Full wwPDB X-ray Structure Validation Report (i)

Jun 19, 2024 – 10:44 AM EDT

PDB ID	:	4JF7
Title	:	Structure of the parainfluenza virus 5 (PIV5) hemagglutinin-neuraminidase (HN) ectodomain
Authors	:	Welch, B.D.; Yuan, P.; Bose, S.; Kors, C.A.; Lamb, R.A.; Jardetzky, T.S.
Deposited on	:	2013-02-27
Resolution	:	2.50 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 (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 (i)) were used in the production of this report:

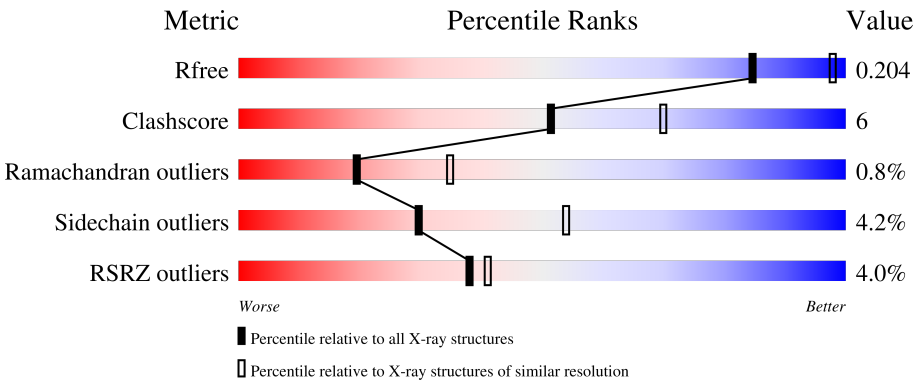
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	A	513	5% 86% 11% • •
1	B	513	4% 85% 11% • •
1	C	513	4% 84% 11% • •
1	D	513	3% 81% 13% • •
2	E	3	33% 67%

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Mol	Chain	Length	Quality of chain
2	F	3	67% 33%
3	G	2	100%
3	H	2	50% 50%
3	I	2	50% 50%
3	J	2	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	NAG	A	608	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 16400 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.

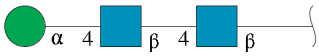
- Molecule 1 is a protein called Hemagglutinin-neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	D	492	3816	2431	630	728	27	0	0	0
1	A	501	3888	2477	642	741	28	0	0	0
1	B	501	3888	2474	643	743	28	0	0	0
1	C	493	3822	2436	631	727	28	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	53	SER	-	expression tag	UNP P04850
D	54	PRO	-	expression tag	UNP P04850
D	55	SER	ASN	conflict	UNP P04850
A	53	SER	-	expression tag	UNP P04850
A	54	PRO	-	expression tag	UNP P04850
A	55	SER	ASN	conflict	UNP P04850
B	53	SER	-	expression tag	UNP P04850
B	54	PRO	-	expression tag	UNP P04850
B	55	SER	ASN	conflict	UNP P04850
C	53	SER	-	expression tag	UNP P04850
C	54	PRO	-	expression tag	UNP P04850
C	55	SER	ASN	conflict	UNP P04850

- Molecule 2 is an oligosaccharide called alpha-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
			Total	C	N	O			
2	E	3	39	22	2	15	0	0	0
2	F	3	39	22	2	15	0	0	0

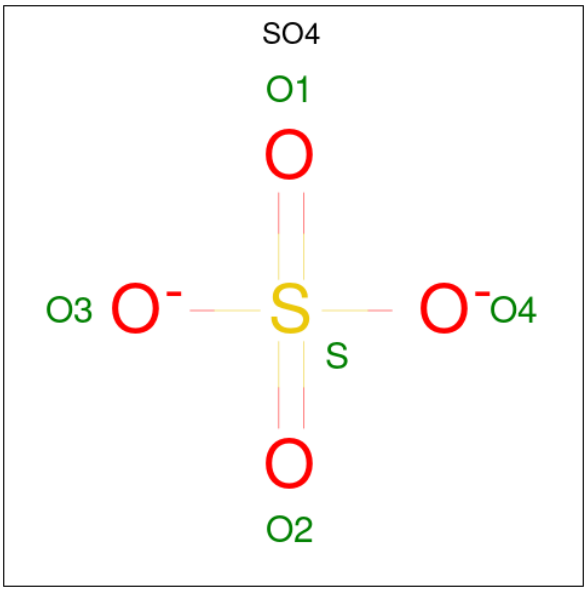
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	2	28	16	2	10	0	0	0
3	H	2	28	16	2	10	0	0	0
3	I	2	28	16	2	10	0	0	0
3	J	2	28	16	2	10	0	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

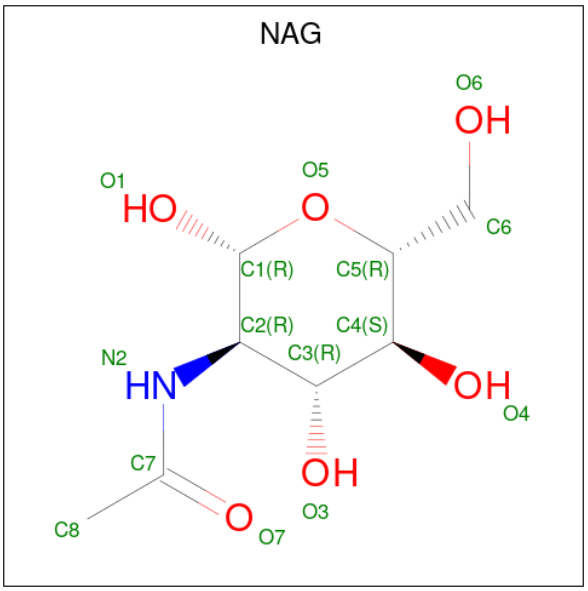
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	D	1	1	1	0	0
4	A	1	1	1	0	0
4	B	1	1	1	0	0
4	C	1	1	1	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
5	D	1	5	4	1		0	0
			Total	O	S			
5	A	1	5	4	1		0	0
			Total	O	S			
5	B	1	5	4	1		0	0
			Total	O	S			
5	C	1	5	4	1		0	0

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



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

- Molecule 7 is water.

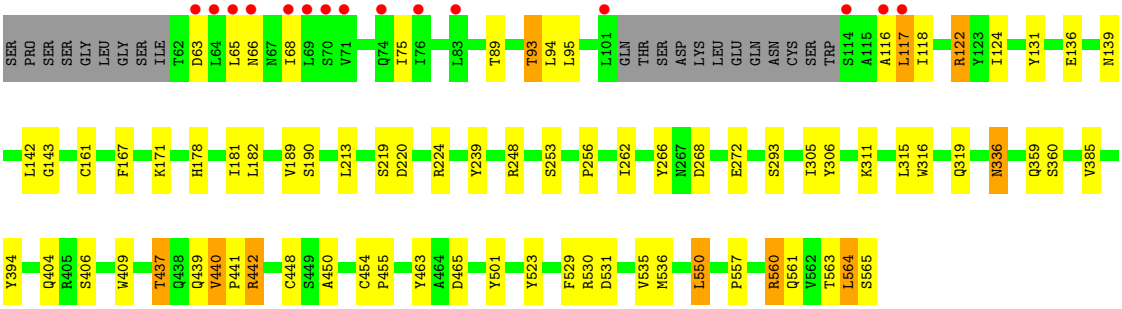
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	D	226	226	226	0	0
7	A	189	189	189	0	0
7	B	115	115	115	0	0
7	C	158	158	158	0	0

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.

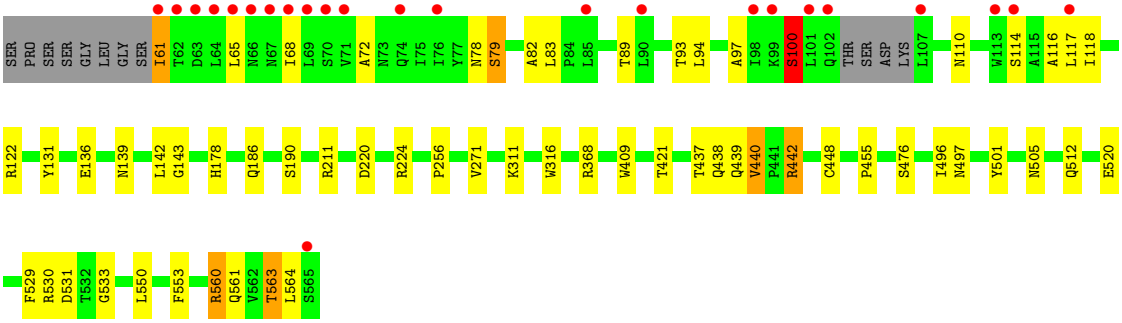
• Molecule 1: Hemagglutinin-neuraminidase

Chain D:



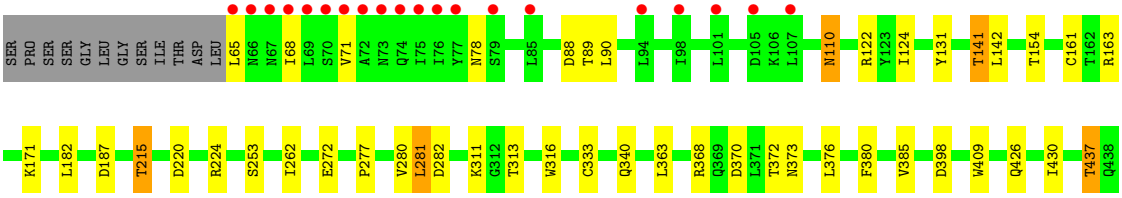
• Molecule 1: Hemagglutinin-neuraminidase

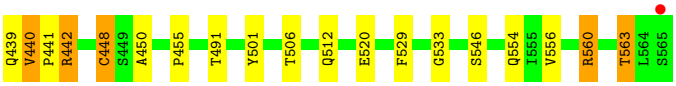
Chain A:



• Molecule 1: Hemagglutinin-neuraminidase

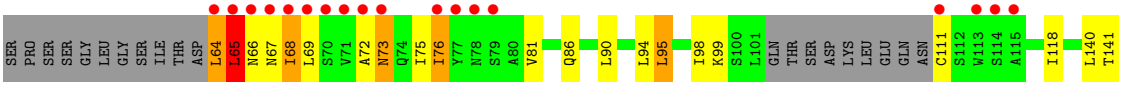
Chain B:

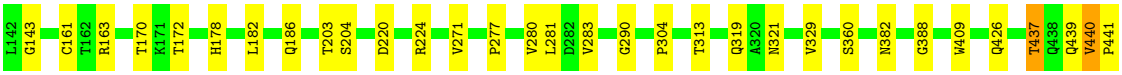


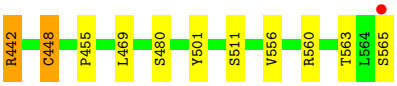


• Molecule 1: Hemagglutinin-neuraminidase

Chain C:

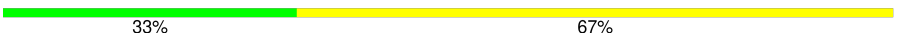






• Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

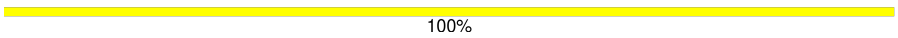


• Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

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

Chain G:



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

Chain H:

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

Chain I:

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

Chain J:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α, β, γ	194.39Å 194.39Å 185.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.36 – 2.50 34.36 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (34.36-2.50) 97.7 (34.36-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.68 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.166 , 0.207 0.165 , 0.204	Depositor DCC
R_{free} test set	2010 reflections (1.70%)	wwPDB-VP
Wilson B-factor (Å^2)	39.7	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 29.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.028 for l,-k,h 0.029 for -l,-k,-h 0.028 for -h,-l,-k 0.028 for -h,l,k 0.106 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	16400	wwPDB-VP
Average B, all atoms (Å^2)	50.0	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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, MAN, NAG, SO4

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	0.42	0/3985	0.60	0/5442
1	B	0.39	0/3986	0.55	0/5442
1	C	0.40	0/3919	0.60	2/5351 (0.0%)
1	D	0.43	0/3911	0.60	0/5340
All	All	0.41	0/15801	0.59	2/21575 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	64	LEU	CA-CB-CG	5.77	128.57	115.30
1	C	64	LEU	CB-CG-CD1	-5.47	101.70	111.00

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	3888	0	3765	46	0
1	B	3888	0	3762	42	0
1	C	3822	0	3700	34	0
1	D	3816	0	3703	52	0
2	E	39	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	39	0	34	2	0
3	G	28	0	25	0	0
3	H	28	0	25	0	0
3	I	28	0	25	0	0
3	J	28	0	26	4	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	A	28	0	26	10	0
6	B	14	0	13	0	0
6	C	28	0	26	0	0
6	D	14	0	13	2	0
7	A	189	0	0	3	0
7	B	115	0	0	2	0
7	C	158	0	0	3	0
7	D	226	0	0	3	0
All	All	16400	0	15177	167	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.

All (167) 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:A:110:ASN:HD21	6:A:608:NAG:C2	1.14	1.58
1:D:139:ASN:HD21	6:D:609:NAG:C1	1.08	1.57
1:A:110:ASN:HD21	6:A:608:NAG:C1	1.30	1.44
1:A:110:ASN:ND2	6:A:608:NAG:C2	1.91	1.31
1:A:110:ASN:ND2	6:A:608:NAG:H2	1.45	1.25
2:F:2:NAG:O4	2:F:3:MAN:C2	2.20	0.89
1:D:437:THR:HG23	1:D:439:GLN:H	1.41	0.84
1:A:110:ASN:HD22	6:A:608:NAG:H2	1.43	0.82
1:C:442:ARG:NH2	1:C:448:CYS:O	2.15	0.79
3:J:1:NAG:C4	3:J:2:NAG:C1	2.60	0.79
1:C:437:THR:HG23	1:C:439:GLN:H	1.45	0.79
1:A:442:ARG:NH2	1:A:448:CYS:O	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1:NAG:O4	3:J:2:NAG:C2	2.33	0.76
1:B:437:THR:HG23	1:B:439:GLN:H	1.49	0.76
1:D:442:ARG:NH2	1:D:448:CYS:O	2.18	0.75
1:D:116:ALA:O	1:D:118:ILE:N	2.20	0.74
1:A:439:GLN:O	7:A:808:HOH:O	2.06	0.74
1:B:442:ARG:NH2	1:B:448:CYS:O	2.21	0.73
1:A:110:ASN:CG	6:A:608:NAG:C1	2.56	0.73
1:C:111:CYS:N	7:C:835:HOH:O	2.24	0.69
1:A:440:VAL:HG21	1:A:501:TYR:CE1	2.28	0.68
1:D:440:VAL:HG21	1:D:501:TYR:CE1	2.28	0.68
1:A:437:THR:HG22	1:A:439:GLN:H	1.58	0.67
1:B:88:ASP:OD1	1:C:86:GLN:NE2	2.27	0.67
1:A:437:THR:HG23	1:A:505:ASN:HA	1.79	0.65
1:C:72:ALA:HA	1:C:75:ILE:HD12	1.79	0.64
1:D:68:ILE:HD11	1:C:68:ILE:HG21	1.80	0.64
1:D:336:ASN:OD1	1:D:336:ASN:N	2.23	0.64
1:C:440:VAL:HG21	1:C:501:TYR:CE1	2.33	0.63
1:B:520:GLU:HB2	1:B:546:SER:HB2	1.80	0.63
1:A:78:ASN:HA	1:A:82:ALA:HB3	1.81	0.62
1:B:372:THR:OG1	1:B:373:ASN:N	2.30	0.62
1:C:277:PRO:HG2	1:C:280:VAL:HG21	1.82	0.62
1:B:142:LEU:HD22	1:B:560:ARG:HD2	1.81	0.61
1:B:426:GLN:NE2	7:B:803:HOH:O	2.33	0.61
1:A:409:TRP:CD2	1:A:455:PRO:HA	2.38	0.59
1:A:122:ARG:HD3	1:A:533:GLY:HA3	1.85	0.59
1:B:313:THR:HG23	1:B:316:TRP:H	1.68	0.59
1:B:333:CYS:SG	1:B:340:GLN:NE2	2.76	0.59
1:A:110:ASN:ND2	6:A:608:NAG:N2	2.50	0.59
1:B:277:PRO:HG2	1:B:280:VAL:HG21	1.86	0.57
2:F:2:NAG:O4	2:F:3:MAN:H2	2.05	0.57
1:A:116:ALA:O	1:A:118:ILE:N	2.34	0.57
1:D:136:GLU:HG2	1:D:564:LEU:HD11	1.87	0.56
1:C:64:LEU:O	1:C:66:ASN:N	2.39	0.55
1:D:75:ILE:HD11	1:C:76:ILE:HD12	1.89	0.55
1:A:100:SER:O	1:A:100:SER:OG	2.17	0.55
1:D:117:LEU:HD12	1:D:213:LEU:HD12	1.89	0.55
1:A:72:ALA:HB1	1:B:71:VAL:HG11	1.89	0.54
1:A:220:ASP:OD1	1:A:224:ARG:NH2	2.41	0.54
1:B:311:LYS:HE2	1:B:316:TRP:CZ2	2.43	0.54
1:D:122:ARG:NH2	7:D:781:HOH:O	2.42	0.53
1:D:139:ASN:ND2	6:D:609:NAG:C2	2.68	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:LEU:HD22	1:D:560:ARG:HD2	1.90	0.53
1:A:110:ASN:OD1	6:A:608:NAG:C1	2.57	0.53
1:B:560:ARG:NH2	7:B:767:HOH:O	2.41	0.52
1:A:61:ILE:HG23	1:A:65:LEU:HD13	1.91	0.52
1:A:220:ASP:CG	1:A:224:ARG:HH22	2.14	0.51
1:D:385:VAL:HG13	1:D:404:GLN:HE22	1.76	0.51
1:B:281:LEU:HD22	1:B:282:ASP:H	1.76	0.50
1:D:220:ASP:OD1	1:D:224:ARG:NH2	2.44	0.50
1:A:211:ARG:HG3	1:B:215:THR:HG22	1.94	0.50
1:B:262:ILE:HG13	1:B:272:GLU:HG3	1.92	0.50
1:C:220:ASP:OD1	1:C:224:ARG:NH2	2.44	0.50
1:B:220:ASP:CG	1:B:224:ARG:HH22	2.15	0.50
1:D:75:ILE:HD12	1:C:75:ILE:HG22	1.95	0.49
1:D:248:ARG:NH2	7:D:804:HOH:O	2.45	0.49
1:D:561:GLN:CD	1:D:563:THR:HG22	2.32	0.49
1:A:131:TYR:OH	1:A:529:PHE:HA	2.12	0.49
1:C:409:TRP:CD2	1:C:455:PRO:HA	2.47	0.49
1:D:239:TYR:HE2	1:D:305:ILE:HG22	1.78	0.49
1:A:79:SER:HB3	1:B:78:ASN:HD22	1.79	0.48
1:D:440:VAL:HG21	1:D:501:TYR:CZ	2.47	0.48
1:B:311:LYS:HA	1:B:316:TRP:CD2	2.48	0.48
1:D:219:SER:O	1:C:204:SER:HB3	2.13	0.48
1:B:409:TRP:CD2	1:B:455:PRO:HA	2.49	0.47
1:D:66:ASN:N	1:D:66:ASN:OD1	2.48	0.47
1:D:143:GLY:O	1:D:560:ARG:HD3	2.14	0.47
1:C:220:ASP:CG	1:C:224:ARG:HH22	2.17	0.47
1:D:409:TRP:CD2	1:D:455:PRO:HA	2.49	0.47
1:A:114:SER:HB2	1:B:110:ASN:OD1	2.14	0.47
1:A:256:PRO:HD3	7:A:745:HOH:O	2.15	0.47
1:B:440:VAL:HG21	1:B:501:TYR:CE1	2.49	0.47
3:J:1:NAG:H4	3:J:2:NAG:C1	2.42	0.47
1:D:536:MET:HG2	1:D:561:GLN:NE2	2.30	0.47
1:A:89:THR:O	1:A:93:THR:HG23	2.15	0.47
1:B:520:GLU:HB2	1:B:546:SER:CB	2.43	0.47
1:D:394:TYR:OH	1:D:465:ASP:HB2	2.15	0.47
1:B:368:ARG:NH2	1:B:370:ASP:OD2	2.46	0.47
1:A:561:GLN:HG2	1:A:563:THR:HG22	1.97	0.46
1:B:440:VAL:HG21	1:B:501:TYR:CZ	2.50	0.46
1:C:94:LEU:O	1:C:98:ILE:HG12	2.15	0.46
1:B:437:THR:CG2	1:B:439:GLN:H	2.24	0.46
1:D:68:ILE:HG23	1:A:68:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:117:LEU:HD13	1:D:266:TYR:CD1	2.51	0.46
1:B:122:ARG:HD3	1:B:533:GLY:HA3	1.98	0.46
1:D:93:THR:HG22	7:C:820:HOH:O	2.15	0.46
1:B:441:PRO:HB2	1:B:450:ALA:HB1	1.97	0.45
1:B:220:ASP:OD1	1:B:224:ARG:NH2	2.50	0.45
1:D:441:PRO:HB2	1:D:450:ALA:HB1	1.99	0.45
1:C:69:LEU:O	1:C:73:ASN:HB2	2.17	0.45
1:D:262:ILE:HG13	1:D:272:GLU:HG3	1.98	0.45
1:D:131:TYR:OH	1:D:529:PHE:HA	2.17	0.45
1:D:117:LEU:HD22	1:D:266:TYR:HB2	1.98	0.45
1:A:139:ASN:ND2	6:A:602:NAG:O5	2.41	0.44
1:A:116:ALA:C	1:A:118:ILE:H	2.19	0.44
1:B:154:THR:HG22	1:B:554:GLN:HG3	1.99	0.44
1:D:440:VAL:HA	1:D:441:PRO:HD2	1.83	0.44
1:C:161:CYS:SG	1:C:163:ARG:HG3	2.57	0.44
1:A:139:ASN:ND2	6:A:602:NAG:C2	2.66	0.44
1:D:306:TYR:HA	1:D:359:GLN:O	2.17	0.44
1:B:363:LEU:HD12	1:B:376:LEU:O	2.18	0.44
1:B:439:GLN:NE2	1:B:506:THR:O	2.48	0.44
1:D:65:LEU:O	1:D:68:ILE:HG22	2.17	0.44
1:A:437:THR:HG22	1:A:438:GLN:N	2.33	0.44
1:C:118:ILE:HD12	1:C:172:THR:HA	1.99	0.43
1:A:136:GLU:HG2	1:A:564:LEU:HD11	2.00	0.43
1:A:122:ARG:HD2	1:A:531:ASP:OD1	2.19	0.43
1:C:440:VAL:HA	1:C:441:PRO:HD2	1.86	0.43
1:B:409:TRP:CG	1:B:455:PRO:HA	2.54	0.43
1:A:311:LYS:HA	1:A:316:TRP:CD2	2.54	0.43
1:C:99:LYS:HD2	1:C:118:ILE:HG12	2.00	0.42
1:B:124:ILE:HG23	1:B:171:LYS:HG2	2.01	0.42
1:B:161:CYS:SG	1:B:163:ARG:HG3	2.60	0.42
1:C:64:LEU:HB3	1:C:65:LEU:H	1.55	0.42
1:C:95:LEU:HD12	1:C:95:LEU:HA	1.85	0.42
1:D:161:CYS:HB3	1:D:181:ILE:HB	2.01	0.42
1:C:283:VAL:HA	1:C:313:THR:HG21	2.00	0.42
1:D:454:CYS:HA	1:D:455:PRO:HD3	1.90	0.42
1:D:256:PRO:HD3	7:D:715:HOH:O	2.18	0.42
1:A:143:GLY:O	1:A:560:ARG:HD3	2.19	0.42
1:D:124:ILE:O	1:D:171:LYS:HG3	2.20	0.42
1:D:550:LEU:CD1	1:C:556:VAL:HG21	2.49	0.42
1:A:122:ARG:NH2	7:A:860:HOH:O	2.53	0.42
1:D:95:LEU:HD11	1:A:94:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:ARG:NH1	1:D:531:ASP:OD2	2.53	0.42
1:D:406:SER:O	1:D:442:ARG:HD2	2.20	0.42
1:A:437:THR:HG22	1:A:439:GLN:N	2.29	0.42
1:C:143:GLY:O	1:C:560:ARG:HD3	2.20	0.42
1:C:409:TRP:CG	1:C:455:PRO:HA	2.54	0.42
1:B:380:PHE:CE1	1:B:430:ILE:HD12	2.55	0.41
1:C:426:GLN:NE2	7:C:856:HOH:O	2.53	0.41
1:D:89:THR:O	1:D:93:THR:HG23	2.20	0.41
1:D:311:LYS:HA	1:D:316:TRP:CD2	2.54	0.41
1:D:315:LEU:O	1:D:319:GLN:HB2	2.21	0.41
1:D:437:THR:CG2	1:D:439:GLN:H	2.23	0.41
1:D:463:TYR:HB3	1:D:523:TYR:CG	2.55	0.41
3:J:1:NAG:O4	3:J:2:NAG:N2	2.54	0.41
1:D:167:PHE:O	1:D:293:SER:HB3	2.21	0.41
1:B:281:LEU:HD22	1:B:282:ASP:N	2.35	0.41
1:D:131:TYR:O	1:D:530:ARG:NH2	2.48	0.41
1:B:439:GLN:HE21	1:B:506:THR:C	2.24	0.41
1:C:319:GLN:HG2	1:C:382:ASN:ND2	2.36	0.41
1:A:131:TYR:O	1:A:530:ARG:NH2	2.54	0.41
1:A:496:ILE:HD12	1:A:520:GLU:HA	2.03	0.41
1:A:550:LEU:CD1	1:B:556:VAL:HG21	2.50	0.41
1:B:171:LYS:HB2	1:B:171:LYS:HE3	1.75	0.41
1:C:140:LEU:HD13	1:C:469:LEU:HD13	2.03	0.41
1:C:290:GLY:N	1:C:304:PRO:O	2.52	0.41
1:C:86:GLN:O	1:C:90:LEU:HB2	2.20	0.41
1:C:329:VAL:HG21	1:C:409:TRP:HH2	1.86	0.41
1:A:142:LEU:HD22	1:A:560:ARG:HD2	2.02	0.40
1:B:131:TYR:OH	1:B:529:PHE:HA	2.21	0.40
1:B:141:THR:HG22	1:B:563:THR:HG23	2.01	0.40
1:A:496:ILE:HG23	1:A:497:ASN:CG	2.42	0.40
1:D:94:LEU:HA	1:D:94:LEU:HD23	1.89	0.40
1:C:360:SER:OG	1:C:388:GLY:HA2	2.22	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	497/513 (97%)	463 (93%)	29 (6%)	5 (1%)	15	28
1	B	499/513 (97%)	472 (95%)	25 (5%)	2 (0%)	34	54
1	C	489/513 (95%)	460 (94%)	26 (5%)	3 (1%)	25	43
1	D	488/513 (95%)	466 (96%)	17 (4%)	5 (1%)	15	28
All	All	1973/2052 (96%)	1861 (94%)	97 (5%)	15 (1%)	19	35

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	117	LEU
1	D	190	SER
1	A	190	SER
1	C	65	LEU
1	A	117	LEU
1	A	97	ALA
1	A	100	SER
1	C	203	THR
1	D	440	VAL
1	B	440	VAL
1	D	535	VAL
1	C	440	VAL
1	D	557	PRO
1	B	68	ILE
1	A	440	VAL

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	435/447 (97%)	420 (97%)	15 (3%)	37	63
1	B	435/447 (97%)	416 (96%)	19 (4%)	28	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	427/447 (96%)	405 (95%)	22 (5%)	23	44
1	D	427/447 (96%)	411 (96%)	16 (4%)	34	60
All	All	1724/1788 (96%)	1652 (96%)	72 (4%)	30	54

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	63	ASP
1	D	93	THR
1	D	122	ARG
1	D	178	HIS
1	D	182	LEU
1	D	189	VAL
1	D	253	SER
1	D	268	ASP
1	D	336	ASN
1	D	360	SER
1	D	437	THR
1	D	442	ARG
1	D	550	LEU
1	D	560	ARG
1	D	564	LEU
1	D	565	SER
1	A	61	ILE
1	A	79	SER
1	A	83	LEU
1	A	100	SER
1	A	178	HIS
1	A	186	GLN
1	A	271	VAL
1	A	368	ARG
1	A	421	THR
1	A	442	ARG
1	A	476	SER
1	A	512	GLN
1	A	553	PHE
1	A	560	ARG
1	A	563	THR
1	B	65	LEU
1	B	89	THR
1	B	90	LEU

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Mol	Chain	Res	Type
1	B	110	ASN
1	B	141	THR
1	B	182	LEU
1	B	187	ASP
1	B	215	THR
1	B	253	SER
1	B	281	LEU
1	B	385	VAL
1	B	398	ASP
1	B	437	THR
1	B	442	ARG
1	B	448	CYS
1	B	491	THR
1	B	512	GLN
1	B	560	ARG
1	B	563	THR
1	C	65	LEU
1	C	67	ASN
1	C	68	ILE
1	C	73	ASN
1	C	76	ILE
1	C	81	VAL
1	C	95	LEU
1	C	141	THR
1	C	170	THR
1	C	178	HIS
1	C	182	LEU
1	C	186	GLN
1	C	271	VAL
1	C	281	LEU
1	C	321	ASN
1	C	437	THR
1	C	442	ARG
1	C	448	CYS
1	C	480	SER
1	C	511	SER
1	C	563	THR
1	C	565	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	139	ASN
1	A	110	ASN
1	B	74	GLN
1	B	78	ASN
1	C	369	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

14 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	1,2	14,14,15	0.53	0	17,19,21	1.43	3 (17%)
2	NAG	E	2	2	14,14,15	0.39	0	17,19,21	1.00	1 (5%)
2	MAN	E	3	2	11,11,12	0.57	0	15,15,17	0.84	0
2	NAG	F	1	1,2	14,14,15	0.48	0	17,19,21	0.94	1 (5%)
2	NAG	F	2	2	14,14,15	0.52	0	17,19,21	1.09	3 (17%)
2	MAN	F	3	2	11,11,12	0.60	0	15,15,17	0.69	0
3	NAG	G	1	1,3	14,14,15	0.53	0	17,19,21	1.40	2 (11%)
3	NAG	G	2	3	14,14,15	0.52	0	17,19,21	1.12	2 (11%)
3	NAG	H	1	1,3	14,14,15	0.54	0	17,19,21	1.31	2 (11%)
3	NAG	H	2	3	14,14,15	0.64	0	17,19,21	0.88	0
3	NAG	I	1	1,3	14,14,15	0.47	0	17,19,21	1.23	1 (5%)
3	NAG	I	2	3	14,14,15	0.43	0	17,19,21	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	J	1	1,3	14,14,15	0.58	0	17,19,21	1.08	1 (5%)
3	NAG	J	2	3	14,14,15	0.45	0	17,19,21	1.03	1 (5%)

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	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	MAN	E	3	2	-	2/2/19/22	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	MAN	F	3	2	-	2/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	1/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	G	1	NAG	C1-O5-C5	4.23	117.85	112.19
3	I	1	NAG	C1-O5-C5	3.71	117.16	112.19
3	H	1	NAG	C2-N2-C7	-3.42	118.32	122.90
2	E	1	NAG	C1-O5-C5	3.27	116.57	112.19
2	E	1	NAG	C2-N2-C7	-3.20	118.61	122.90
3	G	2	NAG	C2-N2-C7	-3.08	118.77	122.90
2	F	1	NAG	C1-O5-C5	2.81	115.95	112.19
3	J	2	NAG	C1-O5-C5	2.79	115.92	112.19
2	E	2	NAG	C1-O5-C5	2.72	115.84	112.19
3	J	1	NAG	C2-N2-C7	-2.64	119.37	122.90
2	F	2	NAG	C1-O5-C5	2.55	115.60	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	H	1	NAG	C1-O5-C5	2.51	115.55	112.19
2	E	1	NAG	C6-C5-C4	-2.23	107.55	113.02
3	G	2	NAG	C1-O5-C5	2.20	115.13	112.19
2	F	2	NAG	C2-N2-C7	-2.10	120.08	122.90
2	F	2	NAG	O5-C1-C2	2.05	114.47	111.29
3	G	1	NAG	C2-N2-C7	-2.05	120.16	122.90

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	2	NAG	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	E	1	NAG	C8-C7-N2-C2
2	F	3	MAN	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
2	E	1	NAG	O7-C7-N2-C2
2	E	3	MAN	O5-C5-C6-O6
3	G	1	NAG	C8-C7-N2-C2
2	E	3	MAN	C4-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	G	1	NAG	O7-C7-N2-C2
3	I	1	NAG	C8-C7-N2-C2
3	H	2	NAG	C1-C2-N2-C7
3	I	1	NAG	O7-C7-N2-C2
3	H	2	NAG	C3-C2-N2-C7
2	F	2	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
2	F	3	MAN	C4-C5-C6-O6
2	F	2	NAG	O5-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6

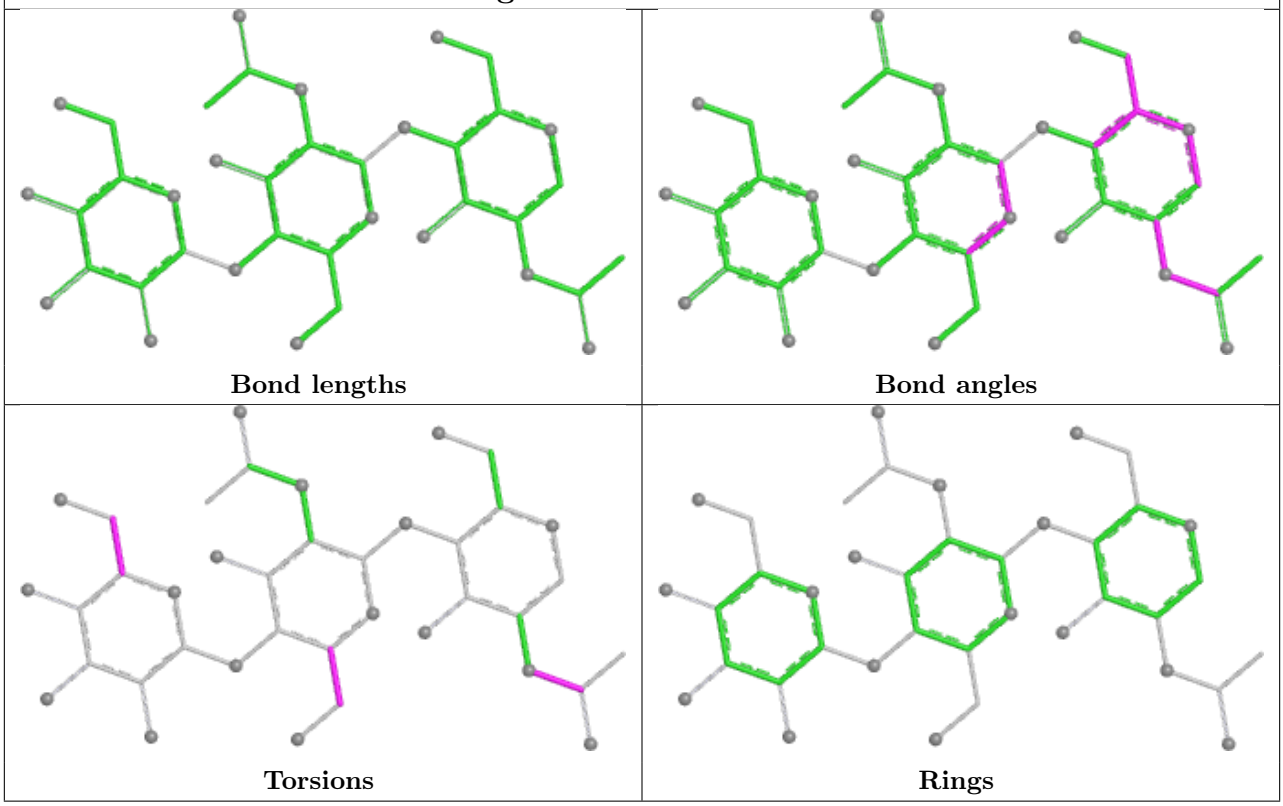
There are no ring outliers.

4 monomers are involved in 6 short contacts:

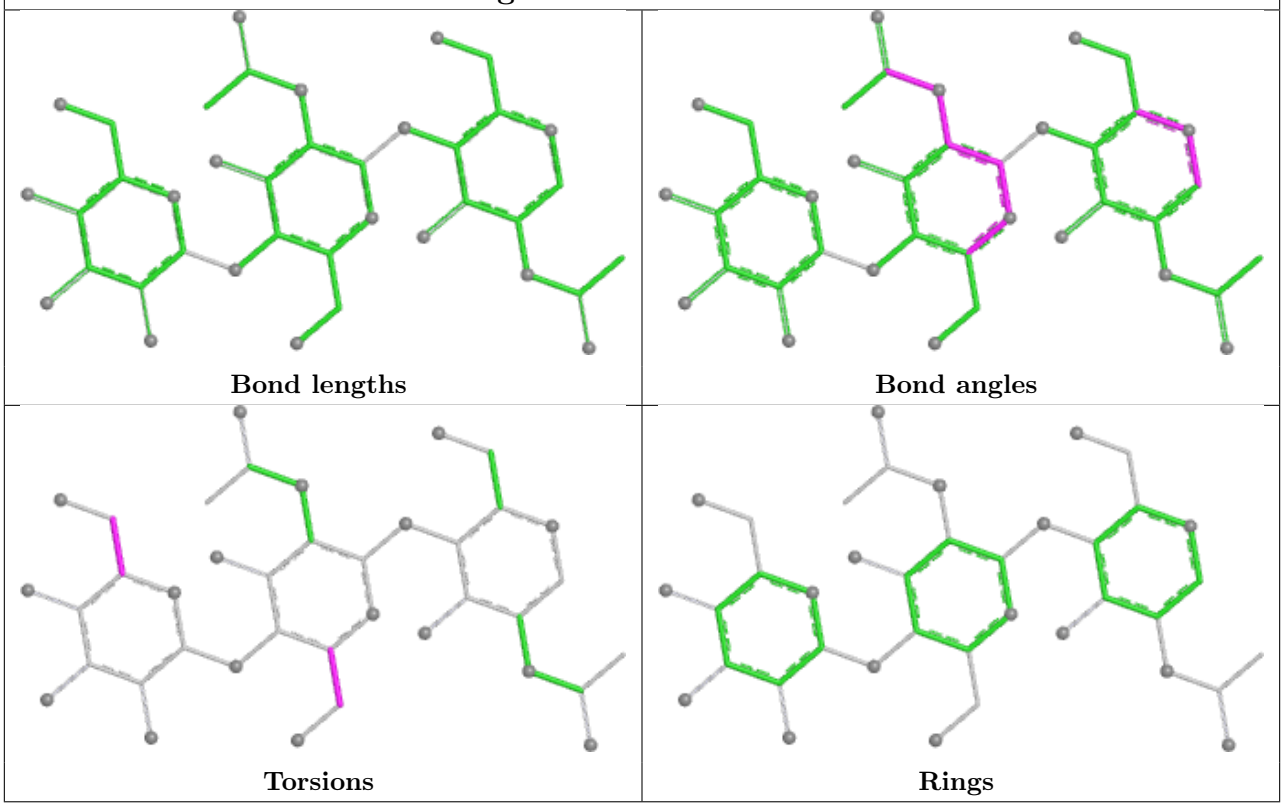
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	NAG	2	0
2	F	3	MAN	2	0
3	J	1	NAG	4	0
3	J	2	NAG	4	0

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

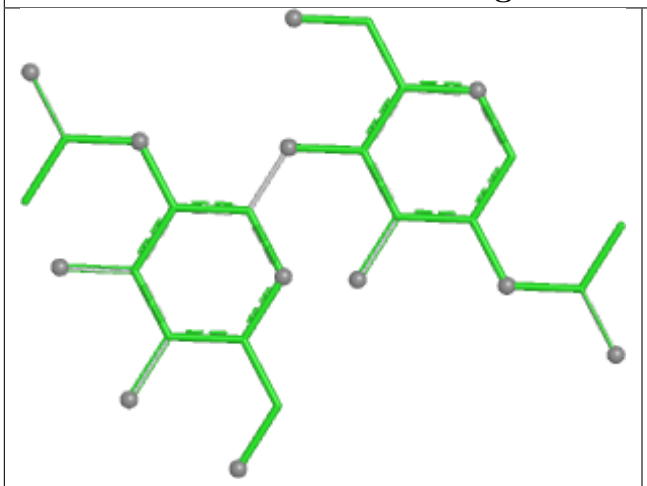
Oligosaccharide Chain E



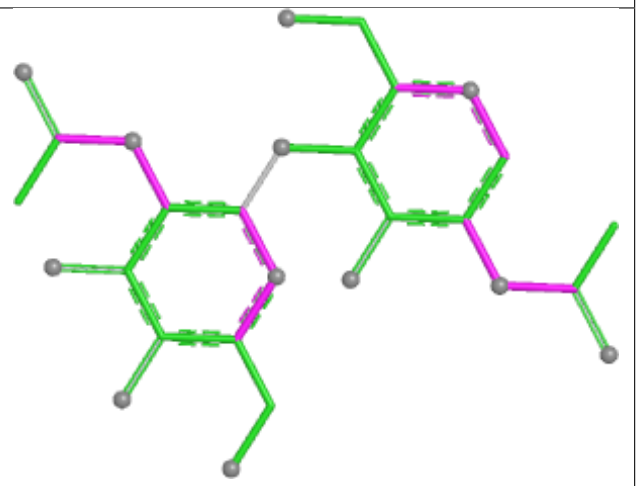
Oligosaccharide Chain F



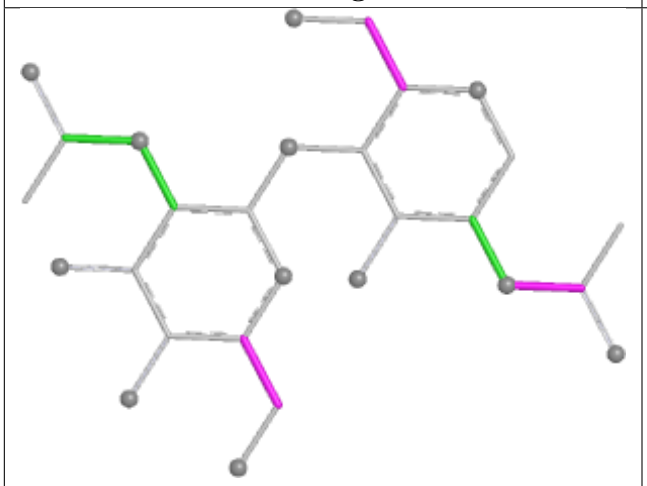
Oligosaccharide Chain G



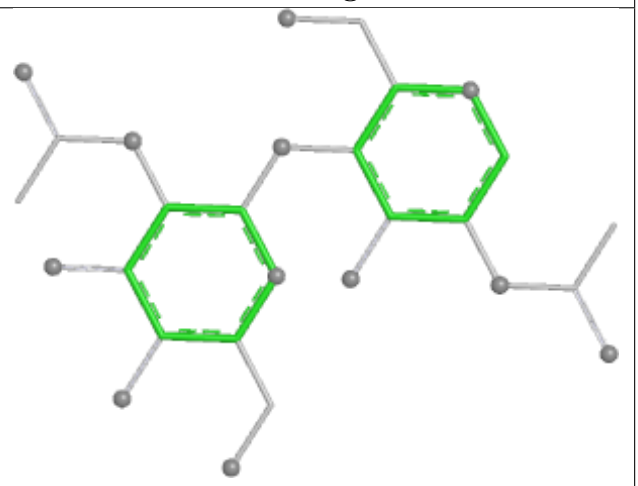
Bond lengths



Bond angles

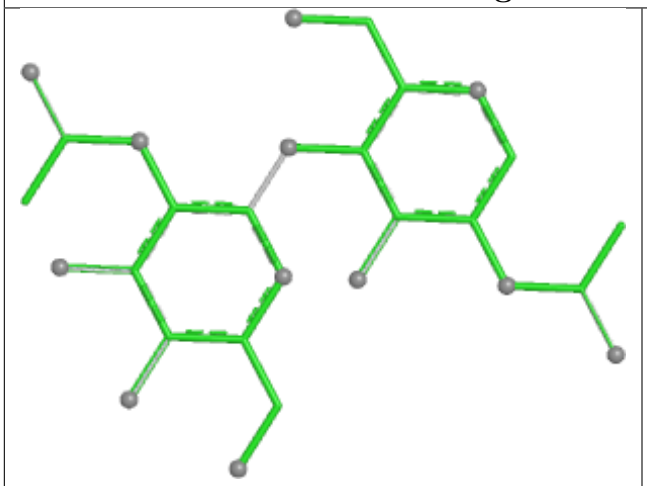


Torsions

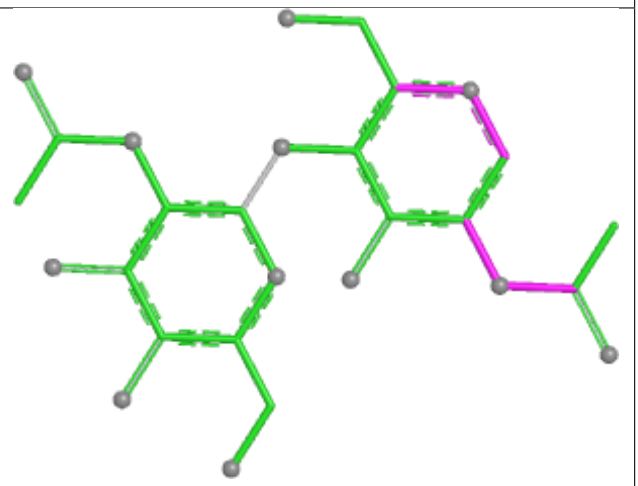


Rings

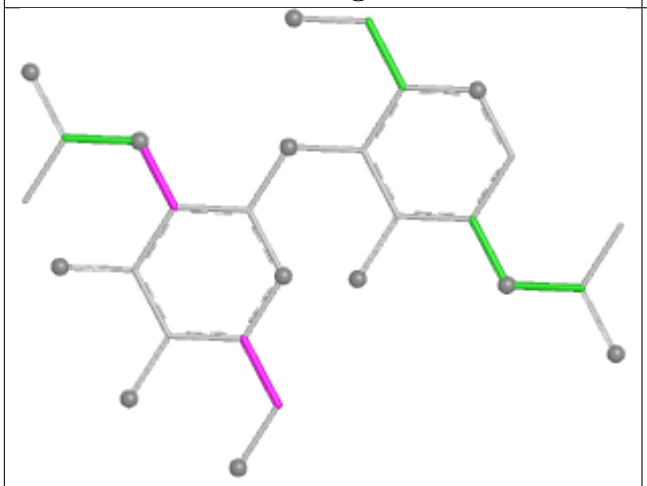
Oligosaccharide Chain H



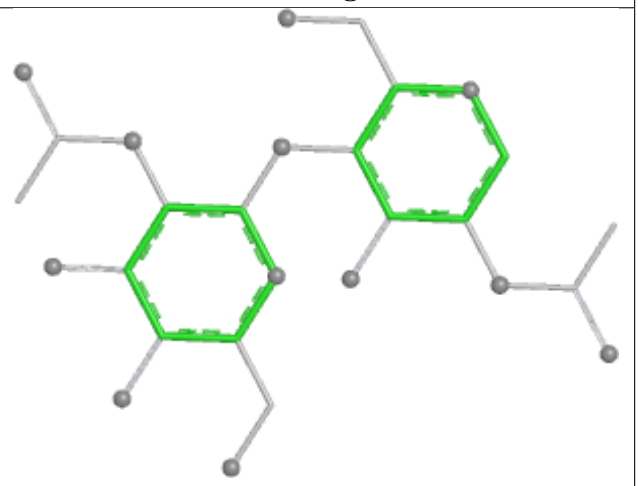
Bond lengths



Bond angles

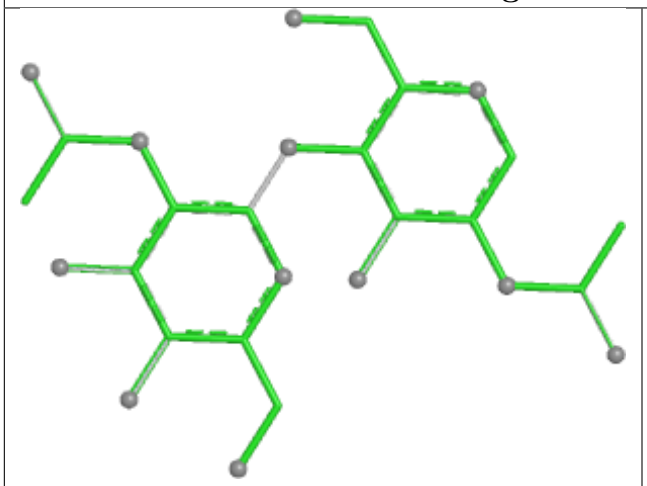


Torsions

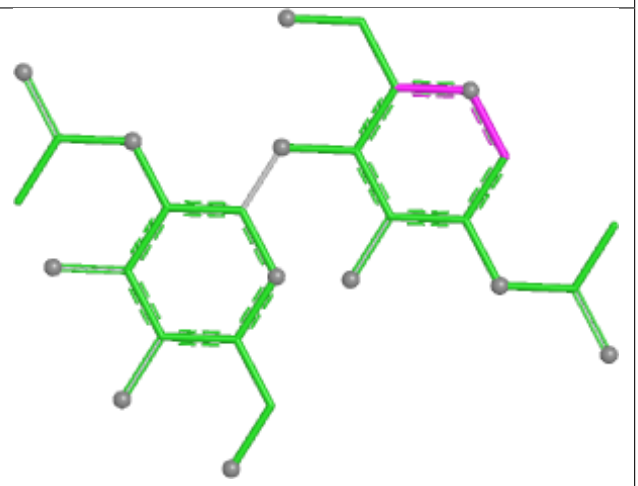


Rings

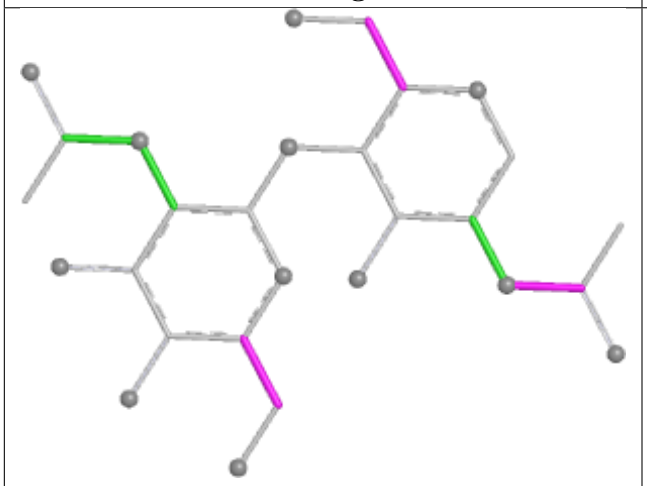
Oligosaccharide Chain I



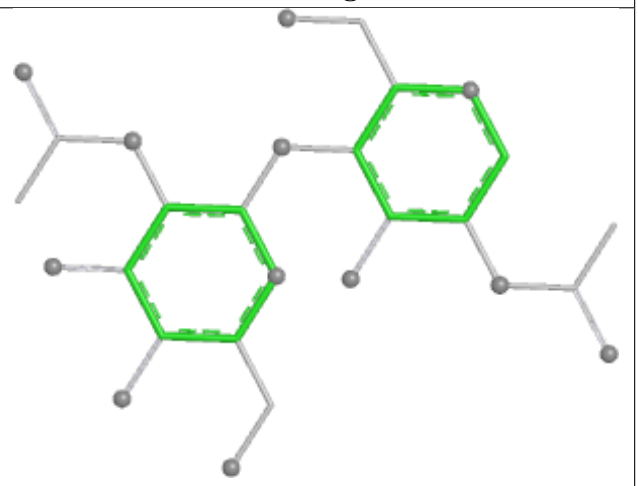
Bond lengths



Bond angles

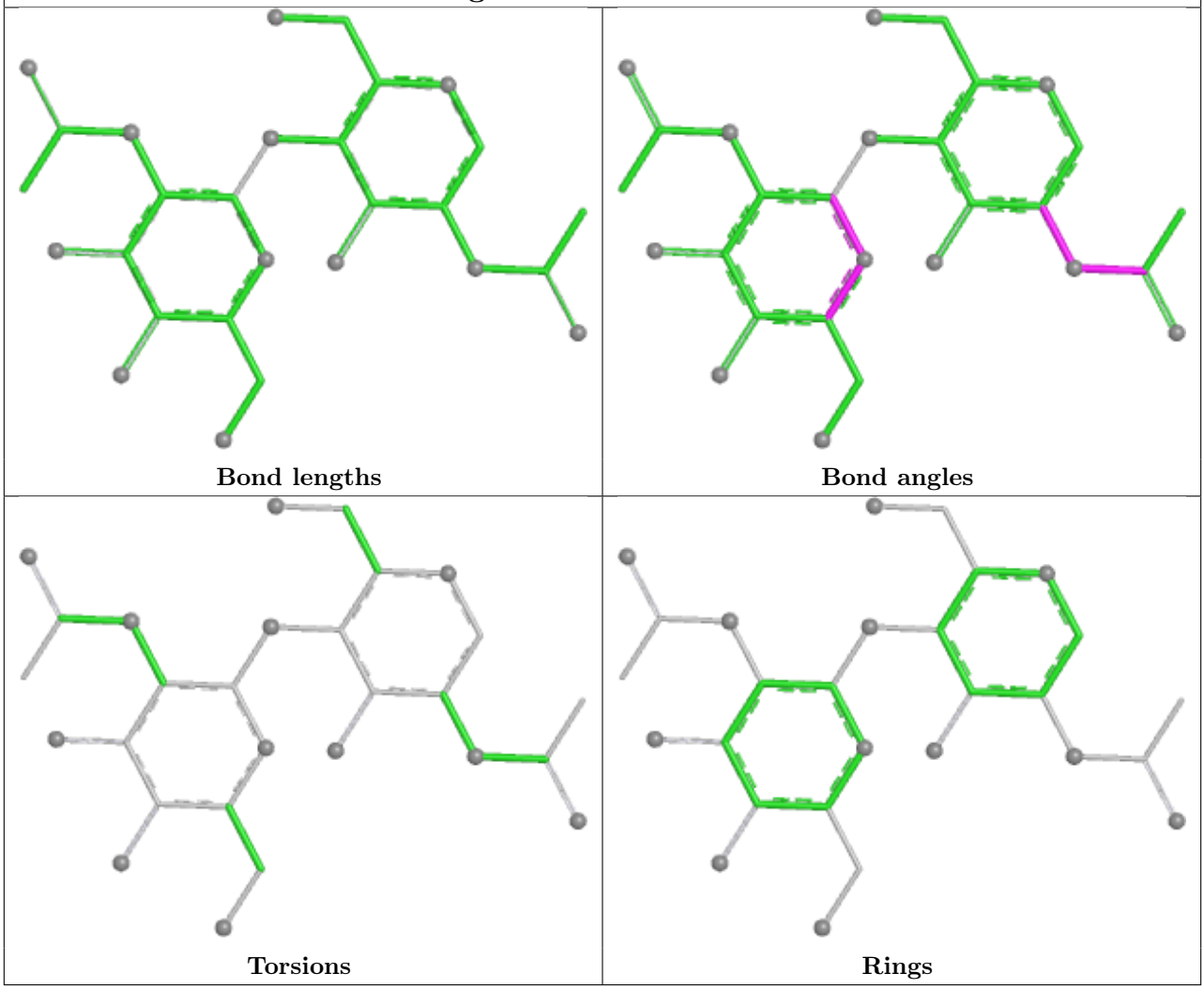


Torsions



Rings

Oligosaccharide Chain J



5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 for Mogul analysis.

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	D	609	1	14,14,15	0.42	0	17,19,21	1.24	1 (5%)
6	NAG	C	604	1	14,14,15	0.41	0	17,19,21	1.46	3 (17%)
5	SO4	A	607	-	4,4,4	0.22	0	6,6,6	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	SO4	B	602	-	4,4,4	0.27	0	6,6,6	0.22	0
6	NAG	A	602	1	14,14,15	0.44	0	17,19,21	1.12	1 (5%)
5	SO4	D	608	-	4,4,4	0.32	0	6,6,6	0.15	0
6	NAG	B	605	1	14,14,15	0.55	0	17,19,21	0.89	1 (5%)
6	NAG	C	603	1	14,14,15	0.47	0	17,19,21	1.32	2 (11%)
5	SO4	C	602	-	4,4,4	0.25	0	6,6,6	0.37	0
6	NAG	A	608	1	14,14,15	0.65	0	17,19,21	1.40	2 (11%)

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	D	609	1	-	0/6/23/26	0/1/1/1
6	NAG	C	604	1	-	1/6/23/26	0/1/1/1
6	NAG	A	602	1	-	0/6/23/26	0/1/1/1
6	NAG	B	605	1	-	0/6/23/26	0/1/1/1
6	NAG	C	603	1	-	4/6/23/26	0/1/1/1
6	NAG	A	608	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	D	609	NAG	C1-O5-C5	4.00	117.55	112.19
6	C	604	NAG	C1-O5-C5	3.73	117.19	112.19
6	C	603	NAG	C2-N2-C7	3.29	127.31	122.90
6	A	608	NAG	O5-C1-C2	3.27	116.36	111.29
6	A	602	NAG	C1-O5-C5	3.23	116.52	112.19
6	A	608	NAG	C4-C3-C2	2.96	115.36	111.02
6	C	604	NAG	C4-C3-C2	-2.83	106.88	111.02
6	C	603	NAG	C1-O5-C5	2.58	115.64	112.19
6	C	604	NAG	C2-N2-C7	-2.47	119.59	122.90
6	B	605	NAG	C1-O5-C5	2.11	115.01	112.19

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	608	NAG	C1-C2-N2-C7
6	A	608	NAG	C8-C7-N2-C2
6	A	608	NAG	O7-C7-N2-C2
6	C	603	NAG	C3-C2-N2-C7
6	C	603	NAG	C8-C7-N2-C2
6	C	603	NAG	O7-C7-N2-C2
6	C	604	NAG	O5-C5-C6-O6
6	A	608	NAG	C4-C5-C6-O6
6	C	603	NAG	C4-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	609	NAG	2	0
6	A	602	NAG	2	0
6	A	608	NAG	8	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 (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	501/513 (97%)	-0.02	24 (4%)	30	32	23, 43, 118, 181	0
1	B	501/513 (97%)	0.00	21 (4%)	36	39	24, 53, 109, 171	0
1	C	493/513 (96%)	-0.05	19 (3%)	39	42	22, 45, 98, 169	0
1	D	492/513 (95%)	-0.09	15 (3%)	50	53	23, 37, 93, 169	0
All	All	1987/2052 (96%)	-0.04	79 (3%)	38	41	22, 44, 106, 181	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	64	LEU	9.9
1	A	62	THR	8.3
1	D	64	LEU	8.1
1	B	65	LEU	7.1
1	C	69	LEU	7.1
1	A	65	LEU	7.0
1	C	70	SER	6.9
1	C	67	ASN	6.4
1	B	69	LEU	6.4
1	B	70	SER	6.1
1	D	101	LEU	6.1
1	B	66	ASN	6.0
1	D	76	ILE	5.8
1	B	68	ILE	5.6
1	D	66	ASN	5.5
1	C	73	ASN	5.5
1	A	63	ASP	5.4
1	C	113	TRP	5.3
1	C	111	CYS	5.3
1	A	61	ILE	5.3
1	B	565	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	72	ALA	4.6
1	D	68	ILE	4.6
1	B	75	ILE	4.5
1	A	66	ASN	4.5
1	C	66	ASN	4.4
1	A	69	LEU	4.3
1	C	71	VAL	4.3
1	A	67	ASN	4.2
1	D	65	LEU	4.0
1	D	114	SER	4.0
1	C	115	ALA	3.9
1	C	72	ALA	3.8
1	C	64	LEU	3.7
1	A	71	VAL	3.7
1	B	67	ASN	3.7
1	C	68	ILE	3.6
1	B	73	ASN	3.5
1	A	107	LEU	3.5
1	A	113	TRP	3.5
1	B	105	ASP	3.4
1	D	71	VAL	3.4
1	A	101	LEU	3.4
1	C	77	TYR	3.3
1	B	79	SER	3.3
1	D	70	SER	3.2
1	D	63	ASP	3.2
1	A	70	SER	3.1
1	A	565	SER	3.1
1	A	102	GLN	3.0
1	D	117	LEU	3.0
1	A	68	ILE	2.9
1	B	71	VAL	2.9
1	A	76	ILE	2.9
1	A	90	LEU	2.9
1	A	117	LEU	2.8
1	B	94	LEU	2.8
1	B	98	ILE	2.7
1	C	114	SER	2.7
1	C	65	LEU	2.7
1	B	107	LEU	2.7
1	B	74	GLN	2.7
1	B	85	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	69	LEU	2.5
1	C	79	SER	2.5
1	D	116	ALA	2.5
1	D	83	LEU	2.4
1	C	565	SER	2.4
1	A	85	LEU	2.4
1	C	76	ILE	2.3
1	C	78	ASN	2.3
1	B	77	TYR	2.2
1	A	99	LYS	2.2
1	B	101	LEU	2.2
1	A	74	GLN	2.1
1	A	114	SER	2.1
1	D	74	GLN	2.1
1	A	98	ILE	2.1
1	B	76	ILE	2.1

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	MAN	E	3	11/12	0.82	0.14	91,108,111,112	0
2	MAN	F	3	11/12	0.83	0.12	103,111,115,115	0
3	NAG	I	2	14/15	0.85	0.19	88,101,109,112	0
3	NAG	H	2	14/15	0.87	0.16	57,91,97,98	0
2	NAG	E	2	14/15	0.90	0.12	73,78,82,83	0
3	NAG	J	2	14/15	0.90	0.19	42,80,99,103	0
2	NAG	F	2	14/15	0.94	0.10	58,76,91,101	0
3	NAG	H	1	14/15	0.95	0.14	50,63,73,75	0
3	NAG	G	2	14/15	0.95	0.18	64,77,94,95	0
3	NAG	I	1	14/15	0.97	0.12	51,57,67,78	0
2	NAG	F	1	14/15	0.97	0.12	43,53,61,69	0
2	NAG	E	1	14/15	0.97	0.15	38,51,63,73	0

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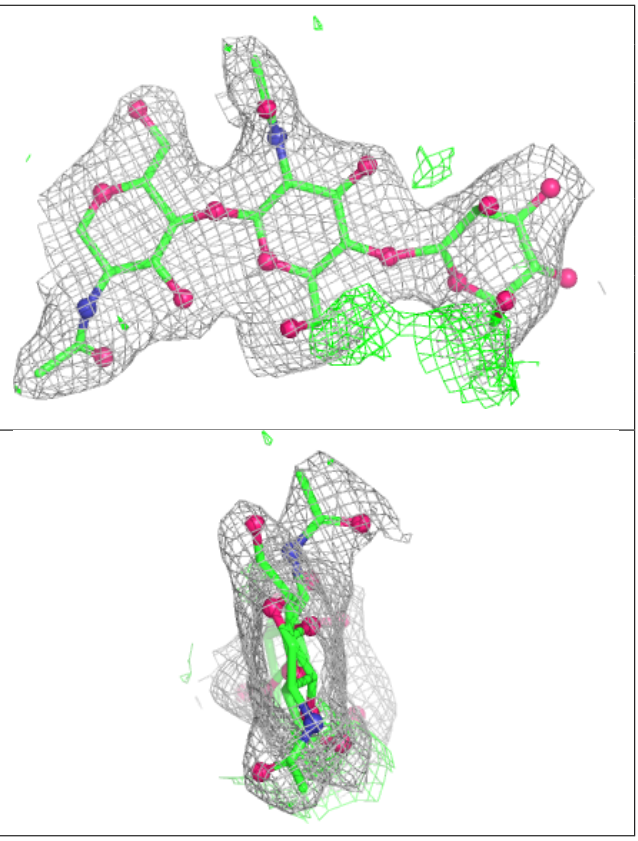
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	J	1	14/15	0.98	0.12	41,53,62,67	0
3	NAG	G	1	14/15	0.98	0.14	36,46,56,66	0

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.

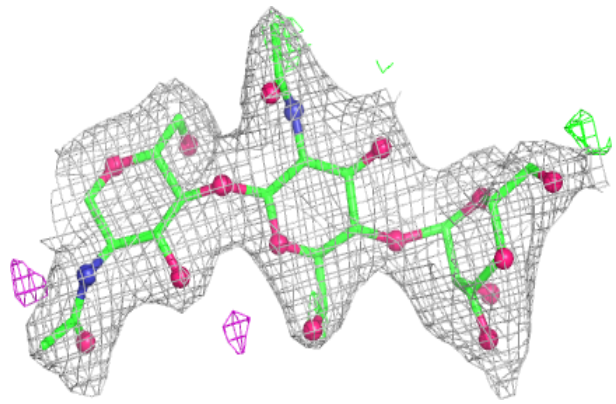
Electron density around Chain E:

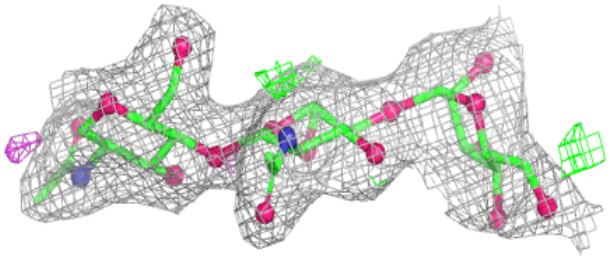
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

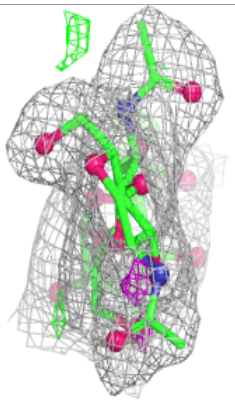


Electron density around Chain F:

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

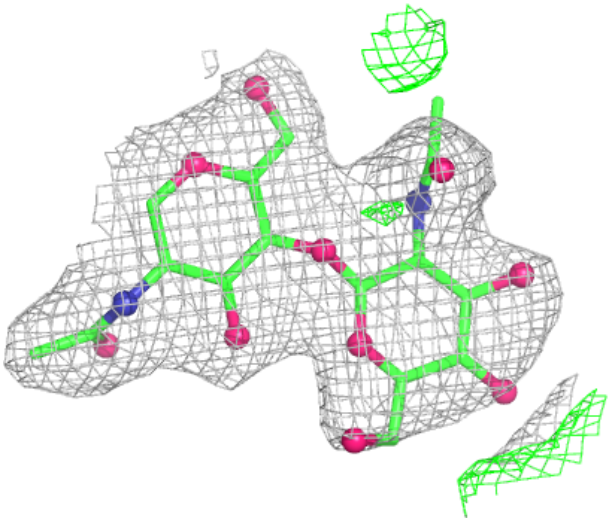


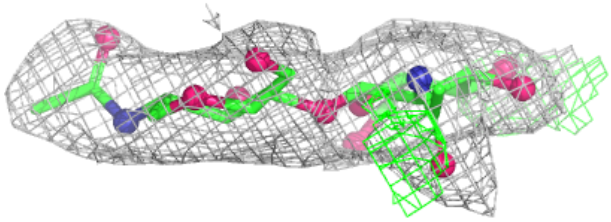


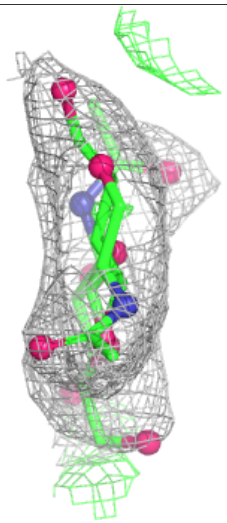


Electron density around Chain G:

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

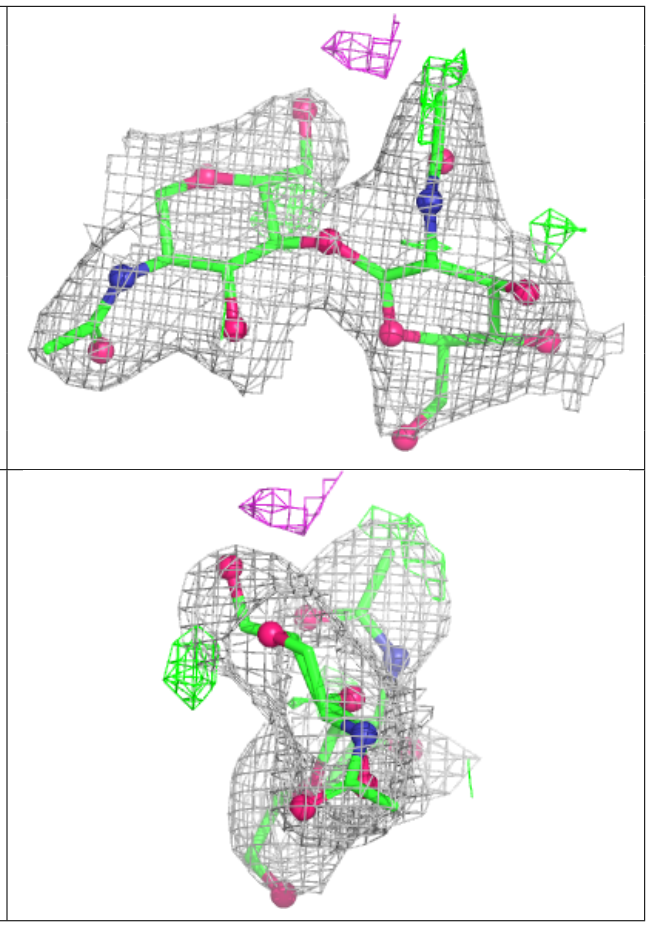


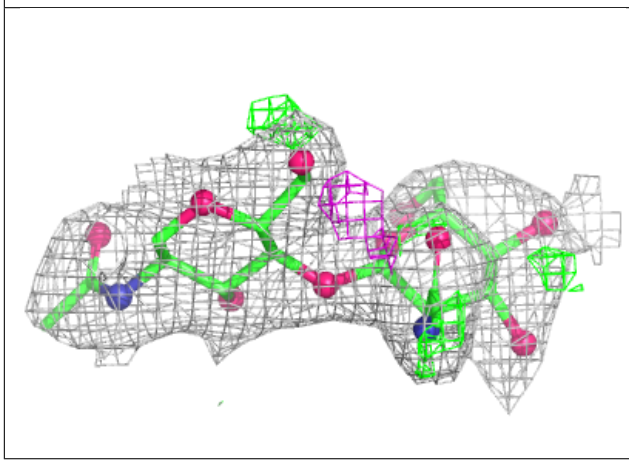




Electron density around Chain H:

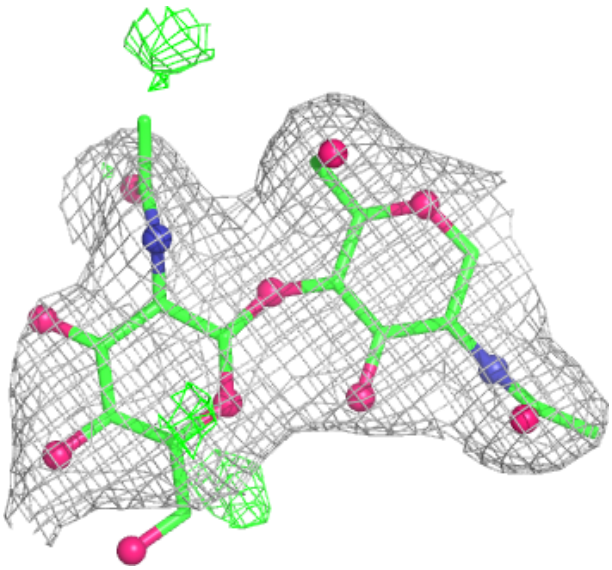
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

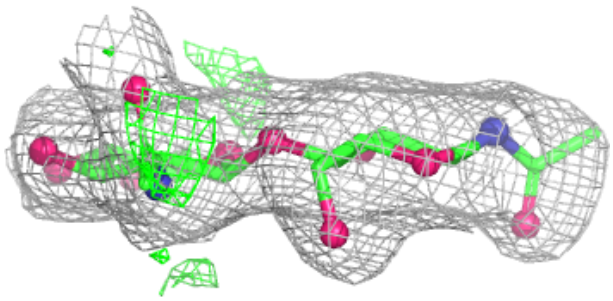


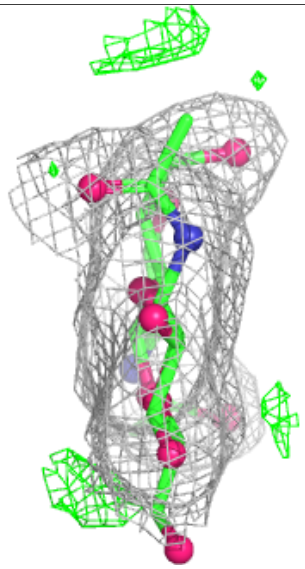


Electron density around Chain I:

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

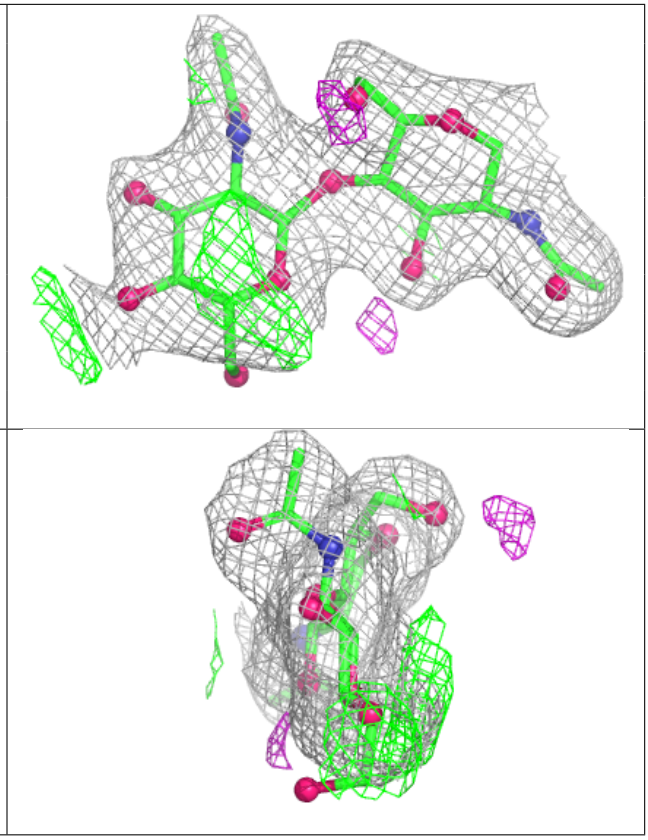






Electron density around Chain J:

$2mF_o$-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
4	CA	B	601	1/1	0.44	0.17	92,92,92,92	0
6	NAG	A	602	14/15	0.84	0.20	66,89,100,101	0
4	CA	A	601	1/1	0.87	0.09	74,74,74,74	0
6	NAG	C	603	14/15	0.87	0.11	81,94,100,100	0
6	NAG	A	608	14/15	0.88	0.13	99,108,112,112	0
6	NAG	D	609	14/15	0.88	0.13	66,81,91,92	0
6	NAG	B	605	14/15	0.91	0.21	45,68,77,80	0
4	CA	C	601	1/1	0.91	0.08	81,81,81,81	0
4	CA	D	601	1/1	0.93	0.10	80,80,80,80	0
6	NAG	C	604	14/15	0.96	0.13	64,69,77,80	0
5	SO4	B	602	5/5	0.97	0.17	66,72,78,86	0
5	SO4	A	607	5/5	0.98	0.12	44,54,65,65	0
5	SO4	D	608	5/5	0.98	0.13	48,60,61,67	0
5	SO4	C	602	5/5	0.98	0.17	50,57,71,80	0

6.5 Other polymers (i)

There are no such residues in this entry.