



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 25, 2022 – 07:05 pm GMT

PDB ID : 6SMC
Title : mouse Interleukin-12 subunit beta - p80 homodimer in space group P1
Authors : Bloch, Y.; Savvides, S.N.
Deposited on : 2019-08-21
Resolution : 3.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.26
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

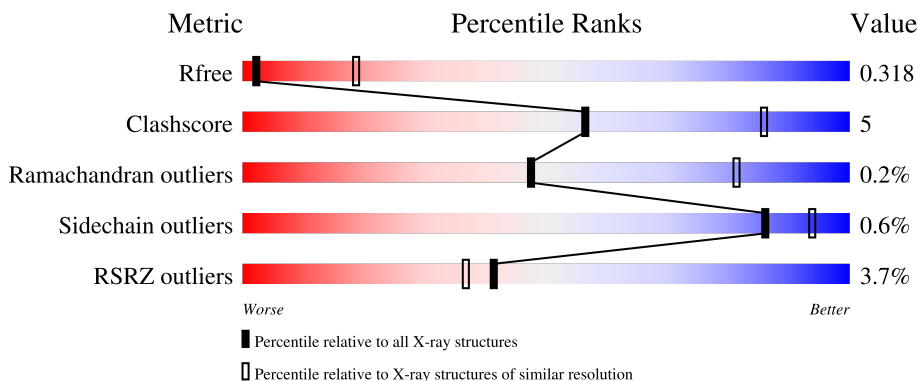
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	344	 3% 77% 10% 12%
1	B	344	 3% 76% 11% 12%
1	C	344	 3% 77% 11% 12%
1	D	344	 4% 75% 12% 13%
2	E	4	 25% 75%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain	
2	F	4		
2	G	4		
2	H	4		

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
3	CL	B	401	-	-	-	X
3	CL	C	401	-	-	-	X

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 19089 atoms, of which 9305 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 Interleukin-12 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	301	4681	1503	2285	404	472	17	0	0	0
1	B	301	4637	1496	2256	397	471	17	0	0	0
1	C	303	4700	1511	2293	407	472	17	0	0	0
1	D	300	4697	1507	2299	405	469	17	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

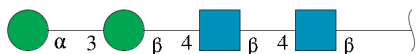
Chain	Residue	Modelled	Actual	Comment	Reference
A	336	GLY	-	expression tag	UNP P43432
A	337	THR	-	expression tag	UNP P43432
A	338	LYS	-	expression tag	UNP P43432
A	339	HIS	-	expression tag	UNP P43432
A	340	HIS	-	expression tag	UNP P43432
A	341	HIS	-	expression tag	UNP P43432
A	342	HIS	-	expression tag	UNP P43432
A	343	HIS	-	expression tag	UNP P43432
A	344	HIS	-	expression tag	UNP P43432
B	336	GLY	-	expression tag	UNP P43432
B	337	THR	-	expression tag	UNP P43432
B	338	LYS	-	expression tag	UNP P43432
B	339	HIS	-	expression tag	UNP P43432
B	340	HIS	-	expression tag	UNP P43432
B	341	HIS	-	expression tag	UNP P43432
B	342	HIS	-	expression tag	UNP P43432
B	343	HIS	-	expression tag	UNP P43432
B	344	HIS	-	expression tag	UNP P43432
C	336	GLY	-	expression tag	UNP P43432
C	337	THR	-	expression tag	UNP P43432
C	338	LYS	-	expression tag	UNP P43432

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	339	HIS	-	expression tag	UNP P43432
C	340	HIS	-	expression tag	UNP P43432
C	341	HIS	-	expression tag	UNP P43432
C	342	HIS	-	expression tag	UNP P43432
C	343	HIS	-	expression tag	UNP P43432
C	344	HIS	-	expression tag	UNP P43432
D	336	GLY	-	expression tag	UNP P43432
D	337	THR	-	expression tag	UNP P43432
D	338	LYS	-	expression tag	UNP P43432
D	339	HIS	-	expression tag	UNP P43432
D	340	HIS	-	expression tag	UNP P43432
D	341	HIS	-	expression tag	UNP P43432
D	342	HIS	-	expression tag	UNP P43432
D	343	HIS	-	expression tag	UNP P43432
D	344	HIS	-	expression tag	UNP P43432

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranos e-(1-4)-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	H	N				O
2	E	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			
2	F	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			
2	G	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			
2	H	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			

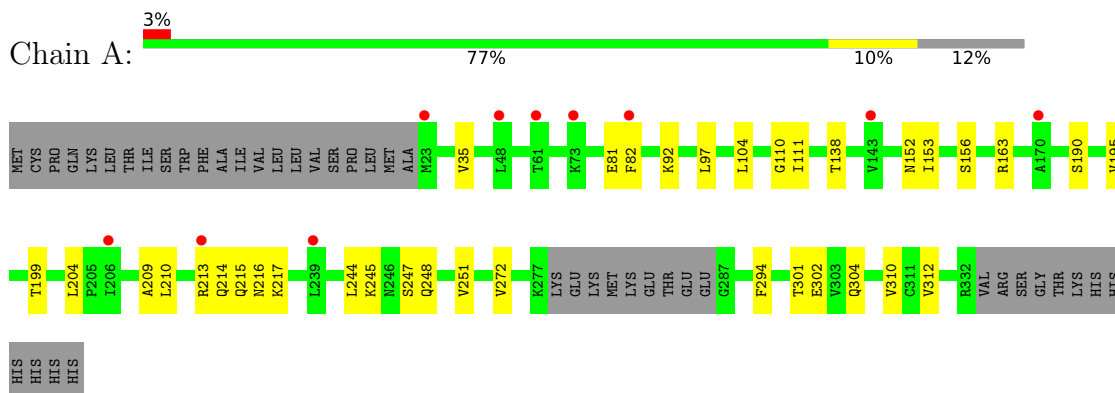
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0

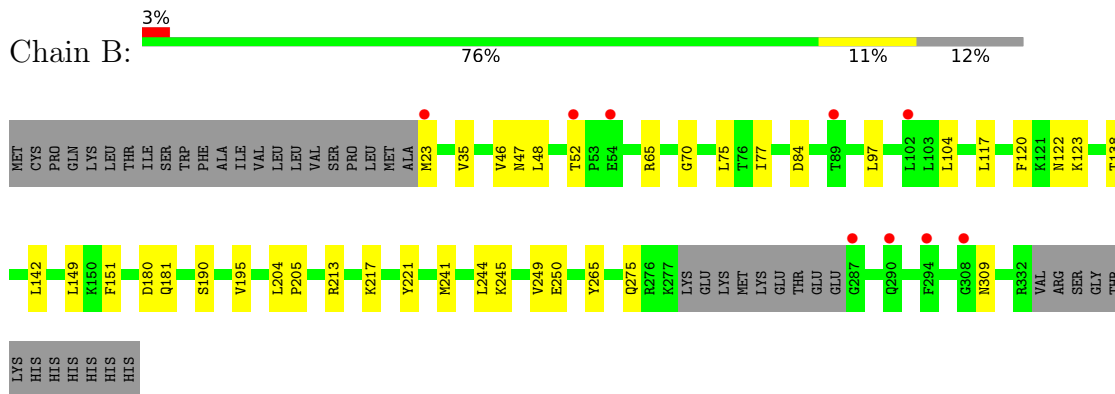
3 Residue-property plots [i](#)

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.

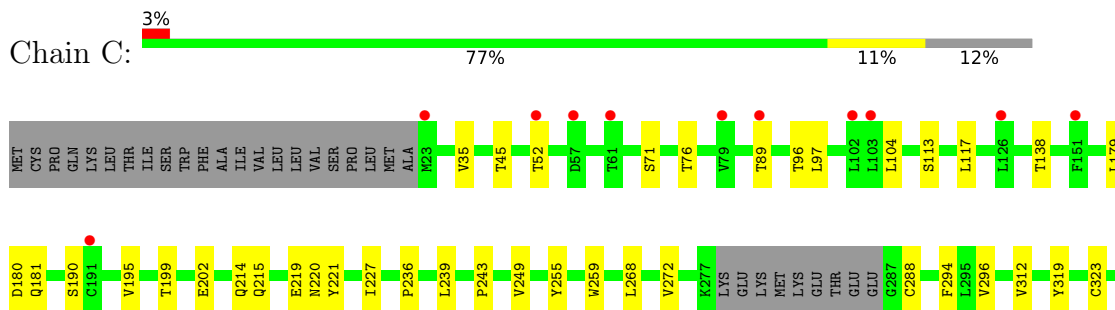
- Molecule 1: Interleukin-12 subunit beta

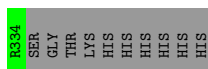


- Molecule 1: Interleukin-12 subunit beta

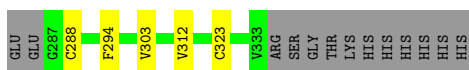
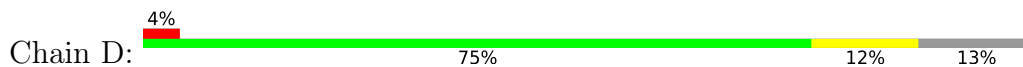


- Molecule 1: Interleukin-12 subunit beta





- Molecule 1: Interleukin-12 subunit beta



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



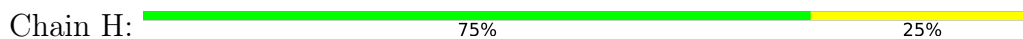
- Molecule 2: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.07Å 96.79Å 107.78Å 68.59° 76.84° 85.83°	Depositor
Resolution (Å)	48.76 – 3.50 48.76 – 3.50	Depositor EDS
% Data completeness (in resolution range)	92.8 (48.76-3.50) 92.8 (48.76-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 3.48Å)	Xtriage
Refinement program	BUSTER, PHENIX 1.16_3549	Depositor
R, R_{free}	0.279 , 0.310 0.286 , 0.318	Depositor DCC
R_{free} test set	2153 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	119.7	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	19089	wwPDB-VP
Average B, all atoms (Å ²)	132.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.34% 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: CL, BMA, 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	0.26	0/2452	0.48	0/3325
1	B	0.27	0/2437	0.47	0/3307
1	C	0.27	0/2463	0.47	0/3340
1	D	0.26	0/2453	0.46	0/3324
All	All	0.27	0/9805	0.47	0/13296

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2396	2285	2282	25	0
1	B	2381	2256	2256	23	0
1	C	2407	2293	2294	22	0
1	D	2398	2299	2300	28	0
2	E	50	43	43	0	0
2	F	50	43	43	0	0
2	G	50	43	43	1	0
2	H	50	43	43	0	0
3	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
All	All	9784	9305	9304	95	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 5.

All (95) 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:35:VAL:HG21	1:B:104:LEU:HD22	1.71	0.70
1:B:244:LEU:HD12	1:B:245:LYS:HG2	1.73	0.69
1:A:244:LEU:HD23	1:A:245:LYS:H	1.58	0.68
1:B:241:MET:HE3	1:B:249:VAL:HG21	1.76	0.66
1:D:35:VAL:HG21	1:D:104:LEU:HD22	1.78	0.65
1:A:199:THR:HG23	1:C:199:THR:HG21	1.79	0.63
1:C:52:THR:HG21	1:C:97:LEU:HB3	1.81	0.62
1:A:294:PHE:HZ	1:A:301:THR:HG21	1.64	0.61
1:A:138:THR:HG22	1:A:190:SER:HA	1.83	0.60
1:C:138:THR:HG22	1:C:190:SER:HA	1.82	0.60
1:B:52:THR:HG21	1:B:97:LEU:HB3	1.83	0.60
1:C:288:CYS:SG	1:C:323:CYS:N	2.76	0.58
1:A:110:GLY:O	1:A:111:ILE:HD13	2.04	0.57
1:C:113:SER:OG	1:C:219:GLU:OE2	2.21	0.57
1:A:81:GLU:N	1:A:81:GLU:OE1	2.39	0.56
1:D:180:ASP:O	1:D:181:GLN:NE2	2.38	0.56
1:D:288:CYS:SG	1:D:323:CYS:N	2.78	0.56
1:D:138:THR:HG22	1:D:190:SER:HA	1.87	0.55
1:A:35:VAL:HG21	1:A:104:LEU:HD22	1.89	0.55
1:B:65:ARG:NH2	1:B:84:ASP:OD1	2.39	0.55
1:B:180:ASP:O	1:B:181:GLN:HG3	2.08	0.54
1:A:199:THR:CG2	1:C:199:THR:HG21	2.37	0.54
1:D:272:VAL:HG22	1:D:312:VAL:HG12	1.90	0.53
1:A:153:ILE:HD12	1:A:209:ALA:O	2.09	0.53
1:D:35:VAL:CG2	1:D:104:LEU:HD22	2.38	0.52
1:B:138:THR:HG22	1:B:190:SER:HA	1.90	0.52
1:B:117:LEU:HD13	1:B:221:TYR:CE1	2.44	0.52
1:B:244:LEU:HD12	1:B:245:LYS:CG	2.39	0.52
1:C:35:VAL:HG21	1:C:104:LEU:HD22	1.92	0.52
1:C:243:PRO:HA	1:C:249:VAL:HG12	1.92	0.52
1:D:154:LYS:HD3	1:D:155:SER:H	1.75	0.52
1:A:92:LYS:HB3	1:A:97:LEU:HD11	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:202:GLU:OE2	1:D:227:ILE:HB	2.11	0.51
1:D:239:LEU:HD21	1:D:312:VAL:CG2	2.41	0.50
1:D:121:LYS:HG3	1:D:122:ASN:N	2.27	0.50
1:A:251:VAL:HG21	1:A:310:VAL:HG11	1.92	0.50
1:C:220:ASN:HD22	2:G:1:NAG:C7	2.25	0.49
1:B:265:TYR:HD1	1:D:264:SER:HG	1.57	0.49
1:D:43:GLY:CA	1:D:80:LYS:HG2	2.43	0.49
1:A:97:LEU:HD12	1:A:97:LEU:N	2.28	0.49
1:A:214:GLN:O	1:A:216:ASN:N	2.44	0.49
1:D:92:LYS:HB3	1:D:97:LEU:HD21	1.95	0.49
1:D:213:ARG:HA	1:D:217:LYS:O	2.13	0.49
1:A:244:LEU:HD22	1:A:248:GLN:HB2	1.95	0.48
1:A:272:VAL:HG22	1:A:312:VAL:HG22	1.95	0.47
1:C:195:VAL:HG23	1:C:195:VAL:O	2.15	0.47
1:D:274:ILE:HD11	1:D:303:VAL:HG21	1.96	0.47
1:C:89:THR:HG22	1:C:96:THR:HG23	1.97	0.47
1:C:202:GLU:OE2	1:C:227:ILE:HB	2.14	0.47
1:C:259:TRP:CZ2	1:C:268:LEU:HD21	2.50	0.47
1:B:70:GLY:HA3	1:B:75:LEU:HD13	1.97	0.47
1:D:77:ILE:CD1	1:D:88:TYR:HE2	2.27	0.47
1:B:23:MET:SD	1:B:46:VAL:HG11	2.56	0.46
1:D:106:LYS:HB2	1:D:113:SER:HB3	1.98	0.46
1:C:239:LEU:HD21	1:C:312:VAL:CG2	2.45	0.46
1:A:152:ASN:O	1:A:210:LEU:HD12	2.16	0.46
1:B:149:LEU:HD23	1:B:151:PHE:CZ	2.51	0.46
1:B:97:LEU:HD12	1:B:97:LEU:N	2.31	0.45
1:C:255:TYR:HE1	1:C:268:LEU:HB2	1.81	0.45
1:C:272:VAL:HG23	1:C:296:VAL:HG12	1.97	0.45
1:B:244:LEU:HD23	1:B:250:GLU:N	2.31	0.45
1:D:123:LYS:O	1:D:123:LYS:HG2	2.16	0.45
1:D:197:CYS:SG	1:D:200:ALA:HB2	2.56	0.45
1:A:294:PHE:CZ	1:A:301:THR:HG21	2.49	0.45
1:D:38:THR:O	1:D:80:LYS:NZ	2.50	0.45
1:D:43:GLY:HA3	1:D:80:LYS:HG2	1.99	0.45
1:A:156:SER:HB3	1:A:209:ALA:HB2	1.98	0.45
1:A:195:VAL:O	1:A:195:VAL:HG23	2.17	0.44
1:A:92:LYS:N	1:A:97:LEU:HD11	2.32	0.44
1:C:117:LEU:HD23	1:C:221:TYR:CE1	2.51	0.44
1:C:214:GLN:O	1:C:215:GLN:C	2.56	0.44
1:A:163:ARG:HD2	1:A:204:LEU:O	2.17	0.44
1:B:275:GLN:O	1:B:309:ASN:N	2.48	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:ARG:HA	1:A:217:LYS:O	2.19	0.43
1:D:195:VAL:O	1:D:195:VAL:HG23	2.18	0.43
1:A:82:PHE:CD1	1:A:104:LEU:HD12	2.54	0.43
1:B:75:LEU:HG	1:B:77:ILE:HG23	2.00	0.43
1:C:179:LEU:O	1:C:181:GLN:N	2.52	0.43
1:D:241:MET:HE3	1:D:249:VAL:HG21	2.00	0.43
1:D:79:VAL:HG11	1:D:104:LEU:HD21	2.01	0.42
1:A:247:SER:HB2	1:A:304:GLN:OE1	2.19	0.42
1:B:213:ARG:HA	1:B:217:LYS:O	2.20	0.42
1:B:120:PHE:CZ	1:B:142:LEU:HD13	2.55	0.42
1:D:33:VAL:HB	1:D:104:LEU:HD23	2.01	0.42
1:C:236:PRO:HB2	1:C:239:LEU:HD11	2.01	0.42
1:B:123:LYS:HG2	1:B:123:LYS:O	2.20	0.41
1:D:122:ASN:ND2	1:D:124:THR:HG22	2.35	0.41
1:A:244:LEU:HD13	1:A:302:GLU:HG2	2.02	0.41
1:B:204:LEU:HD13	1:B:205:PRO:HD2	2.03	0.41
1:C:45:THR:CG2	1:C:76:THR:CG2	2.98	0.41
1:B:47:ASN:C	1:B:48:LEU:HD22	2.41	0.41
1:C:272:VAL:HG22	1:C:312:VAL:HG12	2.03	0.41
1:D:52:THR:HG22	1:D:54:GLU:H	1.86	0.41
1:D:180:ASP:O	1:D:181:GLN:CD	2.59	0.41
1:B:195:VAL:O	1:B:195:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	297/344 (86%)	280 (94%)	16 (5%)	1 (0%)	41 75
1	B	297/344 (86%)	283 (95%)	14 (5%)	0	100 100
1	C	299/344 (87%)	284 (95%)	14 (5%)	1 (0%)	41 75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	294/344 (86%)	280 (95%)	14 (5%)	0	100	100
All	All	1187/1376 (86%)	1127 (95%)	58 (5%)	2 (0%)	47	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	215	GLN
1	C	180	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	A	272/315 (86%)	272 (100%)	0	100	100
1	B	269/315 (85%)	268 (100%)	1 (0%)	91	96
1	C	272/315 (86%)	269 (99%)	3 (1%)	73	88
1	D	274/315 (87%)	272 (99%)	2 (1%)	84	93
All	All	1087/1260 (86%)	1081 (99%)	6 (1%)	86	94

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	122	ASN
1	C	71	SER
1	C	294	PHE
1	C	319	TYR
1	D	154	LYS
1	D	294	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	91	HIS

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](#)

16 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	E	1	2,1	14,14,15	0.23	0	17,19,21	0.70	0
2	NAG	E	2	2	14,14,15	0.31	0	17,19,21	0.72	1 (5%)
2	BMA	E	3	2	11,11,12	0.33	0	15,15,17	0.70	1 (6%)
2	MAN	E	4	2	11,11,12	0.24	0	15,15,17	0.76	1 (6%)
2	NAG	F	1	2,1	14,14,15	0.25	0	17,19,21	0.79	1 (5%)
2	NAG	F	2	2	14,14,15	0.26	0	17,19,21	0.75	0
2	BMA	F	3	2	11,11,12	0.33	0	15,15,17	0.59	0
2	MAN	F	4	2	11,11,12	0.36	0	15,15,17	0.70	0
2	NAG	G	1	2,1	14,14,15	0.34	0	17,19,21	0.85	1 (5%)
2	NAG	G	2	2	14,14,15	0.30	0	17,19,21	0.67	0
2	BMA	G	3	2	11,11,12	0.30	0	15,15,17	0.58	0
2	MAN	G	4	2	11,11,12	0.24	0	15,15,17	0.77	1 (6%)
2	NAG	H	1	2,1	14,14,15	0.31	0	17,19,21	0.70	0
2	NAG	H	2	2	14,14,15	0.29	0	17,19,21	0.63	1 (5%)
2	BMA	H	3	2	11,11,12	0.25	0	15,15,17	0.58	0
2	MAN	H	4	2	11,11,12	0.28	0	15,15,17	0.73	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	E	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4	2	-	0/2/19/22	0/1/1/1
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	2/2/19/22	0/1/1/1
2	MAN	F	4	2	-	0/2/19/22	0/1/1/1
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
2	MAN	G	4	2	-	0/2/19/22	0/1/1/1
2	NAG	H	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1
2	BMA	H	3	2	-	0/2/19/22	0/1/1/1
2	MAN	H	4	2	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	4	MAN	C1-O5-C5	2.74	115.91	112.19
2	E	2	NAG	O5-C1-C2	-2.58	107.22	111.29
2	G	1	NAG	C1-O5-C5	2.51	115.60	112.19
2	G	4	MAN	C1-O5-C5	2.33	115.34	112.19
2	E	3	BMA	C1-O5-C5	2.31	115.32	112.19
2	H	2	NAG	C1-O5-C5	2.10	115.04	112.19
2	F	1	NAG	C1-O5-C5	2.08	115.01	112.19

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	2	NAG	O5-C5-C6-O6
2	H	2	NAG	C4-C5-C6-O6
2	F	3	BMA	O5-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	F	3	BMA	C4-C5-C6-O6
2	G	3	BMA	C4-C5-C6-O6
2	G	3	BMA	O5-C5-C6-O6
2	H	4	MAN	C4-C5-C6-O6

Continued on next page...

Continued from previous page...

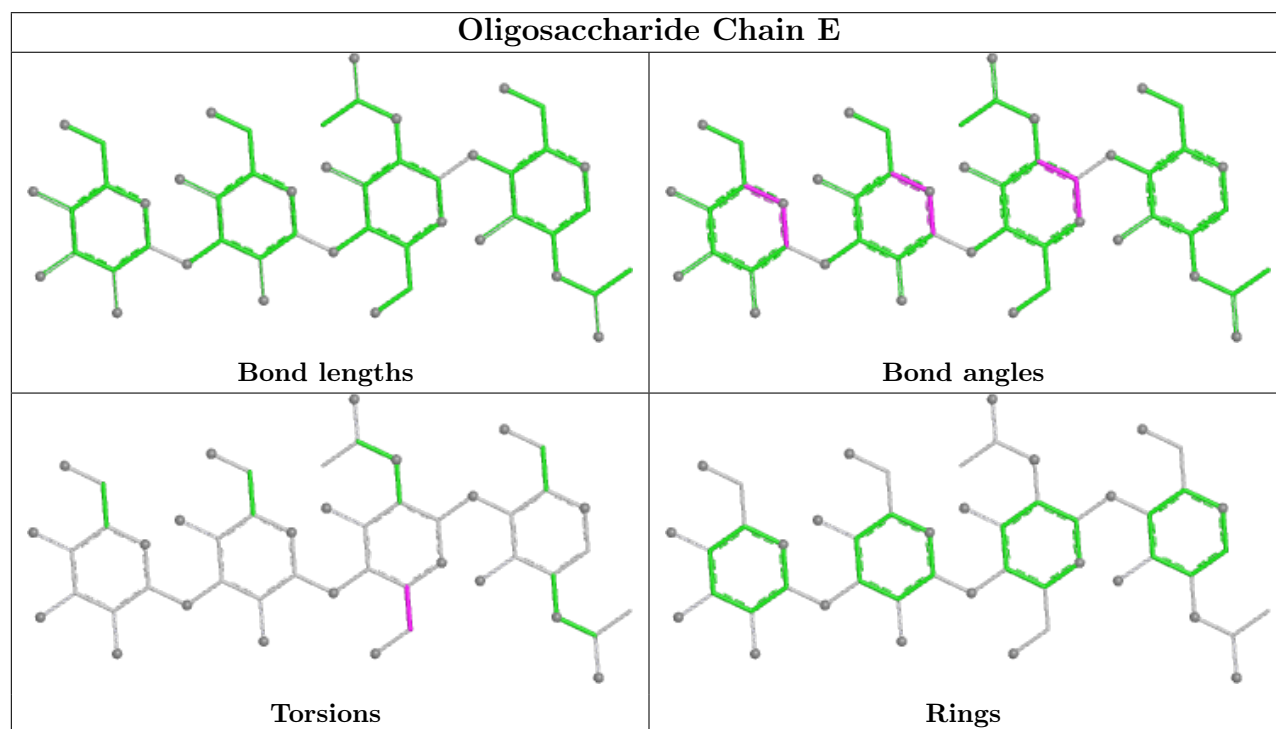
Mol	Chain	Res	Type	Atoms
2	E	2	NAG	C4-C5-C6-O6
2	H	4	MAN	O5-C5-C6-O6

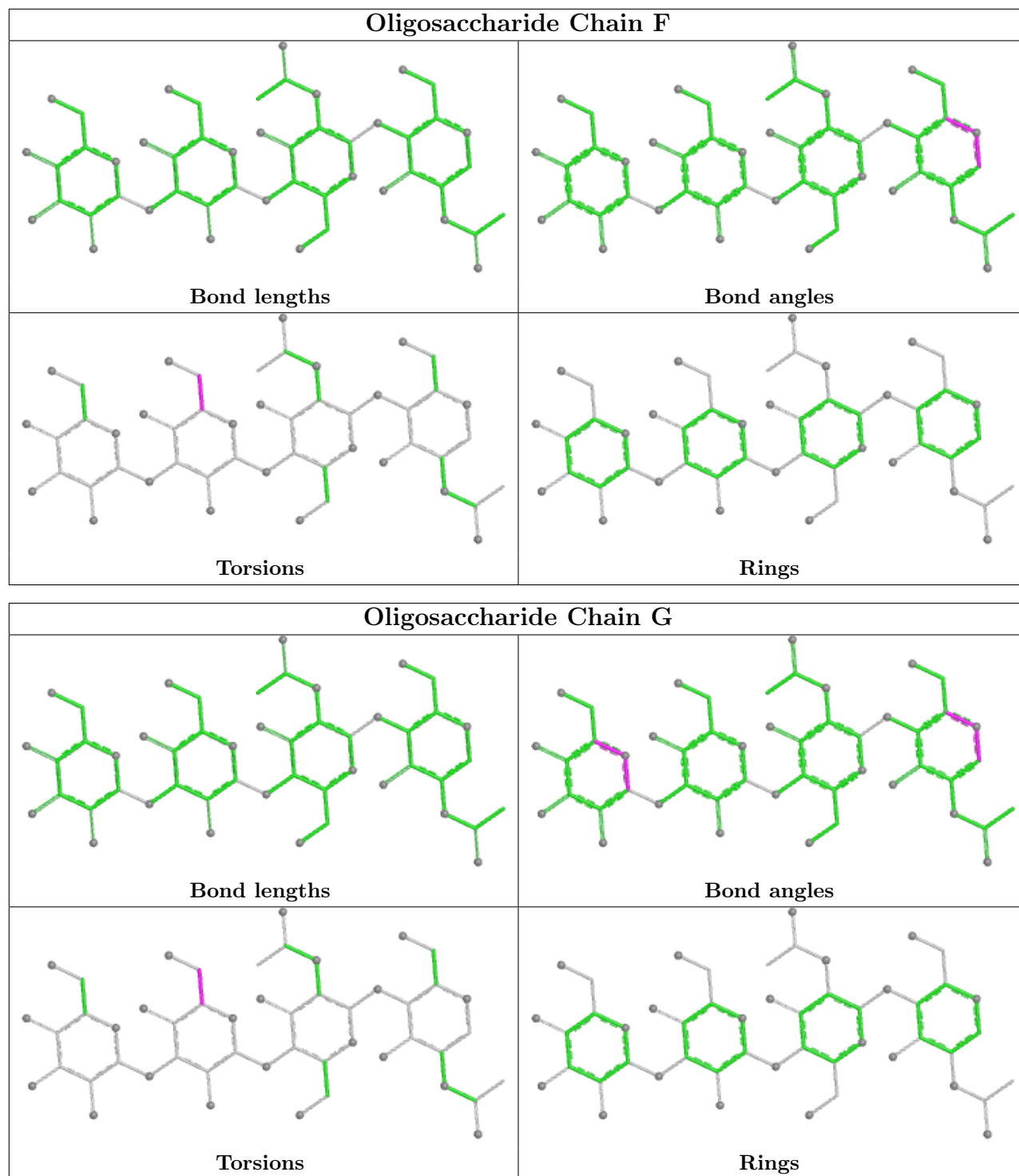
There are no ring outliers.

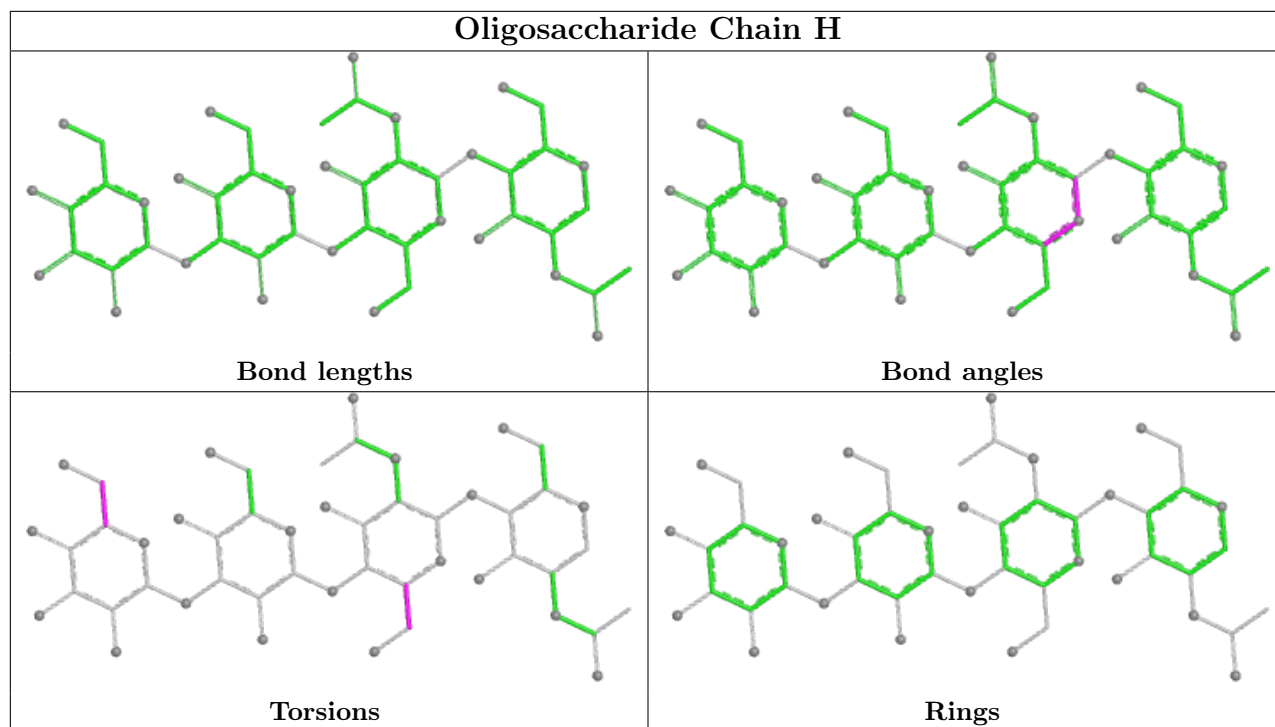
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	A	301/344 (87%)	0.27	10 (3%) 46 41	113, 147, 191, 215	0
1	B	301/344 (87%)	0.23	9 (2%) 50 44	104, 134, 178, 200	0
1	C	303/344 (88%)	0.32	11 (3%) 42 38	111, 149, 201, 230	0
1	D	300/344 (87%)	0.36	15 (5%) 28 25	142, 165, 199, 210	0
All	All	1205/1376 (87%)	0.29	45 (3%) 41 37	104, 151, 196, 230	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	79	VAL	4.2
1	D	216	ASN	4.0
1	C	102	LEU	3.7
1	D	76	THR	3.3
1	D	126	LEU	3.1
1	C	89	THR	3.1
1	D	189	VAL	2.9
1	C	23	MET	2.9
1	A	23	MET	2.8
1	D	23	MET	2.7
1	A	61	THR	2.7
1	A	48	LEU	2.7
1	D	244	LEU	2.6
1	B	54	GLU	2.6
1	D	100	SER	2.6
1	D	241	MET	2.6
1	C	52	THR	2.5
1	C	126	LEU	2.5
1	D	223	THR	2.5
1	D	88	TYR	2.5
1	A	206	ILE	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	99	HIS	2.4
1	C	151	PHE	2.4
1	A	73	LYS	2.4
1	B	89	THR	2.4
1	C	57	ASP	2.3
1	B	102	LEU	2.3
1	B	52	THR	2.2
1	B	308	GLY	2.2
1	B	287	GLY	2.2
1	D	153	ILE	2.2
1	D	61	THR	2.1
1	C	103	LEU	2.1
1	B	294	PHE	2.1
1	D	272	VAL	2.1
1	B	290	GLN	2.1
1	C	191	CYS	2.1
1	A	170	ALA	2.1
1	A	143	VAL	2.1
1	A	239	LEU	2.1
1	D	52	THR	2.1
1	C	61	THR	2.1
1	B	23	MET	2.0
1	A	82	PHE	2.0
1	A	213	ARG	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.

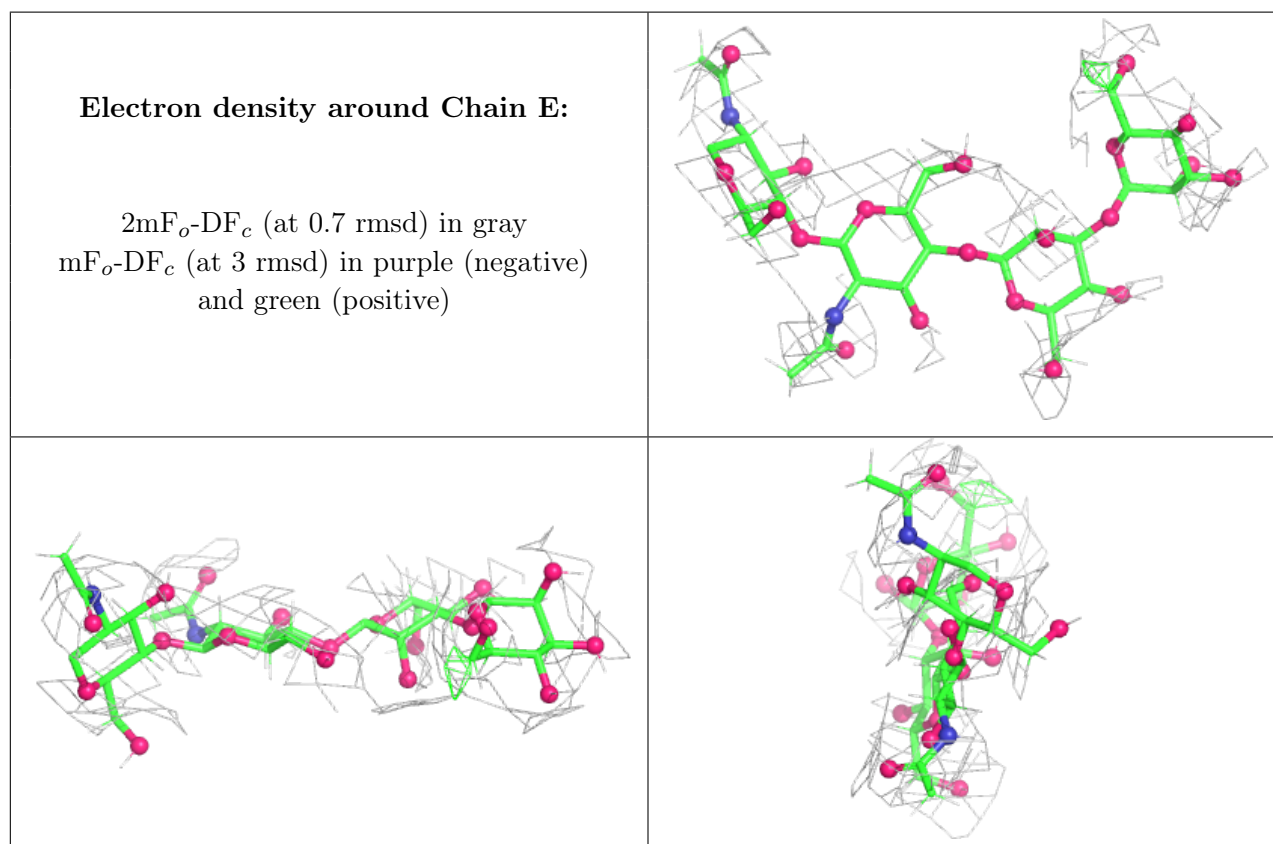
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	E	1	14/15	0.73	0.38	168,182,190,192	0
2	BMA	G	3	11/12	0.80	0.14	217,247,270,276	0
2	MAN	G	4	11/12	0.80	0.25	247,256,274,280	0
2	NAG	H	1	14/15	0.81	0.28	185,199,218,222	0

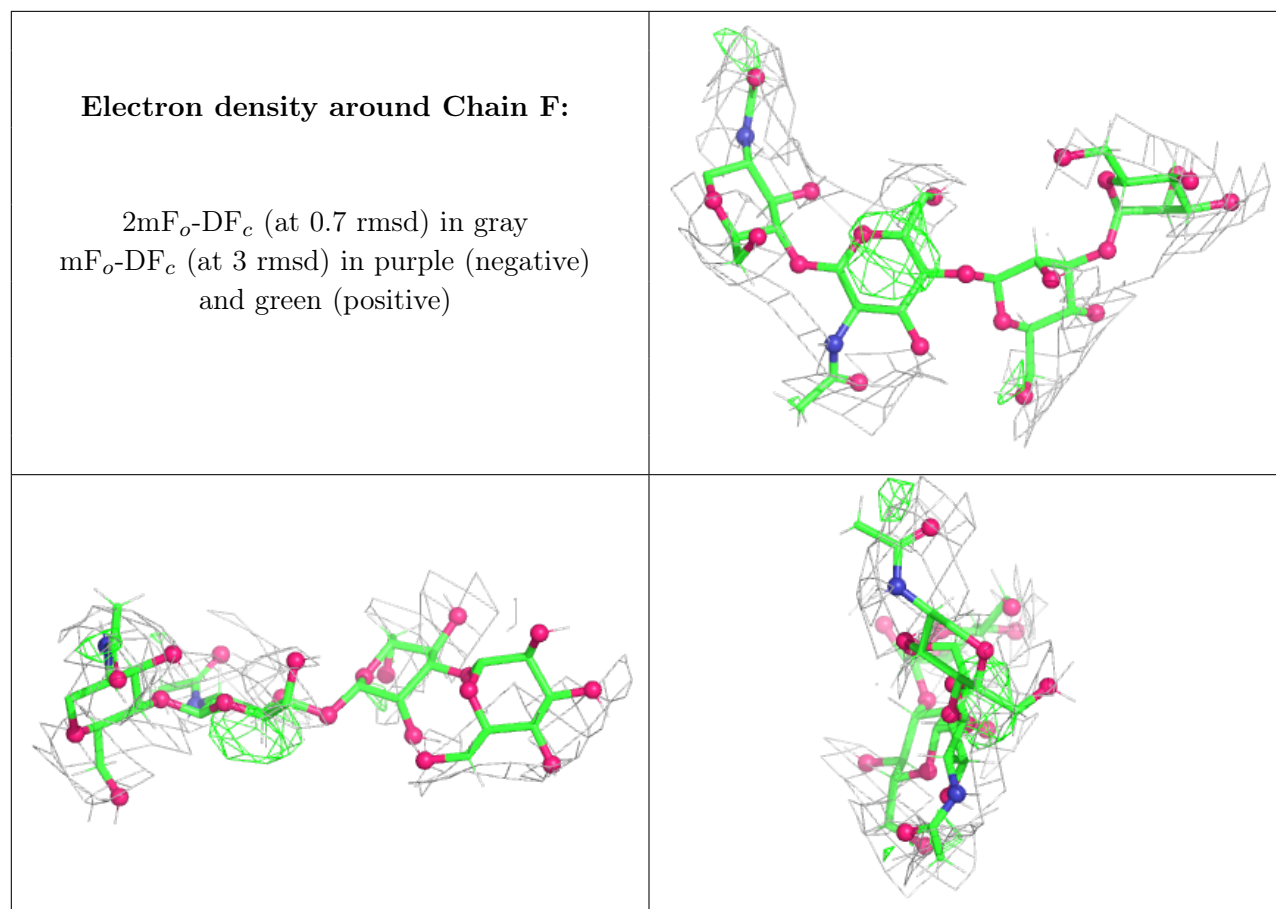
Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	G	1	14/15	0.83	0.19	183,195,209,211	0
2	MAN	F	4	11/12	0.83	0.17	203,217,222,226	0
2	BMA	H	3	11/12	0.85	0.26	225,234,244,246	0
2	BMA	F	3	11/12	0.86	0.16	202,208,216,219	0
2	NAG	G	2	14/15	0.86	0.17	200,214,222,229	0
2	NAG	E	2	14/15	0.87	0.26	192,203,214,218	0
2	BMA	E	3	11/12	0.87	0.25	216,245,262,264	0
2	NAG	H	2	14/15	0.88	0.18	209,223,234,237	0
2	MAN	E	4	11/12	0.89	0.19	224,250,255,259	0
2	NAG	F	2	14/15	0.91	0.21	187,196,203,207	0
2	NAG	F	1	14/15	0.91	0.29	166,174,182,183	0
2	MAN	H	4	11/12	0.91	0.18	222,226,237,238	0

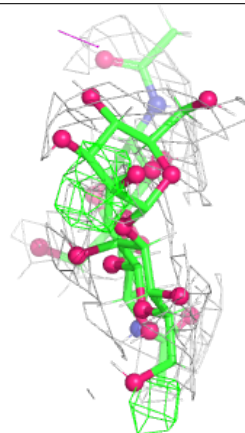
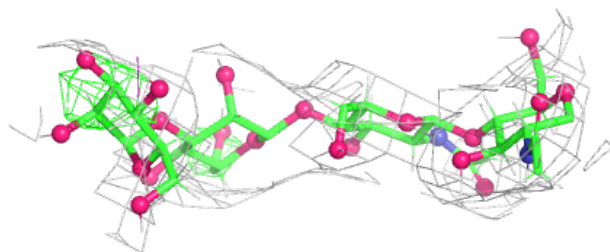
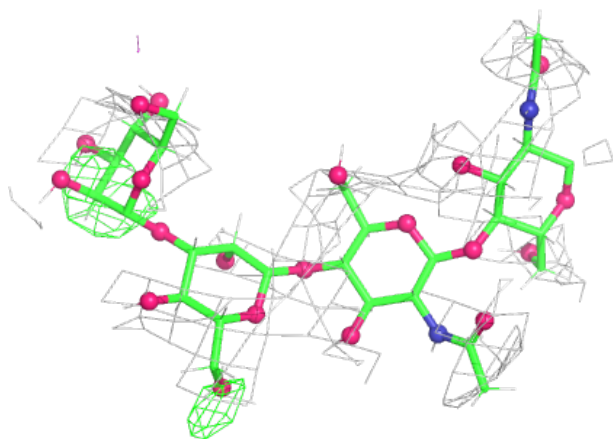
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

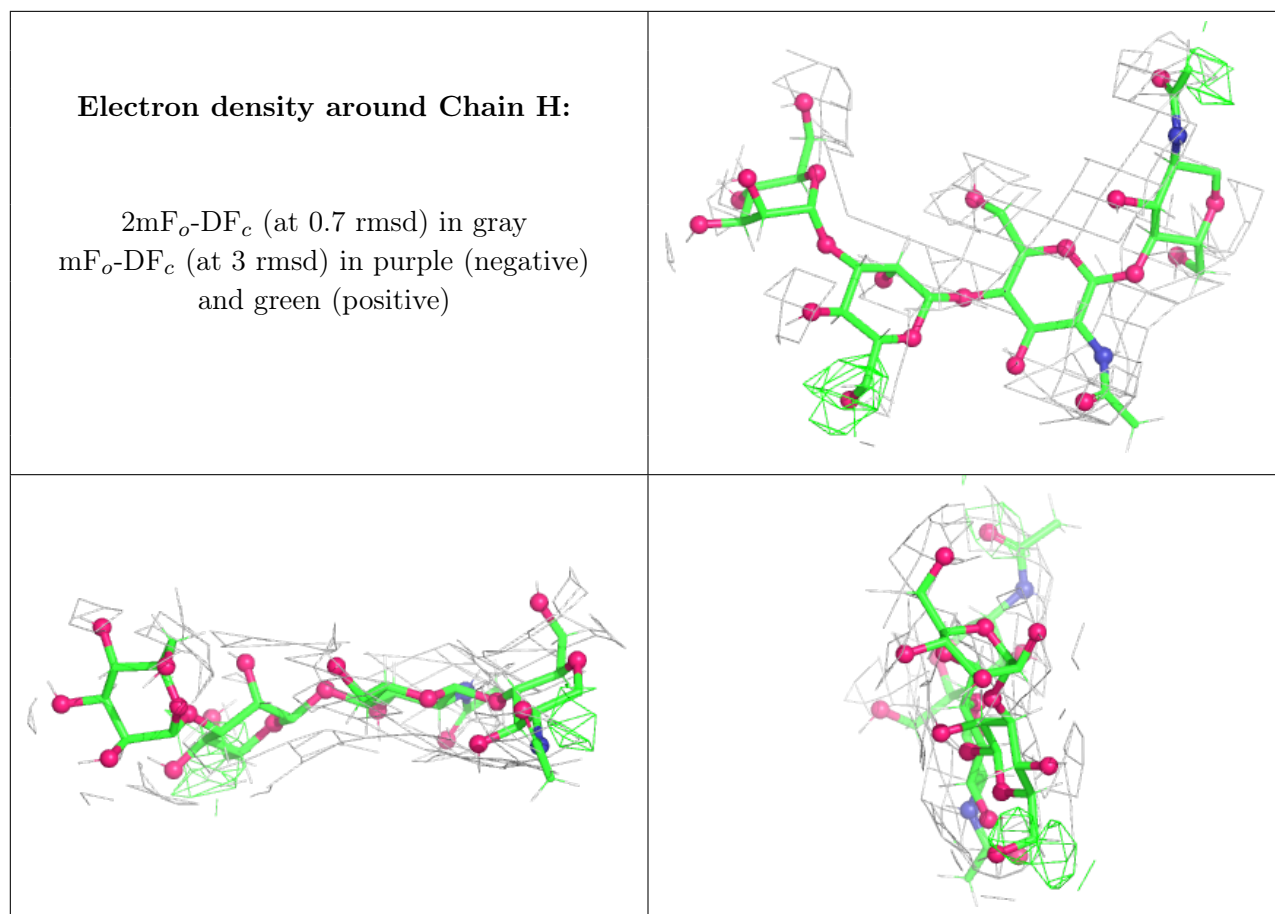




Electron density around Chain G:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CL	C	401	1/1	0.16	0.51	80,80,80,80	0
3	CL	B	401	1/1	0.67	0.72	80,80,80,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.