,106,107	0
7	NAG	E	703	14/15	0.91	0.18	43,57,61,64	0
7	NAG	B	704	14/15	0.91	0.32	74,83,98,100	0

6.5 Other polymers (i)

There are no such residues in this entry.