Full wwPDB X-ray Structure Validation Report (i)

Aug 7, 2023 – 07:56 PM EDT

PDB ID	:	1OYH
Title	:	Crystal Structure of P13 Alanine Variant of Antithrombin
Authors	:	Johnson, D.J.D.; Huntington, J.A.
Deposited on	:	2003-04-04
Resolution	:	2.62 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 (i) 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 (1)) were used in the production of this report:

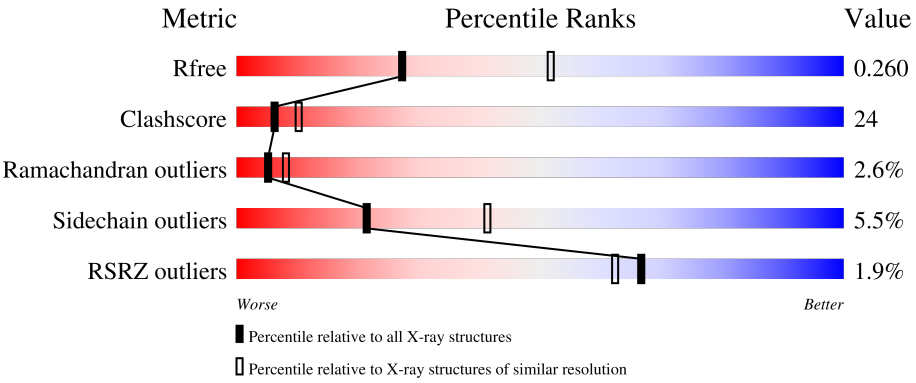
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 <=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	I	432	% 61% 31% 5% .
2	L	432	3% 53% 37% 5% 5%
3	A	2	50% 50%
3	B	2	100%
4	C	5	60% 40%

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	C	1	X	-	-	-
4	NAG	C	2	-	-	-	X
4	MAN	C	4	-	-	-	X
5	NAG	I	861	-	-	-	X
5	NAG	L	831	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6661 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 Antithrombin-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	416	Total	C	N	O	S	0	0	0
			3259	2083	545	615	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	137	ALA	SER	engineered mutation	UNP P01008
I	381	ALA	GLU	engineered mutation	UNP P01008

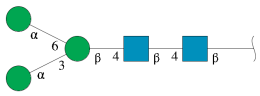
- Molecule 2 is a protein called Antithrombin-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	410	Total	C	N	O	S	0	0	0
			3175	2028	518	611	18			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

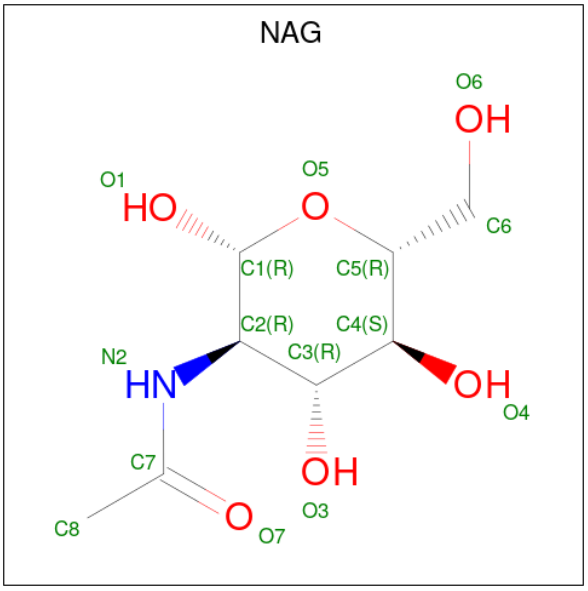
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	A	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(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
4	C	5	Total C N O 61 34 2 25	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	I	1	Total C N O 14 8 1 5	0	0
5	I	1	Total C N O 14 8 1 5	0	0
5	L	1	Total C N O 14 8 1 5	0	0
5	L	1	Total C N O 14 8 1 5	0	0

- Molecule 6 is water.

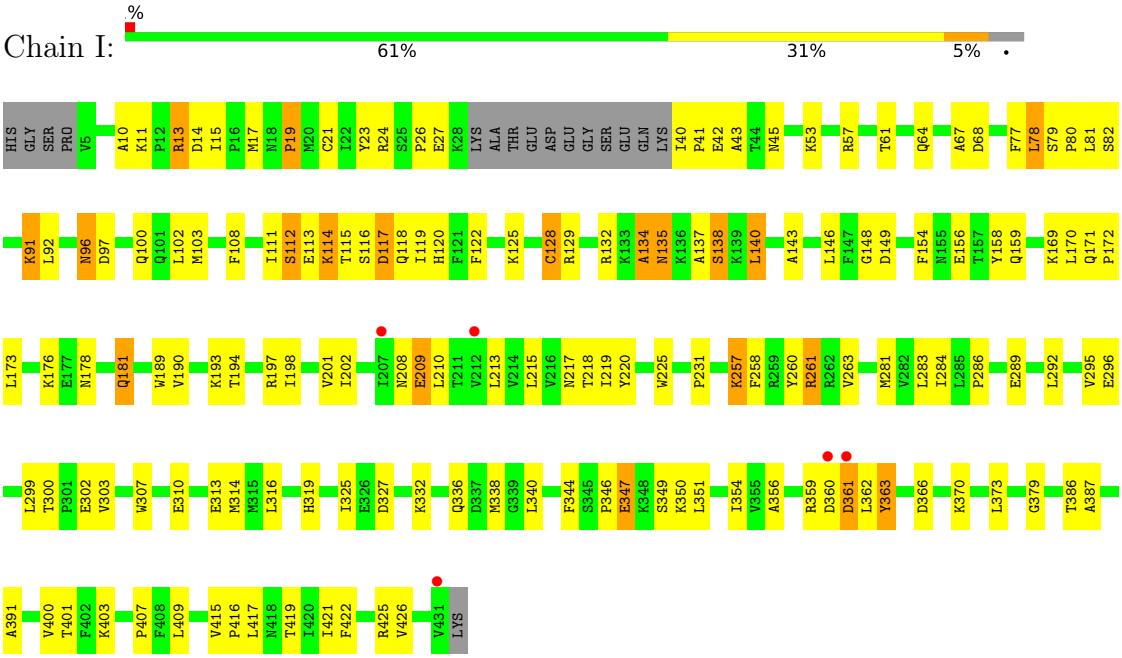
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	I	33	Total O 33 33	0	0
6	L	21	Total O 21 21	0	0

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.

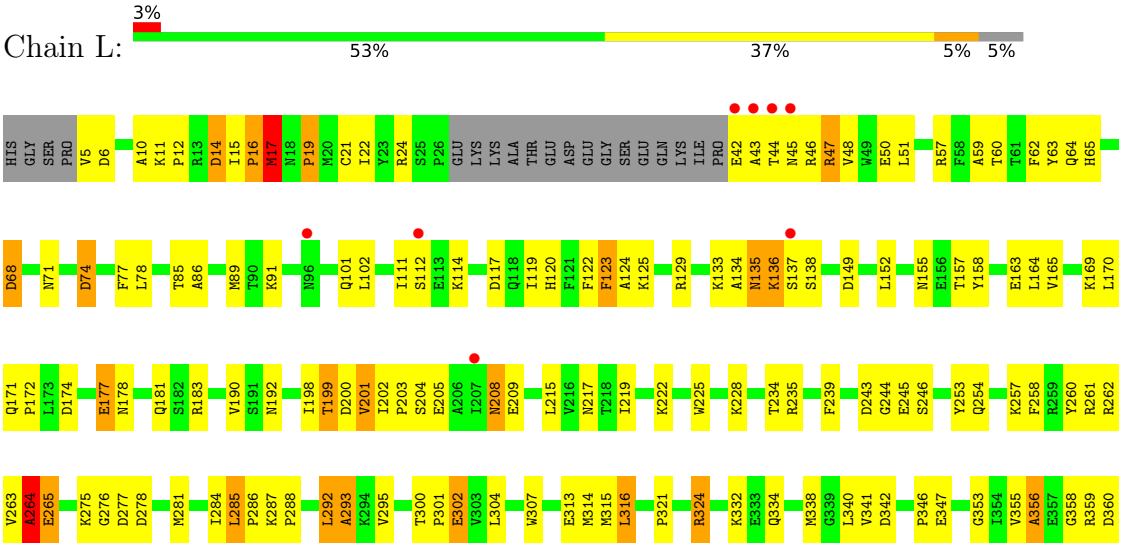
• Molecule 1: Antithrombin-III

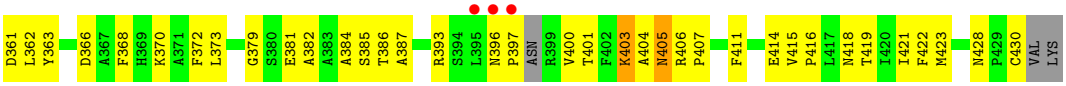
Chain I:



• Molecule 2: Antithrombin-III

Chain L:



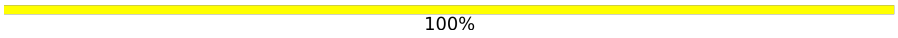


• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain A:

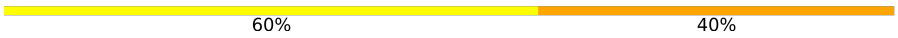
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:



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

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	69.00Å 98.57Å 89.35Å 90.00° 105.53° 90.00°	Depositor
Resolution (Å)	39.00 – 2.62 39.45 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.00-2.62) 99.8 (39.45-2.62)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.91 (at 2.61Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.258 0.223 , 0.260	Depositor DCC
R_{free} test set	1726 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	55.3	Xtriage
Anisotropy	0.472	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 49.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6661	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.19% 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: NAG, BMA, 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	I	0.42	0/3325	0.69	1/4503 (0.0%)
2	L	0.39	0/3238	0.66	2/4392 (0.0%)
All	All	0.41	0/6563	0.67	3/8895 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	L	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	134	ALA	N-CA-C	6.12	127.53	111.00
2	L	414	GLU	N-CA-C	-5.44	96.31	111.00
2	L	264	ALA	N-CA-C	5.02	124.56	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	363	TYR	Sidechain

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	I	3259	0	3200	147	0
2	L	3175	0	3050	168	0
3	A	28	0	25	1	0
3	B	28	0	25	1	0
4	C	61	0	52	7	0
5	I	28	0	26	5	0
5	L	28	0	26	2	0
6	I	33	0	0	2	0
6	L	21	0	0	2	0
All	All	6661	0	6404	316	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 24.

All (316) 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:L:86:ALA:HA	2:L:89:MET:HE3	1.39	1.04
2:L:292:LEU:HD23	2:L:407:PRO:HG2	1.46	0.96
2:L:208:ASN:HB3	2:L:393:ARG:HH12	1.28	0.95
2:L:63:TYR:HB2	2:L:423:MET:HE1	1.50	0.91
2:L:42:GLU:HG2	2:L:45:ASN:HD22	1.35	0.91
2:L:134:ALA:O	2:L:135:ASN:HB2	1.69	0.89
2:L:85:THR:HG22	2:L:89:MET:HE2	1.55	0.88
2:L:111:ILE:HD12	2:L:119:ILE:HG13	1.56	0.84
2:L:102:LEU:HD23	2:L:340:LEU:HD11	1.61	0.83
2:L:91:LYS:NZ	2:L:120:HIS:NE2	2.27	0.82
2:L:324:ARG:HG3	2:L:324:ARG:O	1.79	0.82
1:I:115:THR:H	1:I:118:GLN:HE21	1.30	0.79
1:I:13:ARG:HB3	1:I:13:ARG:HH21	1.48	0.78
1:I:13:ARG:HB3	1:I:13:ARG:NH2	1.98	0.77
2:L:405:ASN:ND2	2:L:406:ARG:H	1.82	0.77
1:I:19:PRO:C	1:I:21:CYS:H	1.89	0.76
2:L:264:ALA:O	2:L:265:GLU:HB2	1.85	0.75
1:I:190:VAL:HG21	1:I:201:VAL:HG21	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:47:ARG:HG2	2:L:122:PHE:CE2	2.24	0.71
1:I:108:PHE:HB3	1:I:119:ILE:HD13	1.71	0.71
2:L:292:LEU:CD2	2:L:407:PRO:HG2	2.19	0.71
1:I:143:ALA:O	1:I:217:ASN:HA	1.89	0.71
2:L:183:ARG:HG2	2:L:183:ARG:HH11	1.54	0.71
2:L:208:ASN:HB3	2:L:393:ARG:NH1	2.05	0.70
1:I:91:LYS:NZ	1:I:120:HIS:NE2	2.31	0.69
2:L:63:TYR:HB2	2:L:423:MET:CE	2.22	0.69
1:I:198:ILE:HG23	1:I:370:LYS:HD3	1.74	0.68
1:I:194:THR:O	1:I:197:ARG:HG2	1.92	0.68
1:I:350:LYS:HG3	5:I:801:NAG:H83	1.73	0.68
2:L:86:ALA:CA	2:L:89:MET:HE3	2.22	0.68
2:L:284:ILE:HD13	2:L:307:TRP:CZ3	2.29	0.68
1:I:189:TRP:O	1:I:193:LYS:HG2	1.93	0.68
1:I:111:ILE:HG22	1:I:114:LYS:HD3	1.76	0.68
1:I:386:THR:HA	2:L:315:MET:O	1.94	0.68
2:L:192:ASN:HA	4:C:1:NAG:N2	2.09	0.67
2:L:17:MET:HG3	2:L:17:MET:O	1.92	0.67
1:I:108:PHE:HB3	1:I:119:ILE:CD1	2.23	0.67
2:L:228:LYS:HE3	2:L:275:LYS:HE3	1.77	0.67
2:L:15:ILE:HD12	2:L:164:LEU:HD21	1.75	0.66
1:I:261:ARG:HG2	1:I:310:GLU:HB3	1.77	0.66
1:I:102:LEU:HD23	1:I:340:LEU:HD11	1.78	0.66
2:L:5:VAL:HG12	2:L:6:ASP:H	1.59	0.66
1:I:15:ILE:HG22	1:I:15:ILE:O	1.95	0.65
1:I:137:ALA:O	1:I:138:SER:CB	2.44	0.65
1:I:26:PRO:O	1:I:112:SER:O	2.15	0.65
2:L:263:VAL:O	2:L:265:GLU:N	2.27	0.65
1:I:67:ALA:HB1	1:I:425:ARG:NH2	2.12	0.65
1:I:292:LEU:O	1:I:296:GLU:HG3	1.97	0.64
2:L:21:CYS:C	2:L:22:ILE:HD12	2.16	0.64
1:I:156:GLU:HA	1:I:159:GLN:HE21	1.62	0.64
2:L:360:ASP:O	2:L:362:LEU:N	2.31	0.64
1:I:178:ASN:HA	1:I:181:GLN:OE1	1.98	0.63
1:I:64:GLN:O	1:I:68:ASP:HB2	1.99	0.63
1:I:128:CYS:O	1:I:132:ARG:HB2	1.99	0.63
2:L:178:ASN:HB3	2:L:181:GLN:HB3	1.80	0.63
2:L:42:GLU:HG2	2:L:45:ASN:ND2	2.12	0.62
2:L:5:VAL:HG12	2:L:6:ASP:N	2.14	0.62
2:L:405:ASN:HD22	2:L:406:ARG:H	1.47	0.62
1:I:347:GLU:HG2	6:I:885:HOH:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:198:ILE:HG23	2:L:370:LYS:HG2	1.82	0.61
1:I:316:LEU:HB2	1:I:400:VAL:O	2.00	0.61
1:I:213:LEU:HD11	1:I:354:ILE:HD13	1.81	0.61
2:L:183:ARG:HG2	2:L:183:ARG:NH1	2.13	0.61
2:L:276:GLY:O	2:L:277:ASP:HB2	1.99	0.61
2:L:208:ASN:CB	2:L:393:ARG:HH12	2.08	0.60
2:L:129:ARG:HH11	2:L:129:ARG:HG3	1.67	0.60
1:I:292:LEU:HD11	1:I:409:LEU:HG	1.82	0.60
1:I:19:PRO:C	1:I:21:CYS:N	2.55	0.60
2:L:192:ASN:HA	4:C:1:NAG:HN2	1.66	0.60
1:I:115:THR:OG1	1:I:118:GLN:HG3	2.03	0.59
1:I:194:THR:HG21	1:I:198:ILE:HD12	1.85	0.59
1:I:387:ALA:O	2:L:316:LEU:HB2	2.03	0.59
1:I:125:LYS:HE2	1:I:129:ARG:HH21	1.68	0.59
1:I:77:PHE:CE2	1:I:373:LEU:HB2	2.38	0.59
1:I:209:GLU:CD	1:I:209:GLU:H	2.06	0.58
1:I:81:LEU:HD22	1:I:419:THR:HG21	1.85	0.58
1:I:17:MET:CB	1:I:117:ASP:HB2	2.34	0.58
4:C:1:NAG:H62	4:C:2:NAG:O7	2.04	0.58
2:L:225:TRP:CD1	2:L:379:GLY:HA2	2.39	0.58
2:L:134:ALA:O	2:L:135:ASN:CB	2.49	0.58
2:L:292:LEU:HD21	2:L:407:PRO:O	2.04	0.57
1:I:356:ALA:HB3	1:I:359:ARG:HB3	1.86	0.57
1:I:125:LYS:HE2	1:I:129:ARG:NH2	2.20	0.57
2:L:137:SER:HB2	5:L:831:NAG:O6	2.05	0.57
1:I:82:SER:HB2	1:I:219:ILE:HG13	1.87	0.56
1:I:11:LYS:HE3	1:I:14:ASP:OD2	2.04	0.56
2:L:129:ARG:HG3	2:L:129:ARG:NH1	2.20	0.56
1:I:363:TYR:CD1	1:I:363:TYR:N	2.72	0.56
2:L:192:ASN:HA	4:C:1:NAG:C7	2.36	0.56
1:I:148:GLY:O	1:I:172:PRO:HA	2.06	0.56
1:I:260:TYR:CG	1:I:261:ARG:N	2.75	0.55
2:L:355:VAL:HG23	2:L:362:LEU:HD11	1.88	0.55
1:I:53:LYS:O	1:I:57:ARG:HG3	2.06	0.55
2:L:91:LYS:CE	2:L:120:HIS:NE2	2.69	0.55
2:L:190:VAL:HG21	2:L:201:VAL:HG21	1.89	0.55
2:L:355:VAL:HG12	2:L:356:ALA:N	2.22	0.55
1:I:140:LEU:HD21	1:I:421:ILE:HD13	1.89	0.55
1:I:257:LYS:HD2	1:I:313:GLU:HB3	1.88	0.54
2:L:136:LYS:C	2:L:138:SER:H	2.11	0.54
1:I:40:ILE:N	1:I:41:PRO:HD2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:190:VAL:HG11	1:I:201:VAL:CG1	2.37	0.54
2:L:59:ALA:O	2:L:423:MET:HE1	2.07	0.54
2:L:62:PHE:HD1	2:L:338:MET:HE1	1.73	0.54
2:L:353:GLY:HA3	6:L:882:HOH:O	2.07	0.54
2:L:62:PHE:HA	2:L:338:MET:CE	2.38	0.53
1:I:129:ARG:HB2	1:I:417:LEU:HD11	1.90	0.53
1:I:181:GLN:CD	1:I:181:GLN:H	2.11	0.53
1:I:112:SER:OG	1:I:113:GLU:N	2.42	0.53
1:I:213:LEU:HD11	1:I:354:ILE:CD1	2.38	0.52
1:I:356:ALA:HB3	1:I:359:ARG:CB	2.39	0.52
2:L:360:ASP:C	2:L:362:LEU:H	2.12	0.52
1:I:284:ILE:HB	1:I:409:LEU:HB2	1.91	0.52
2:L:149:ASP:HB3	2:L:152:LEU:HG	1.92	0.52
2:L:404:ALA:HB2	2:L:428:ASN:HD22	1.74	0.52
1:I:354:ILE:HG22	1:I:362:LEU:HD13	1.90	0.52
2:L:91:LYS:HZ3	2:L:120:HIS:CD2	2.24	0.52
1:I:178:ASN:HB3	1:I:181:GLN:HG2	1.92	0.52
1:I:263:VAL:HG21	1:I:307:TRP:CE2	2.45	0.52
2:L:257:LYS:HD2	2:L:313:GLU:OE2	2.10	0.52
2:L:174:ASP:OD1	2:L:177:GLU:HB2	2.10	0.51
1:I:103:MET:HE1	1:I:119:ILE:CD1	2.40	0.51
2:L:418:ASN:CG	2:L:418:ASN:O	2.47	0.51
3:A:1:NAG:H62	3:A:2:NAG:C1	2.41	0.51
2:L:428:ASN:OD1	2:L:430:CYS:HB2	2.09	0.51
2:L:62:PHE:HA	2:L:338:MET:HE1	1.92	0.51
1:I:225:TRP:CD1	1:I:379:GLY:HA2	2.46	0.51
2:L:334:GLN:CD	2:L:334:GLN:H	2.14	0.51
1:I:96:ASN:OD1	5:I:801:NAG:C2	2.58	0.51
1:I:281:MET:HE3	1:I:283:LEU:HD21	1.93	0.51
2:L:393:ARG:NH1	2:L:393:ARG:HB2	2.25	0.51
1:I:415:VAL:HB	1:I:416:PRO:HD3	1.92	0.51
2:L:200:ASP:O	2:L:201:VAL:C	2.48	0.51
1:I:77:PHE:CZ	1:I:373:LEU:HB2	2.46	0.51
1:I:361:ASP:OD2	1:I:361:ASP:N	2.37	0.51
2:L:170:LEU:C	2:L:170:LEU:HD23	2.32	0.51
1:I:24:ARG:HG3	1:I:24:ARG:NH1	2.26	0.50
1:I:349:SER:OG	1:I:351:LEU:HD13	2.11	0.50
2:L:91:LYS:HE2	2:L:120:HIS:NE2	2.26	0.50
2:L:278:ASP:OD1	2:L:278:ASP:N	2.37	0.50
2:L:401:THR:HG22	2:L:403:LYS:H	1.76	0.50
1:I:361:ASP:HA	6:I:886:HOH:O	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:341:VAL:HG23	2:L:342:ASP:N	2.26	0.50
2:L:208:ASN:C	2:L:208:ASN:HD22	2.14	0.50
1:I:23:TYR:O	1:I:115:THR:HA	2.12	0.50
1:I:292:LEU:HD11	1:I:409:LEU:CD2	2.41	0.50
2:L:125:LYS:O	2:L:129:ARG:HG2	2.11	0.50
1:I:197:ARG:HG3	1:I:220:TYR:CE1	2.46	0.50
2:L:45:ASN:OD1	2:L:129:ARG:NH2	2.45	0.50
2:L:46:ARG:O	2:L:50:GLU:HG3	2.12	0.50
2:L:239:PHE:O	2:L:246:SER:HA	2.12	0.50
1:I:201:VAL:HG23	1:I:202:ILE:HG12	1.94	0.50
2:L:17:MET:CE	2:L:19:PRO:HD3	2.42	0.50
4:C:2:NAG:H61	4:C:3:BMA:C1	2.42	0.50
1:I:96:ASN:OD1	5:I:801:NAG:H2	2.11	0.50
2:L:62:PHE:CD1	2:L:338:MET:HE1	2.46	0.50
2:L:198:ILE:HD12	2:L:370:LYS:HG3	1.93	0.50
2:L:285:LEU:N	2:L:285:LEU:HD23	2.28	0.49
1:I:115:THR:N	1:I:118:GLN:HE21	2.06	0.49
1:I:91:LYS:CB	1:I:102:LEU:HD13	2.42	0.49
2:L:71:ASN:HB3	2:L:74:ASP:HB2	1.94	0.49
2:L:372:PHE:O	2:L:382:ALA:HA	2.12	0.49
1:I:193:LYS:HA	5:I:861:NAG:H82	1.94	0.49
2:L:155:ASN:HB3	2:L:158:TYR:HB3	1.95	0.49
1:I:77:PHE:CE1	1:I:373:LEU:HD22	2.48	0.49
1:I:135:ASN:C	1:I:137:ALA:N	2.65	0.49
1:I:24:ARG:HG3	1:I:24:ARG:HH11	1.78	0.49
1:I:258:PHE:HB2	1:I:316:LEU:HD21	1.95	0.49
1:I:114:LYS:HG3	1:I:118:GLN:NE2	2.28	0.49
1:I:257:LYS:HA	1:I:314:MET:O	2.13	0.49
2:L:234:THR:HG22	2:L:235:ARG:N	2.28	0.49
2:L:358:GLY:O	2:L:359:ARG:C	2.49	0.49
2:L:16:PRO:HG2	2:L:17:MET:H	1.77	0.48
2:L:24:ARG:HA	2:L:114:LYS:O	2.13	0.48
2:L:71:ASN:N	6:L:877:HOH:O	2.28	0.48
1:I:61:THR:HG22	1:I:338:MET:HE1	1.96	0.48
1:I:91:LYS:HZ2	1:I:120:HIS:CE1	2.24	0.48
2:L:183:ARG:NE	2:L:204:SER:HA	2.29	0.48
2:L:404:ALA:HB2	2:L:428:ASN:ND2	2.29	0.47
2:L:421:ILE:HG22	2:L:422:PHE:CD2	2.49	0.47
1:I:286:PRO:HB3	1:I:295:VAL:HG21	1.95	0.47
2:L:71:ASN:O	2:L:74:ASP:HB2	2.14	0.47
2:L:405:ASN:ND2	2:L:406:ARG:N	2.59	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:190:VAL:HG11	1:I:201:VAL:HG13	1.96	0.47
1:I:176:LYS:O	1:I:209:GLU:HB3	2.14	0.47
2:L:22:ILE:HD12	2:L:22:ILE:N	2.30	0.47
2:L:60:THR:O	2:L:64:GLN:HG3	2.14	0.47
1:I:300:THR:OG1	1:I:303:VAL:HG23	2.14	0.47
1:I:114:LYS:HA	1:I:118:GLN:NE2	2.30	0.47
2:L:119:ILE:CD1	2:L:119:ILE:H	2.27	0.47
2:L:324:ARG:O	2:L:324:ARG:CG	2.60	0.47
1:I:77:PHE:HB2	1:I:325:ILE:HG21	1.96	0.46
2:L:260:TYR:CG	2:L:261:ARG:N	2.83	0.46
2:L:51:LEU:HD21	2:L:123:PHE:HA	1.98	0.46
2:L:86:ALA:HA	2:L:89:MET:CE	2.28	0.46
2:L:158:TYR:HB2	2:L:353:GLY:O	2.16	0.46
1:I:79:SER:HB2	1:I:422:PHE:CE1	2.51	0.46
1:I:281:MET:CE	1:I:283:LEU:HD21	2.46	0.46
2:L:17:MET:HE2	2:L:117:ASP:HB2	1.97	0.46
2:L:304:LEU:O	2:L:304:LEU:HD23	2.16	0.46
1:I:292:LEU:HD11	1:I:409:LEU:CG	2.46	0.46
1:I:159:GLN:HG2	1:I:170:LEU:HD12	1.97	0.46
1:I:319:HIS:HB2	1:I:403:LYS:HA	1.96	0.46
2:L:48:VAL:O	2:L:51:LEU:HB3	2.16	0.46
1:I:92:LEU:HB2	1:I:158:TYR:HE1	1.81	0.46
2:L:332:LYS:HB2	2:L:366:ASP:OD1	2.16	0.46
1:I:197:ARG:HG3	1:I:220:TYR:HE1	1.79	0.45
2:L:42:GLU:HG2	2:L:45:ASN:HB2	1.98	0.45
2:L:314:MET:HG2	2:L:315:MET:N	2.31	0.45
1:I:350:LYS:CG	5:I:801:NAG:H83	2.42	0.45
2:L:44:THR:O	2:L:48:VAL:HG23	2.16	0.45
2:L:119:ILE:H	2:L:119:ILE:HD12	1.81	0.45
2:L:163:GLU:OE2	2:L:169:LYS:HG2	2.16	0.45
1:I:169:LYS:HE2	1:I:171:GLN:OE1	2.16	0.45
1:I:283:LEU:C	1:I:284:ILE:HD12	2.37	0.45
1:I:332:LYS:O	1:I:336:GLN:HG3	2.16	0.45
2:L:300:THR:OG1	2:L:302:GLU:HG2	2.16	0.45
2:L:77:PHE:CZ	2:L:373:LEU:HB2	2.52	0.45
1:I:14:ASP:C	1:I:15:ILE:HD12	2.37	0.45
1:I:27:GLU:HA	1:I:113:GLU:HG2	1.99	0.45
1:I:102:LEU:CD2	1:I:340:LEU:HD11	2.44	0.45
1:I:289:GLU:H	1:I:289:GLU:CD	2.19	0.45
2:L:91:LYS:HE2	2:L:120:HIS:CE1	2.52	0.45
2:L:199:THR:O	2:L:199:THR:CG2	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:171:GLN:HA	1:I:172:PRO:HD3	1.77	0.45
2:L:16:PRO:O	2:L:17:MET:O	2.35	0.45
2:L:43:ALA:O	2:L:47:ARG:HB2	2.17	0.44
2:L:201:VAL:CG1	2:L:385:SER:HB3	2.47	0.44
1:I:96:ASN:HB3	1:I:97:ASP:H	1.48	0.44
2:L:222:LYS:HG2	2:L:381:GLU:HG3	1.98	0.44
2:L:346:PRO:HB2	2:L:347:GLU:OE2	2.18	0.44
2:L:17:MET:CE	2:L:117:ASP:HB2	2.47	0.44
2:L:265:GLU:O	2:L:265:GLU:HG2	2.18	0.44
2:L:356:ALA:O	3:B:1:NAG:H81	2.17	0.44
1:I:15:ILE:HD12	1:I:15:ILE:N	2.33	0.44
2:L:17:MET:HE3	2:L:19:PRO:HD3	2.00	0.44
2:L:119:ILE:HD12	2:L:119:ILE:N	2.33	0.44
2:L:243:ASP:OD1	2:L:245:GLU:HG3	2.17	0.44
2:L:393:ARG:HB2	2:L:393:ARG:HH11	1.83	0.44
1:I:407:PRO:HA	1:I:426:VAL:O	2.17	0.44
2:L:370:LYS:O	2:L:384:ALA:HA	2.17	0.44
2:L:281:MET:HA	2:L:411:PHE:O	2.18	0.44
2:L:292:LEU:O	2:L:295:VAL:N	2.48	0.44
2:L:368:PHE:O	2:L:386:THR:HA	2.18	0.44
1:I:23:TYR:HE1	1:I:100:GLN:NE2	2.16	0.43
2:L:135:ASN:CG	5:L:831:NAG:H83	2.37	0.43
2:L:415:VAL:HB	2:L:416:PRO:CD	2.48	0.43
1:I:284:ILE:HD12	1:I:284:ILE:N	2.34	0.43
2:L:204:SER:O	2:L:205:GLU:HB2	2.18	0.43
2:L:124:ALA:HB2	2:L:165:VAL:HG13	2.00	0.43
2:L:355:VAL:CG1	2:L:356:ALA:N	2.82	0.43
4:C:2:NAG:H82	4:C:2:NAG:O3	2.19	0.43
2:L:57:ARG:HA	2:L:301:PRO:HG2	2.00	0.43
2:L:254:GLN:NE2	2:L:258:PHE:HZ	2.17	0.43
2:L:334:GLN:CD	2:L:334:GLN:N	2.71	0.43
1:I:78:LEU:HD12	1:I:80:PRO:HD3	2.01	0.43
1:I:100:GLN:HE21	1:I:100:GLN:HB2	1.68	0.43
2:L:89:MET:HE1	2:L:217:ASN:HB2	2.01	0.43
1:I:359:ARG:HG2	1:I:359:ARG:HH11	1.84	0.43
2:L:5:VAL:CG1	2:L:6:ASP:H	2.31	0.43
2:L:217:ASN:HD21	2:L:219:ILE:HG13	1.84	0.43
2:L:135:ASN:O	2:L:136:LYS:CB	2.67	0.43
2:L:155:ASN:OD1	2:L:157:THR:N	2.52	0.43
1:I:42:GLU:O	1:I:43:ALA:HB3	2.18	0.42
1:I:114:LYS:HG2	1:I:122:PHE:CE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:332:LYS:HG3	1:I:344:PHE:CD1	2.55	0.42
1:I:10:ALA:HB1	1:I:15:ILE:HD11	2.01	0.42
2:L:171:GLN:HA	2:L:172:PRO:HD3	1.84	0.42
2:L:286:PRO:O	2:L:287:LYS:C	2.57	0.42
1:I:91:LYS:HB2	1:I:102:LEU:HD13	2.01	0.42
2:L:11:LYS:O	2:L:14:ASP:HB2	2.20	0.42
2:L:111:ILE:HG22	2:L:112:SER:N	2.34	0.42
1:I:208:ASN:OD1	1:I:210:LEU:HB2	2.19	0.42
2:L:65:HIS:CD2	2:L:338:MET:HG3	2.54	0.42
1:I:92:LEU:HB2	1:I:158:TYR:CE1	2.54	0.42
2:L:192:ASN:CA	4:C:1:NAG:HN2	2.29	0.42
1:I:190:VAL:HG11	1:I:201:VAL:HG11	2.00	0.42
1:I:359:ARG:HD3	1:I:362:LEU:HD21	2.02	0.42
1:I:13:ARG:O	1:I:13:ARG:HG2	2.19	0.42
1:I:346:PRO:O	1:I:361:ASP:CB	2.68	0.42
2:L:253:TYR:CD1	2:L:253:TYR:C	2.92	0.42
1:I:103:MET:HE1	1:I:119:ILE:HD12	2.00	0.42
1:I:391:ALA:O	2:L:321:PRO:HD3	2.20	0.42
1:I:181:GLN:H	1:I:181:GLN:NE2	2.18	0.41
2:L:202:ILE:HA	2:L:203:PRO:HD2	1.89	0.41
2:L:215:LEU:O	2:L:387:ALA:HA	2.20	0.41
1:I:149:ASP:HA	1:I:173:LEU:O	2.21	0.41
1:I:218:THR:HG22	1:I:370:LYS:H	1.85	0.41
1:I:231:PRO:HD2	1:I:386:THR:O	2.20	0.41
2:L:64:GLN:O	2:L:68:ASP:HB2	2.20	0.41
2:L:292:LEU:O	2:L:293:ALA:C	2.58	0.41
1:I:260:TYR:O	1:I:261:ARG:HB2	2.20	0.41
2:L:129:ARG:O	2:L:133:LYS:HE3	2.20	0.41
2:L:421:ILE:HG22	2:L:422:PHE:CE2	2.55	0.41
1:I:172:PRO:O	1:I:173:LEU:HD23	2.21	0.41
2:L:243:ASP:OD1	2:L:244:GLY:N	2.54	0.41
2:L:257:LYS:HA	2:L:314:MET:O	2.21	0.41
2:L:257:LYS:HG3	2:L:315:MET:HG2	2.03	0.41
2:L:264:ALA:O	2:L:265:GLU:CB	2.60	0.41
2:L:302:GLU:CD	2:L:302:GLU:H	2.23	0.41
1:I:103:MET:SD	1:I:119:ILE:CD1	3.09	0.41
1:I:111:ILE:O	1:I:112:SER:C	2.58	0.41
1:I:134:ALA:HB1	1:I:135:ASN:H	1.25	0.41
1:I:292:LEU:HD21	1:I:425:ARG:HG3	2.03	0.41
2:L:51:LEU:CD2	2:L:123:PHE:HA	2.51	0.41
1:I:108:PHE:CB	1:I:119:ILE:HD13	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:114:LYS:N	1:I:114:LYS:HD2	2.36	0.40
1:I:103:MET:HE1	1:I:119:ILE:HD11	2.02	0.40
2:L:287:LYS:O	2:L:288:PRO:C	2.59	0.40
2:L:405:ASN:HD22	2:L:406:ARG:N	2.14	0.40
1:I:116:SER:HA	1:I:119:ILE:HD12	2.03	0.40
1:I:154:PHE:HB3	1:I:170:LEU:HD13	2.04	0.40
1:I:218:THR:HG22	1:I:370:LYS:O	2.21	0.40
2:L:396:ASN:HB2	2:L:397:PRO:HD2	2.03	0.40
1:I:299:LEU:HD23	1:I:299:LEU:HA	1.89	0.40
1:I:146:LEU:HD13	1:I:215:LEU:HD13	2.03	0.40
2:L:101:GLN:OE1	2:L:341:VAL:HG22	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	I	412/432 (95%)	378 (92%)	28 (7%)	6 (2%)	10 19
2	L	404/432 (94%)	355 (88%)	34 (8%)	15 (4%)	3 4
All	All	816/864 (94%)	733 (90%)	62 (8%)	21 (3%)	5 8

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	112	SER
1	I	135	ASN
1	I	138	SER
2	L	10	ALA
2	L	17	MET
2	L	135	ASN
2	L	264	ALA

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Mol	Chain	Res	Type
2	L	265	GLU
2	L	356	ALA
2	L	361	ASP
2	L	400	VAL
1	I	19	PRO
1	I	360	ASP
2	L	16	PRO
2	L	136	LYS
2	L	293	ALA
2	L	403	LYS
2	L	19	PRO
2	L	12	PRO
2	L	14	ASP
1	I	261	ARG

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	I	351/381 (92%)	332 (95%)	19 (5%)	22	42
2	L	338/383 (88%)	319 (94%)	19 (6%)	21	40
All	All	689/764 (90%)	651 (94%)	38 (6%)	21	41

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	13	ARG
1	I	45	ASN
1	I	78	LEU
1	I	91	LYS
1	I	96	ASN
1	I	114	LYS
1	I	117	ASP
1	I	128	CYS
1	I	140	LEU

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Mol	Chain	Res	Type
1	I	181	GLN
1	I	209	GLU
1	I	257	LYS
1	I	302	GLU
1	I	327	ASP
1	I	347	GLU
1	I	361	ASP
1	I	363	TYR
1	I	366	ASP
1	I	401	THR
2	L	17	MET
2	L	47	ARG
2	L	68	ASP
2	L	74	ASP
2	L	78	LEU
2	L	123	PHE
2	L	177	GLU
2	L	199	THR
2	L	201	VAL
2	L	208	ASN
2	L	209	GLU
2	L	262	ARG
2	L	285	LEU
2	L	292	LEU
2	L	302	GLU
2	L	316	LEU
2	L	324	ARG
2	L	405	ASN
2	L	419	THR

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

Mol	Chain	Res	Type
1	I	45	ASN
1	I	100	GLN
1	I	118	GLN
1	I	159	GLN
1	I	178	ASN
1	I	217	ASN
1	I	233	ASN
2	L	55	ASN
2	L	65	HIS

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Mol	Chain	Res	Type
2	L	71	ASN
2	L	100	GLN
2	L	144	ASN
2	L	208	ASN
2	L	217	ASN
2	L	254	GLN
2	L	336	GLN
2	L	405	ASN

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)

9 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	3,1	14,14,15	0.61	0	17,19,21	0.84	1 (5%)
3	NAG	A	2	3	14,14,15	0.64	0	17,19,21	0.68	0
3	NAG	B	1	2,3	14,14,15	0.46	0	17,19,21	0.74	0
3	NAG	B	2	3	14,14,15	0.53	0	17,19,21	0.99	2 (11%)
4	NAG	C	1	2,4	14,14,15	0.71	0	17,19,21	1.00	2 (11%)
4	NAG	C	2	4	14,14,15	0.69	0	17,19,21	0.83	0
4	BMA	C	3	4	11,11,12	0.76	0	15,15,17	0.95	1 (6%)
4	MAN	C	4	4	11,11,12	0.63	0	15,15,17	0.61	1 (6%)
4	MAN	C	5	4	11,11,12	0.54	0	15,15,17	0.67	1 (6%)

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	3,1	-	2/6/23/26	0/1/1/1
3	NAG	A	2	3	-	4/6/23/26	0/1/1/1
3	NAG	B	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	B	2	3	-	4/6/23/26	0/1/1/1
4	NAG	C	1	2,4	1/1/5/7	4/6/23/26	0/1/1/1
4	NAG	C	2	4	-	5/6/23/26	0/1/1/1
4	BMA	C	3	4	-	2/2/19/22	0/1/1/1
4	MAN	C	4	4	-	2/2/19/22	1/1/1/1
4	MAN	C	5	4	-	2/2/19/22	1/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	3	BMA	C1-C2-C3	3.18	113.58	109.67
3	B	2	NAG	C2-N2-C7	-2.68	119.08	122.90
4	C	1	NAG	O5-C1-C2	-2.57	107.23	111.29
4	C	1	NAG	C2-N2-C7	-2.43	119.44	122.90
3	A	1	NAG	C2-N2-C7	-2.18	119.79	122.90
4	C	5	MAN	C1-O5-C5	2.16	115.11	112.19
4	C	4	MAN	C1-O5-C5	2.15	115.10	112.19
3	B	2	NAG	C4-C3-C2	-2.05	108.02	111.02

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	1	NAG	C1

All (27) 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
3	B	2	NAG	C8-C7-N2-C2
3	B	2	NAG	O7-C7-N2-C2
4	C	1	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	C	1	NAG	O7-C7-N2-C2
4	C	2	NAG	C3-C2-N2-C7
4	C	2	NAG	C8-C7-N2-C2
4	C	2	NAG	O7-C7-N2-C2
4	C	1	NAG	O5-C5-C6-O6
3	A	2	NAG	O5-C5-C6-O6
4	C	3	BMA	O5-C5-C6-O6
4	C	3	BMA	C4-C5-C6-O6
4	C	4	MAN	O5-C5-C6-O6
4	C	1	NAG	C4-C5-C6-O6
4	C	5	MAN	O5-C5-C6-O6
3	B	2	NAG	O5-C5-C6-O6
3	A	2	NAG	C4-C5-C6-O6
4	C	5	MAN	C4-C5-C6-O6
3	B	2	NAG	C4-C5-C6-O6
3	B	1	NAG	O5-C5-C6-O6
3	A	1	NAG	C4-C5-C6-O6
4	C	2	NAG	C4-C5-C6-O6
4	C	2	NAG	O5-C5-C6-O6
4	C	4	MAN	C4-C5-C6-O6
3	A	1	NAG	O5-C5-C6-O6
3	B	1	NAG	C4-C5-C6-O6

All (2) ring outliers are listed below:

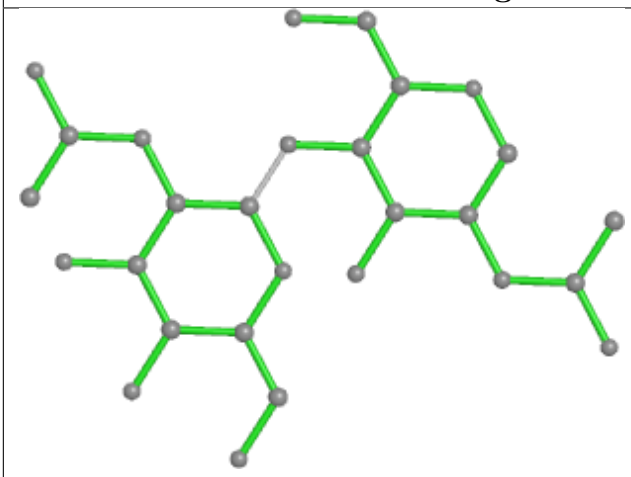
Mol	Chain	Res	Type	Atoms
4	C	5	MAN	C1-C2-C3-C4-C5-O5
4	C	4	MAN	C1-C2-C3-C4-C5-O5

6 monomers are involved in 9 short contacts:

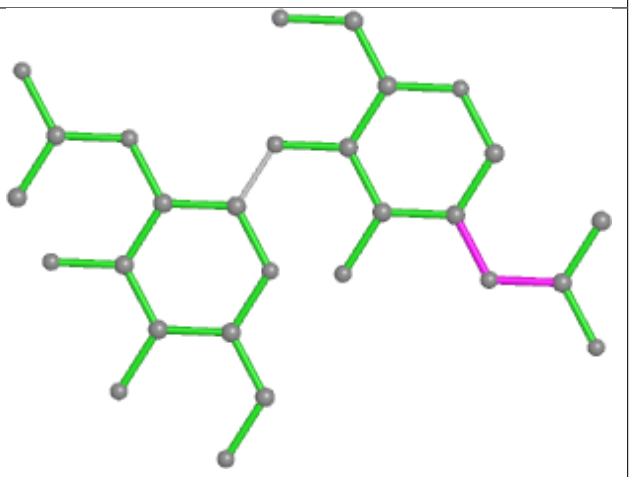
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	NAG	1	0
4	C	2	NAG	3	0
4	C	1	NAG	5	0
3	A	2	NAG	1	0
4	C	3	BMA	1	0
3	B	1	NAG	1	0

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

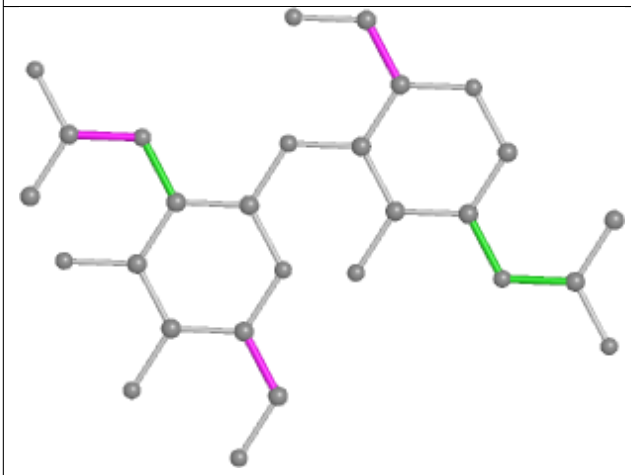
Oligosaccharide Chain A



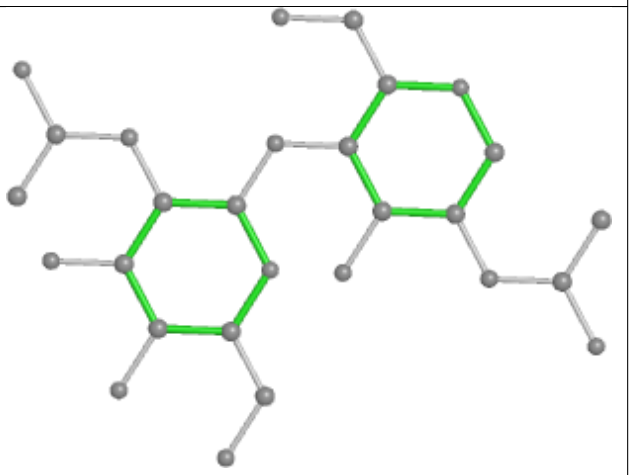
Bond lengths



Bond angles

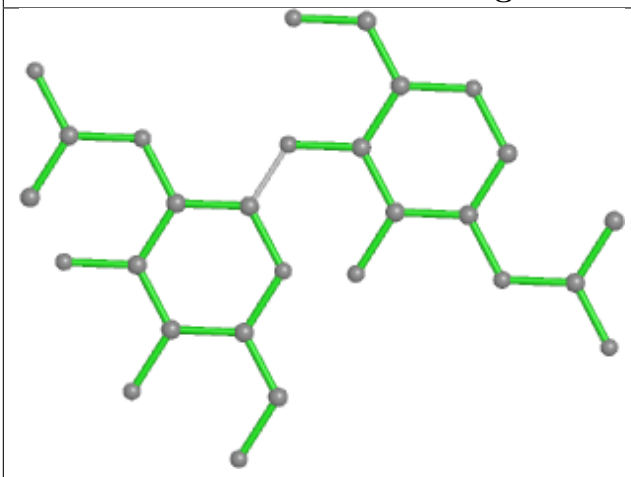


Torsions

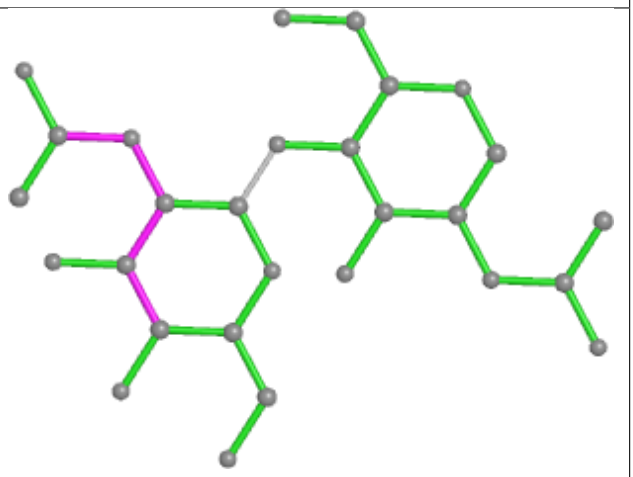


Rings

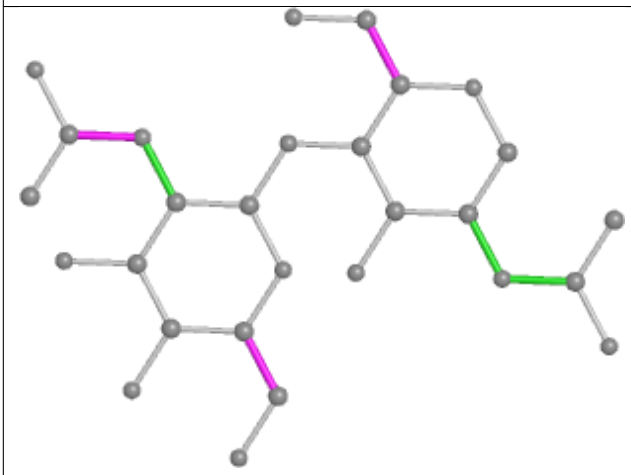
Oligosaccharide Chain B



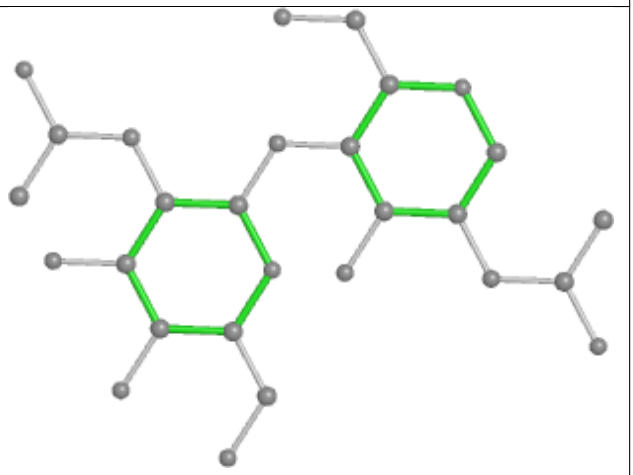
Bond lengths



Bond angles

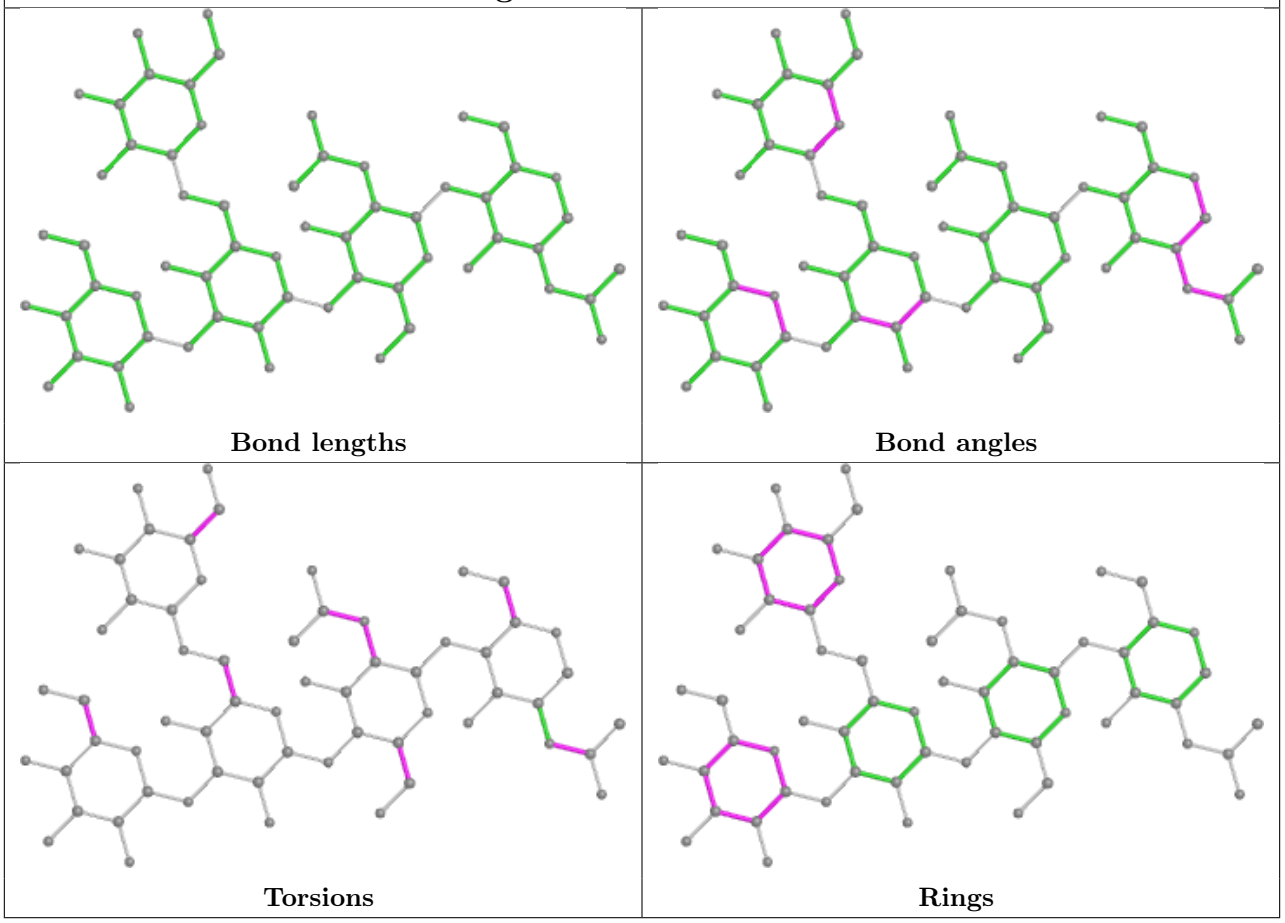


Torsions



Rings

Oligosaccharide Chain C



5.6 Ligand geometry (i)

4 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	$\#\|Z\| > 2$
5	NAG	L	831	2	14,14,15	0.59	0	17,19,21	0.73	0
5	NAG	L	801	2	14,14,15	0.58	0	17,19,21	0.60	0
5	NAG	I	801	1	14,14,15	0.60	0	17,19,21	0.66	0
5	NAG	I	861	1	14,14,15	0.67	0	17,19,21	0.63	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	L	831	2	-	5/6/23/26	0/1/1/1
5	NAG	L	801	2	-	5/6/23/26	0/1/1/1
5	NAG	I	801	1	-	3/6/23/26	0/1/1/1
5	NAG	I	861	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	831	NAG	C8-C7-N2-C2
5	L	831	NAG	O7-C7-N2-C2
5	L	831	NAG	C1-C2-N2-C7
5	L	801	NAG	O5-C5-C6-O6
5	L	801	NAG	C4-C5-C6-O6
5	I	861	NAG	C4-C5-C6-O6
5	I	861	NAG	C8-C7-N2-C2
5	I	861	NAG	O5-C5-C6-O6
5	I	861	NAG	O7-C7-N2-C2
5	L	801	NAG	C8-C7-N2-C2
5	L	801	NAG	O7-C7-N2-C2
5	L	831	NAG	C4-C5-C6-O6
5	L	801	NAG	C3-C2-N2-C7
5	L	831	NAG	O5-C5-C6-O6
5	I	801	NAG	C1-C2-N2-C7
5	I	801	NAG	O5-C5-C6-O6
5	I	801	NAG	C3-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	831	NAG	2	0
5	I	801	NAG	4	0
5	I	861	NAG	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	I	416/432 (96%)	0.02	5 (1%)	79	76	29, 51, 79, 103	0
2	L	410/432 (94%)	0.15	11 (2%)	54	49	32, 56, 99, 108	0
All	All	826/864 (95%)	0.08	16 (1%)	66	62	29, 53, 90, 108	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	207	ILE	5.4
2	L	112	SER	3.3
1	I	360	ASP	2.9
2	L	43	ALA	2.9
2	L	44	THR	2.9
2	L	207	ILE	2.7
2	L	96	ASN	2.6
1	I	431	VAL	2.6
2	L	45	ASN	2.5
2	L	397	PRO	2.4
2	L	137	SER	2.4
2	L	396	ASN	2.3
2	L	395	LEU	2.2
1	I	361	ASP	2.2
2	L	42	GLU	2.1
1	I	212	VAL	2.0

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

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

6.3 Carbohydrates (i)

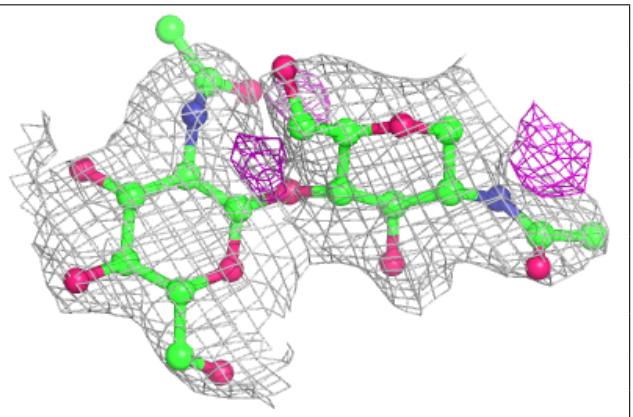
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

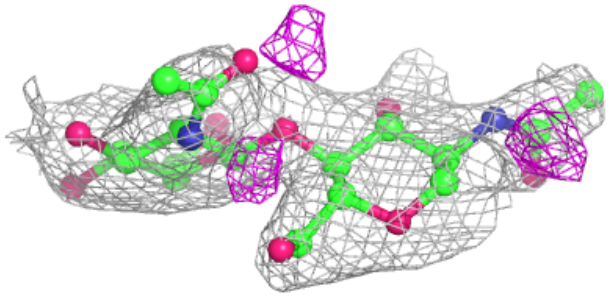
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MAN	C	4	11/12	0.58	0.49	139,140,140,141	0
4	NAG	C	2	14/15	0.64	0.45	122,126,128,131	0
4	NAG	C	1	14/15	0.74	0.29	98,104,108,115	0
3	NAG	B	2	14/15	0.81	0.41	92,96,98,99	0
4	BMA	C	3	11/12	0.82	0.35	134,136,138,140	0
4	MAN	C	5	11/12	0.83	0.55	141,141,142,142	0
3	NAG	A	2	14/15	0.86	0.35	88,92,93,94	0
3	NAG	A	1	14/15	0.87	0.28	64,69,75,82	0
3	NAG	B	1	14/15	0.90	0.14	69,74,79,86	0

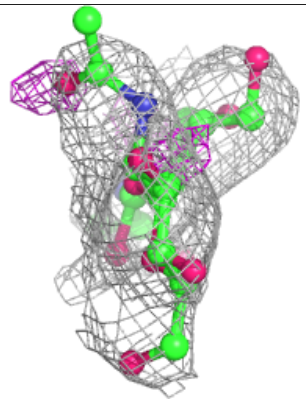
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain A:

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

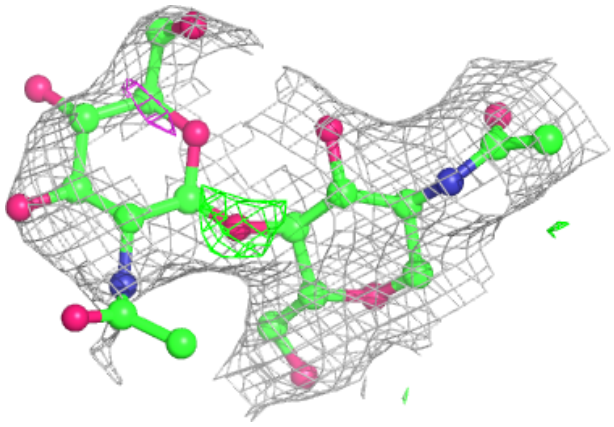


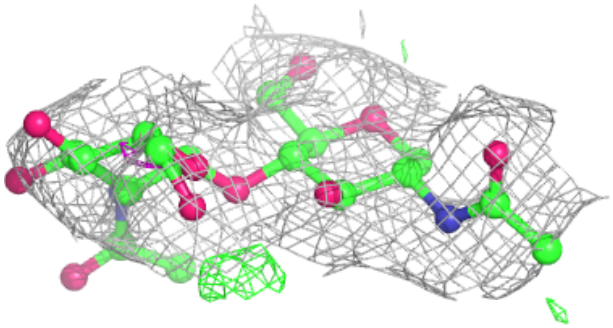


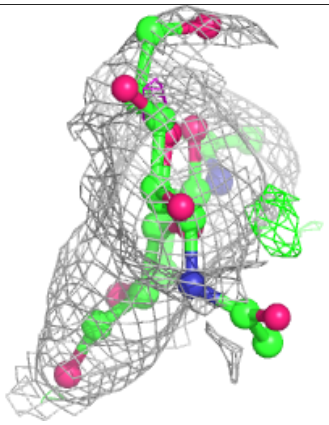


Electron density around Chain B:

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

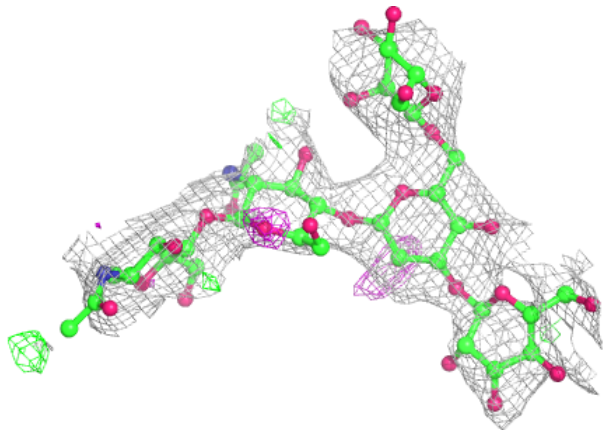


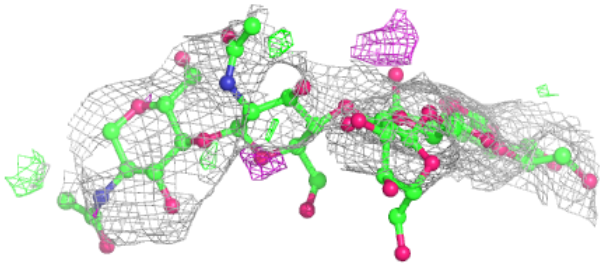


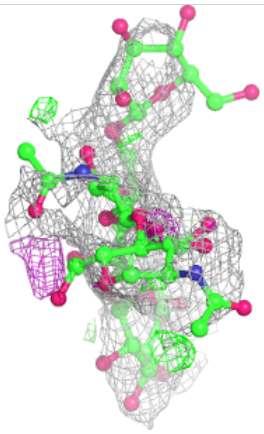


Electron density around Chain C:

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







6.4 Ligands

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, 95^{th} 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	I	861	14/15	0.68	0.41	92,97,100,101	0
5	NAG	L	831	14/15	0.76	0.47	118,120,124,125	0
5	NAG	I	801	14/15	0.84	0.27	77,80,82,83	0
5	NAG	L	801	14/15	0.86	0.31	84,85,86,87	0

6.5 Other polymers

There are no such residues in this entry.