



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 12, 2024 – 12:17 PM EDT

PDB ID : 6MUF
Title : Crystal Structure of HIV-1 B41 SOSIP.664 Prefusion Env Trimer in Complex with Human Antibodies 3H109L and 35O22 at 3.4 Angstrom
Authors : Lai, Y.-T.; Kwong, P.D.
Deposited on : 2018-10-23
Resolution : 2.91 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

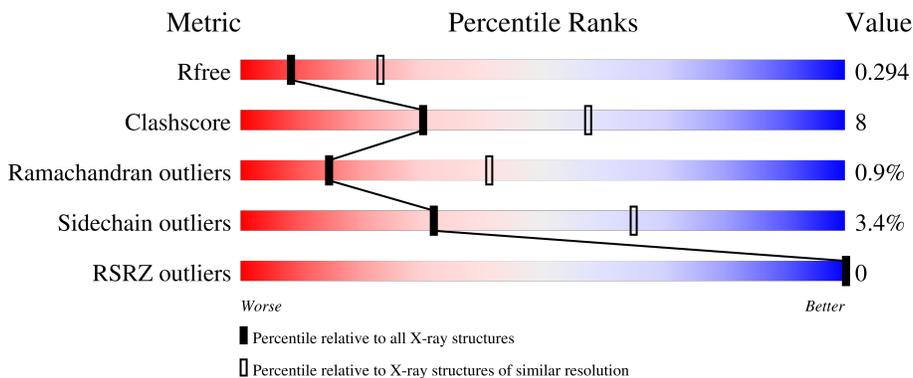
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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}	164625	2797 (2.94-2.90)
Clashscore	180529	3049 (2.94-2.90)
Ramachandran outliers	177936	2981 (2.94-2.90)
Sidechain outliers	177891	2983 (2.94-2.90)
RSRZ outliers	164620	2799 (2.94-2.90)

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	B	153	 65% 14% 20%
2	D	134	 75% 19% 1% 1%
3	E	114	 78% 20% 1% 1%
4	G	489	 63% 21% 14%
5	H	244	 73% 20% 7%

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Mol	Chain	Length	Quality of chain
6	L	217	 <p>79% 18%</p>
7	A	6	 <p>17% 50% 33%</p>
8	C	4	 <p>75% 25%</p>
9	F	2	 <p>100%</p>
10	I	10	 <p>20% 40% 40%</p>

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 9881 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	122	983	627	166	183	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP B3UEZ6
B	605	CYS	THR	engineered mutation	UNP B3UEZ6

- Molecule 2 is a protein called 35O22 scFv heavy chain portion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	128	994	630	168	191	5	0	0	0

- Molecule 3 is a protein called 35O22 scFv light chain portion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	112	851	533	141	171	6	0	0	0

- Molecule 4 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	G	421	3314	2093	583	612	26	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	501	CYS	ALA	conflict	UNP B3UES2
G	508	ARG	-	expression tag	UNP B3UES2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	509	ARG	-	expression tag	UNP B3UES2
G	510	ARG	-	expression tag	UNP B3UES2
G	511	ARG	-	expression tag	UNP B3UES2
G	512	ARG	-	expression tag	UNP B3UES2
G	513	ARG	-	expression tag	UNP B3UES2

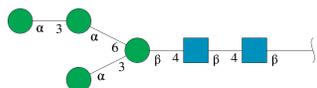
- Molecule 5 is a protein called 3H109L Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	H	226	1715	1093	278	338	6	0	0	0

- Molecule 6 is a protein called 3H109L Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	L	211	1604	1009	276	312	7	0	0	0

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
7	A	6	72	40	2	30	0	0	0

- Molecule 8 is an oligosaccharide called 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.



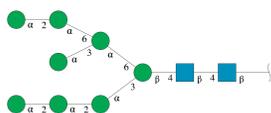
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	C	4	50	28	2	20	0	0	0

- Molecule 9 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



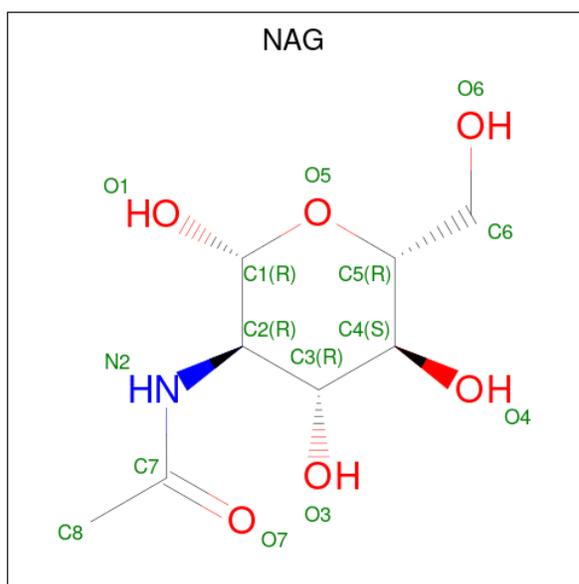
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	F	2	28	16	2	10	0	0	0

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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
			Total	C	N	O			
10	I	10	116	64	2	50	0	0	0

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

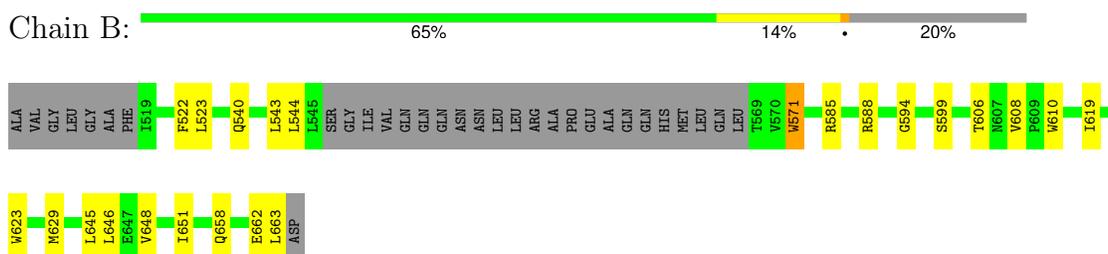


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	0	0
			14	8	1	5		
11	B	1	Total	C	N	O	0	0
			14	8	1	5		
11	G	1	Total	C	N	O	0	0
			14	8	1	5		
11	G	1	Total	C	N	O	0	0
			14	8	1	5		
11	G	1	Total	C	N	O	0	0
			14	8	1	5		
11	G	1	Total	C	N	O	0	0
			14	8	1	5		
11	G	1	Total	C	N	O	0	0
			14	8	1	5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

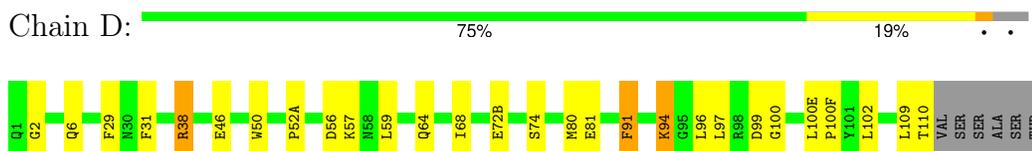
3 Residue-property plots [i](#)

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.

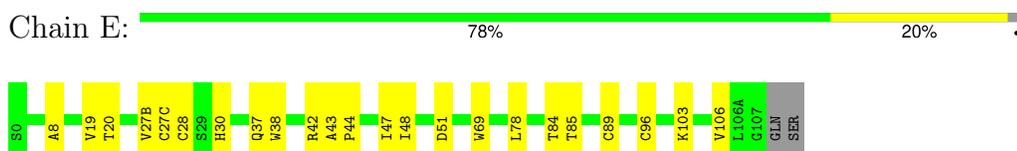
- Molecule 1: Envelope glycoprotein gp160



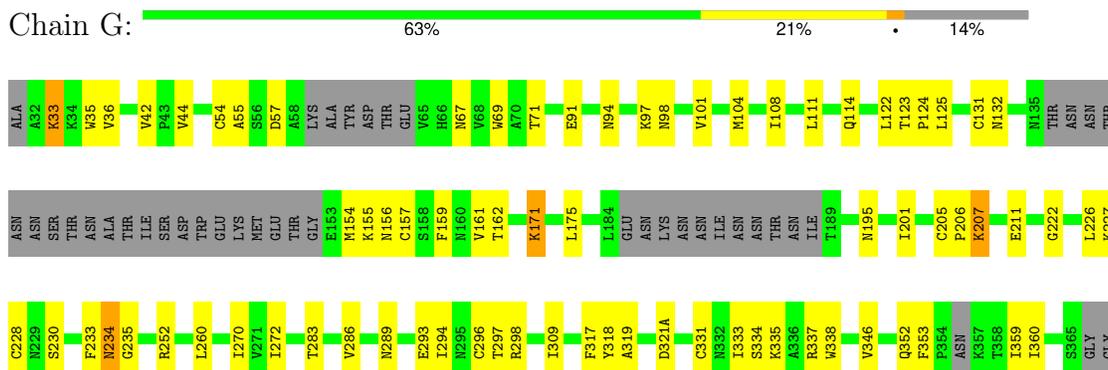
- Molecule 2: 35O22 scFv heavy chain portion

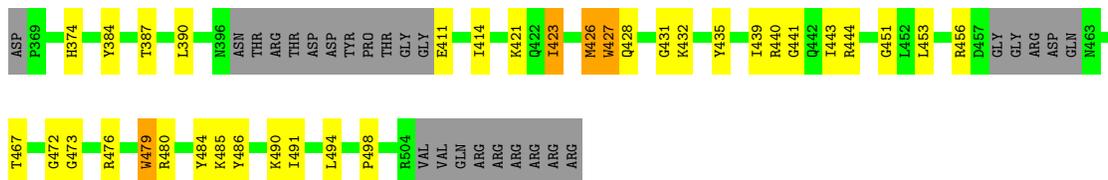


- Molecule 3: 35O22 scFv light chain portion



- Molecule 4: Envelope glycoprotein gp160





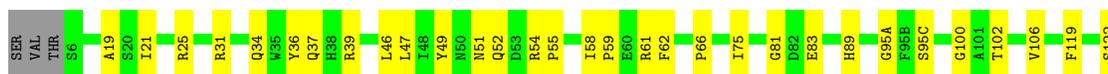
- Molecule 5: 3H109L Fab heavy chain

Chain H: 73% 20% 7%



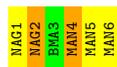
- Molecule 6: 3H109L Fab light chain

Chain L: 79% 18%



- Molecule 7: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[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

Chain A: 17% 50% 33%



- Molecule 8: 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: 75% 25%



- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 100%



- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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 I: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	131.97Å 131.97Å 314.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.84 – 2.91 41.84 – 2.91	Depositor EDS
% Data completeness (in resolution range)	39.7 (41.84-2.91) 39.7 (41.84-2.91)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.81Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.253 , 0.297 0.251 , 0.294	Depositor DCC
R_{free} test set	25553 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtrriage
Anisotropy	0.006	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 3.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.078 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	9881	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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: MAN, BMA, NAG

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	B	0.25	0/1001	0.41	0/1358
2	D	0.24	0/1021	0.47	0/1390
3	E	0.25	0/875	0.44	0/1195
4	G	0.25	0/3382	0.45	0/4591
5	H	0.25	0/1758	0.47	0/2397
6	L	0.24	0/1647	0.44	0/2247
All	All	0.25	0/9684	0.45	0/13178

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	B	983	0	971	18	0
2	D	994	0	958	18	0
3	E	851	0	801	10	0
4	G	3314	0	3268	68	0
5	H	1715	0	1685	28	0
6	L	1604	0	1553	23	0
7	A	72	0	61	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	50	0	43	0	0
9	F	28	0	25	0	0
10	I	116	0	97	6	0
11	B	28	0	26	0	0
11	G	126	0	117	5	0
All	All	9881	0	9605	162	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 8.

The worst 5 of 162 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:629:MET:HG3	4:G:44:VAL:HG23	1.71	0.72
4:G:333:ILE:HD11	4:G:390:LEU:HD21	1.70	0.72
4:G:270:ILE:HG22	4:G:289:ASN:H	1.56	0.70
4:G:346:VAL:HG13	4:G:359:ILE:HD12	1.76	0.67
6:L:197:THR:HA	6:L:202:THR:HA	1.76	0.67

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	B	118/153 (77%)	105 (89%)	13 (11%)	0	100	100
2	D	126/134 (94%)	109 (86%)	17 (14%)	0	100	100
3	E	110/114 (96%)	92 (84%)	16 (14%)	2 (2%)	7	24
4	G	405/489 (83%)	364 (90%)	36 (9%)	5 (1%)	11	33
5	H	222/244 (91%)	204 (92%)	17 (8%)	1 (0%)	25	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	L	209/217 (96%)	187 (90%)	19 (9%)	3 (1%)	9	30
All	All	1190/1351 (88%)	1061 (89%)	118 (10%)	11 (1%)	14	41

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	H	64	LYS
4	G	431	GLY
6	L	95(A)	GLY
6	L	100	GLY
3	E	8	ALA

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	B	106/130 (82%)	104 (98%)	2 (2%)	52	79
2	D	107/112 (96%)	103 (96%)	4 (4%)	29	62
3	E	98/100 (98%)	93 (95%)	5 (5%)	20	50
4	G	375/433 (87%)	357 (95%)	18 (5%)	21	52
5	H	196/212 (92%)	192 (98%)	4 (2%)	50	78
6	L	175/181 (97%)	172 (98%)	3 (2%)	56	82
All	All	1057/1168 (90%)	1021 (97%)	36 (3%)	32	65

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

Mol	Chain	Res	Type
4	G	490	LYS
6	L	180	SER
5	H	57	THR
5	H	162	HIS
4	G	57	ASP

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

Mol	Chain	Res	Type
5	H	198	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](#)

22 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
7	NAG	A	1	7,4	14,14,15	0.31	0	17,19,21	0.43	0
7	NAG	A	2	7	14,14,15	0.44	0	17,19,21	1.34	2 (11%)
7	BMA	A	3	7	11,11,12	0.52	0	15,15,17	0.64	0
7	MAN	A	4	7	11,11,12	0.98	1 (9%)	15,15,17	1.03	1 (6%)
7	MAN	A	5	7	11,11,12	1.52	1 (9%)	15,15,17	1.75	3 (20%)
7	MAN	A	6	7	11,11,12	0.60	0	15,15,17	0.99	2 (13%)
8	NAG	C	1	8,4	14,14,15	0.26	0	17,19,21	0.42	0
8	NAG	C	2	8	14,14,15	0.22	0	17,19,21	0.41	0
8	BMA	C	3	8	11,11,12	0.60	0	15,15,17	0.70	0
8	MAN	C	4	8	11,11,12	0.74	1 (9%)	15,15,17	1.07	2 (13%)
9	NAG	F	1	9,4	14,14,15	0.25	0	17,19,21	0.49	0
9	NAG	F	2	9	14,14,15	0.31	0	17,19,21	0.48	0
10	NAG	I	1	4,10	14,14,15	0.55	0	17,19,21	1.50	2 (11%)
10	MAN	I	10	10	11,11,12	1.03	0	15,15,17	1.10	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	NAG	I	2	10	14,14,15	0.21	0	17,19,21	0.46	0
10	BMA	I	3	10	11,11,12	0.91	0	15,15,17	0.91	0
10	MAN	I	4	10	11,11,12	0.80	1 (9%)	15,15,17	1.24	2 (13%)
10	MAN	I	5	10	11,11,12	0.78	0	15,15,17	0.91	1 (6%)
10	MAN	I	6	10	11,11,12	0.76	0	15,15,17	0.95	2 (13%)
10	MAN	I	7	10	11,11,12	0.70	0	15,15,17	0.94	2 (13%)
10	MAN	I	8	10	11,11,12	0.70	0	15,15,17	0.96	1 (6%)
10	MAN	I	9	10	11,11,12	0.72	0	15,15,17	1.27	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	A	1	7,4	-	0/6/23/26	0/1/1/1
7	NAG	A	2	7	-	6/6/23/26	0/1/1/1
7	BMA	A	3	7	-	2/2/19/22	0/1/1/1
7	MAN	A	4	7	-	2/2/19/22	0/1/1/1
7	MAN	A	5	7	-	2/2/19/22	0/1/1/1
7	MAN	A	6	7	-	0/2/19/22	0/1/1/1
8	NAG	C	1	8,4	-	0/6/23/26	0/1/1/1
8	NAG	C	2	8	-	0/6/23/26	0/1/1/1
8	BMA	C	3	8	-	2/2/19/22	0/1/1/1
8	MAN	C	4	8	-	2/2/19/22	0/1/1/1
9	NAG	F	1	9,4	-	0/6/23/26	0/1/1/1
9	NAG	F	2	9	-	2/6/23/26	0/1/1/1
10	NAG	I	1	4,10	-	4/6/23/26	0/1/1/1
10	MAN	I	10	10	-	0/2/19/22	0/1/1/1
10	NAG	I	2	10	-	2/6/23/26	0/1/1/1
10	BMA	I	3	10	-	0/2/19/22	0/1/1/1
10	MAN	I	4	10	-	2/2/19/22	0/1/1/1
10	MAN	I	5	10	-	2/2/19/22	0/1/1/1
10	MAN	I	6	10	-	0/2/19/22	0/1/1/1
10	MAN	I	7	10	-	0/2/19/22	0/1/1/1
10	MAN	I	8	10	-	2/2/19/22	0/1/1/1
10	MAN	I	9	10	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	5	MAN	C1-C2	4.29	1.62	1.52
10	I	4	MAN	C1-C2	2.36	1.57	1.52
7	A	4	MAN	O5-C1	-2.10	1.40	1.43
8	C	4	MAN	C1-C2	2.08	1.57	1.52

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	1	NAG	C2-N2-C7	4.66	129.15	122.90
7	A	2	NAG	C2-N2-C7	4.57	129.02	122.90
7	A	5	MAN	C1-O5-C5	4.40	118.08	112.19
10	I	9	MAN	C1-O5-C5	3.89	117.40	112.19
7	A	5	MAN	C1-C2-C3	3.64	114.95	109.64

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

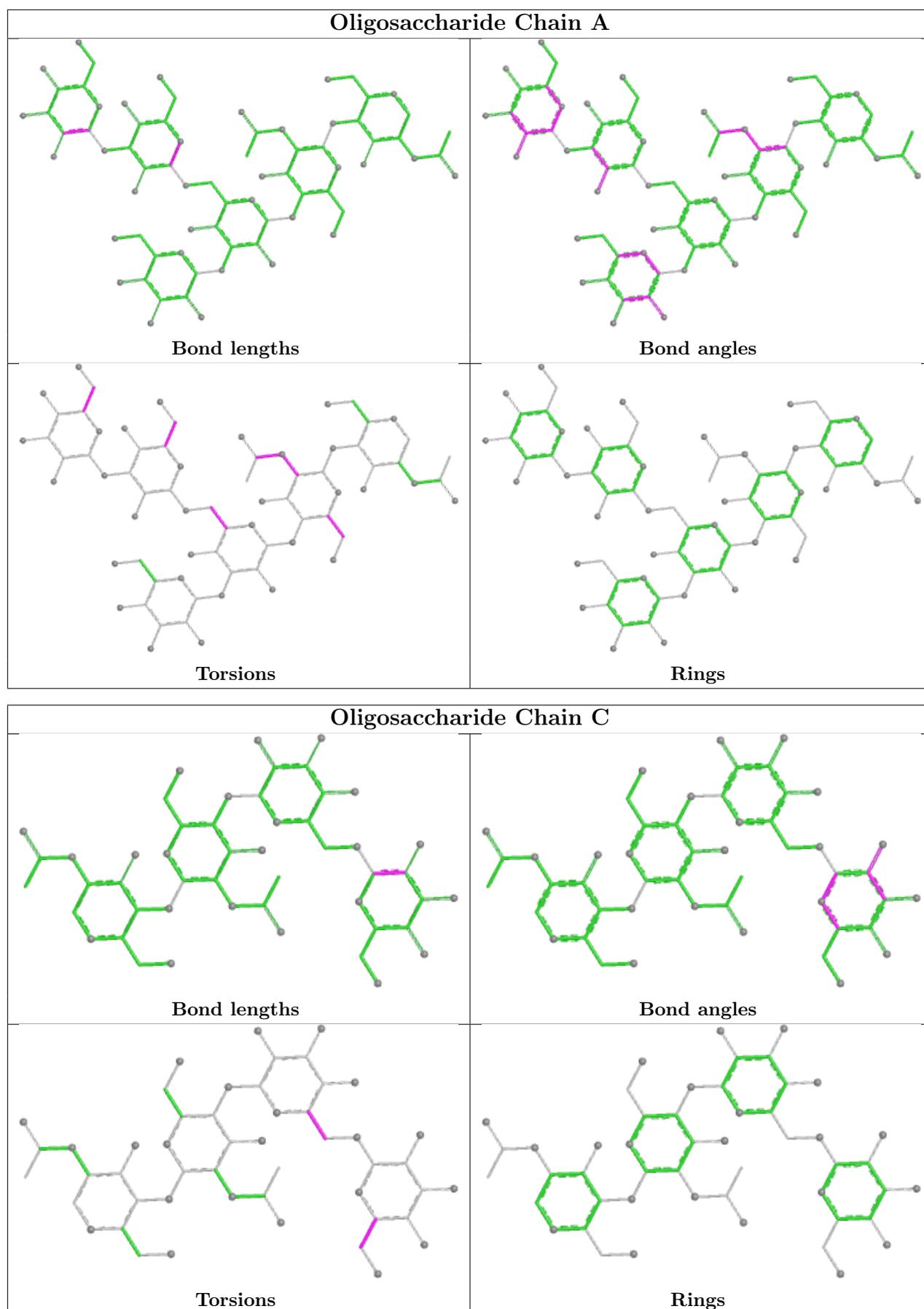
Mol	Chain	Res	Type	Atoms
8	C	4	MAN	O5-C5-C6-O6
7	A	3	BMA	O5-C5-C6-O6
8	C	3	BMA	C4-C5-C6-O6
7	A	2	NAG	O5-C5-C6-O6
10	I	4	MAN	O5-C5-C6-O6

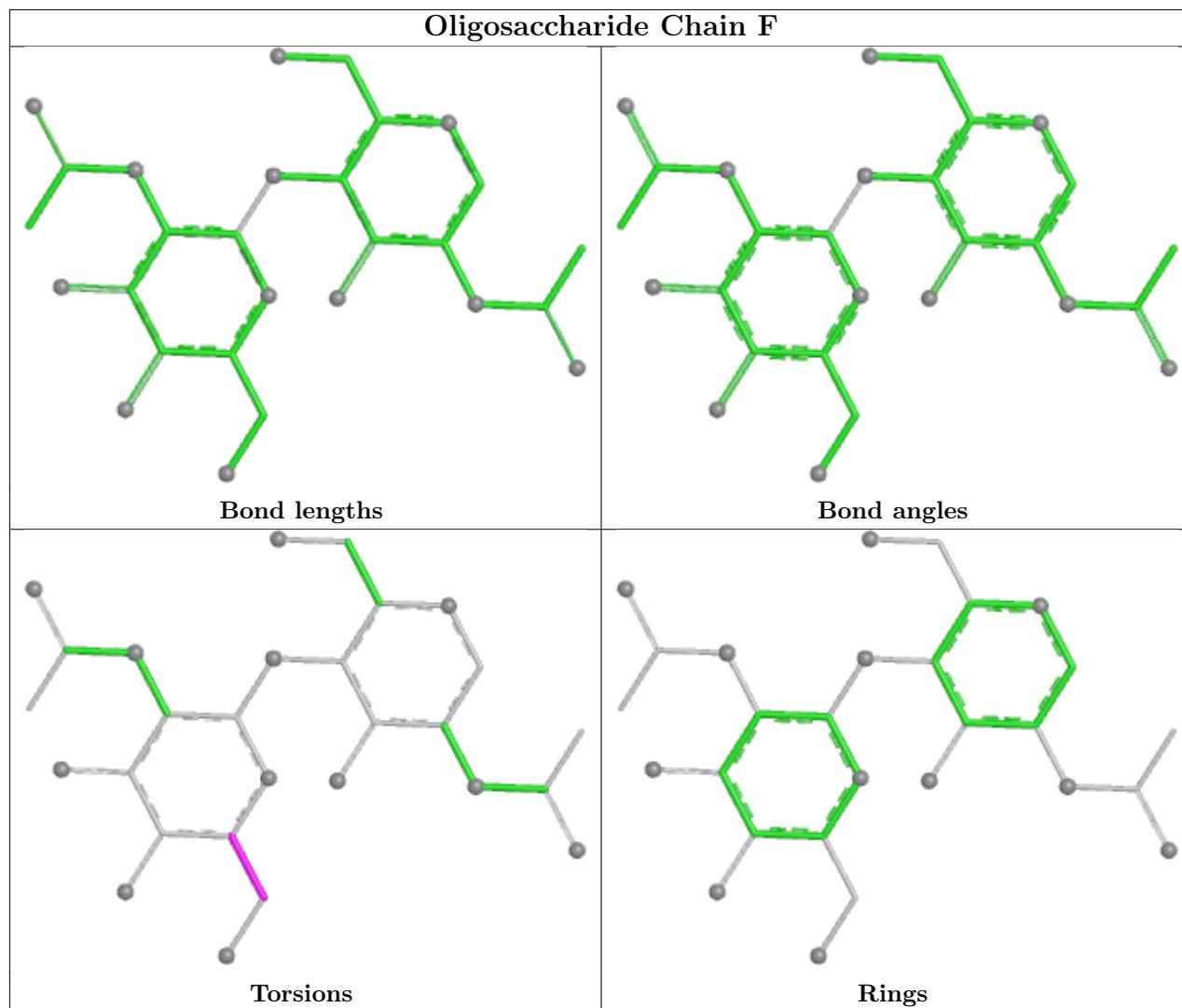
There are no ring outliers.

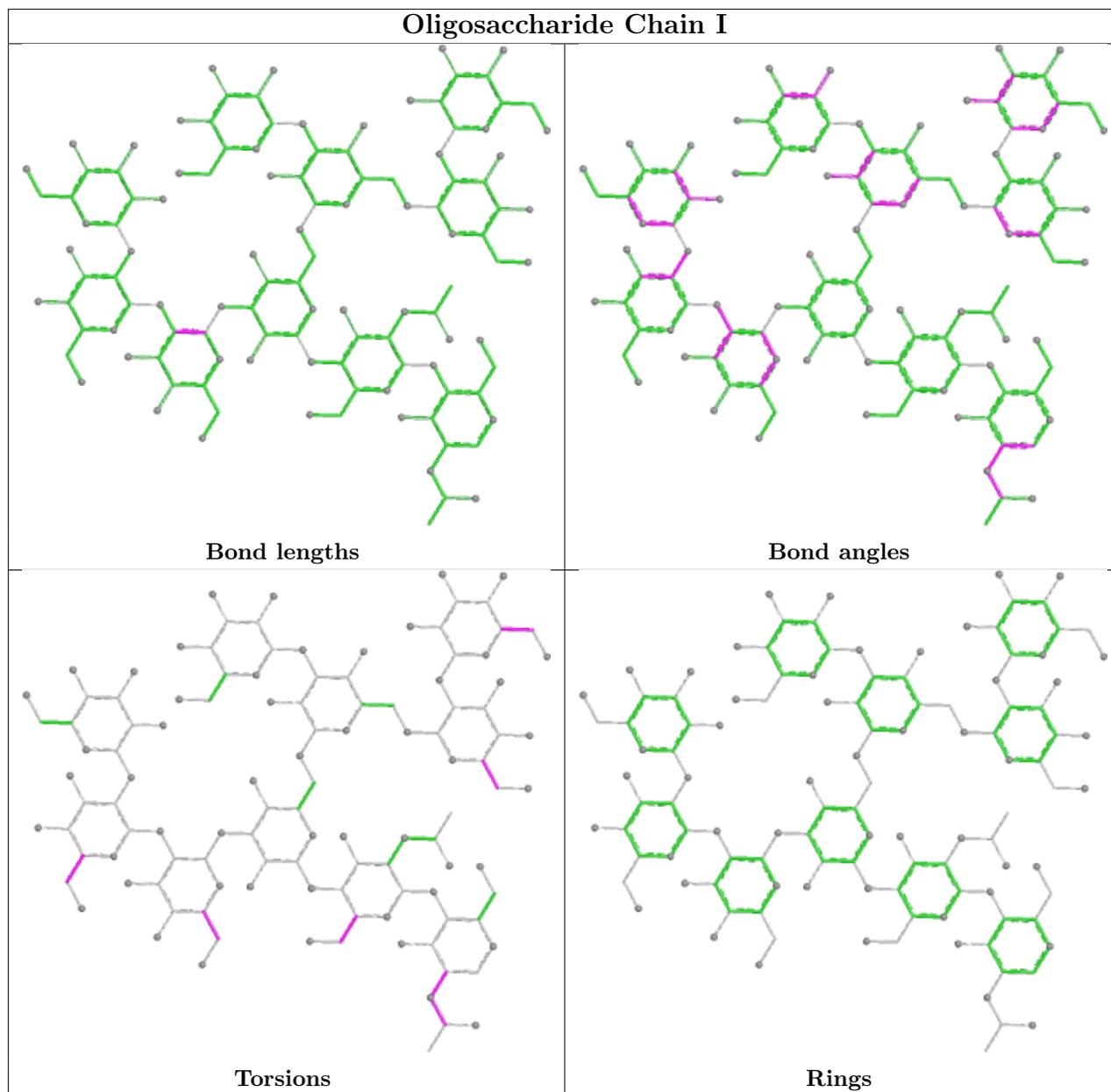
7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1	NAG	1	0
10	I	9	MAN	1	0
10	I	1	NAG	3	0
10	I	6	MAN	1	0
10	I	5	MAN	1	0
7	A	2	NAG	1	0
7	A	4	MAN	3	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](#)

11 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	NAG	G	629	4	14,14,15	0.29	0	17,19,21	0.50	0
11	NAG	G	618	4	14,14,15	0.30	0	17,19,21	0.46	0
11	NAG	G	613	4	14,14,15	0.36	0	17,19,21	0.51	0
11	NAG	G	612	4	14,14,15	0.32	0	17,19,21	0.46	0
11	NAG	G	617	4	14,14,15	0.24	0	17,19,21	0.55	0
11	NAG	G	630	4	14,14,15	0.29	0	17,19,21	0.61	0
11	NAG	G	616	4	14,14,15	0.30	0	17,19,21	0.50	0
11	NAG	G	631	4	14,14,15	0.23	0	17,19,21	0.60	0
11	NAG	B	702	1	14,14,15	0.37	0	17,19,21	0.59	0
11	NAG	B	701	1	14,14,15	0.30	0	17,19,21	0.48	0
11	NAG	G	611	4	14,14,15	0.30	0	17,19,21	0.49	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
11	NAG	G	629	4	-	2/6/23/26	0/1/1/1
11	NAG	G	618	4	-	0/6/23/26	0/1/1/1
11	NAG	G	613	4	-	2/6/23/26	0/1/1/1
11	NAG	G	612	4	-	3/6/23/26	0/1/1/1
11	NAG	G	617	4	-	2/6/23/26	0/1/1/1
11	NAG	G	630	4	-	2/6/23/26	0/1/1/1
11	NAG	G	616	4	-	2/6/23/26	0/1/1/1
11	NAG	G	631	4	-	0/6/23/26	0/1/1/1
11	NAG	B	702	1	-	0/6/23/26	0/1/1/1
11	NAG	B	701	1	-	2/6/23/26	0/1/1/1
11	NAG	G	611	4	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	G	630	NAG	O5-C5-C6-O6
11	G	630	NAG	C4-C5-C6-O6
11	G	612	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
11	B	701	NAG	O5-C5-C6-O6
11	G	612	NAG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	G	613	NAG	1	0
11	G	630	NAG	2	0
11	G	631	NAG	1	0
11	G	611	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 [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	B	122/153 (79%)	-1.69	0 100 100	9, 24, 60, 79	0
2	D	128/134 (95%)	-1.67	0 100 100	30, 76, 118, 130	0
3	E	112/114 (98%)	-1.63	0 100 100	28, 64, 106, 131	0
4	G	421/489 (86%)	-1.71	0 100 100	9, 41, 82, 106	0
5	H	226/244 (92%)	-1.72	0 100 100	22, 56, 93, 106	0
6	L	211/217 (97%)	-1.75	0 100 100	20, 42, 63, 107	0
All	All	1220/1351 (90%)	-1.70	0 100 100	9, 47, 98, 131	0

There are no RSRZ outliers to report.

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](#)

SUGAR-RSR INFOmissingINFO

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
11	NAG	G	611	14/15	0.97	0.05	52,78,95,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
11	NAG	G	616	14/15	0.97	0.05	27,77,98,103	0
11	NAG	B	701	14/15	0.98	0.04	78,103,125,127	0
11	NAG	G	612	14/15	0.98	0.06	97,125,145,168	0
11	NAG	B	702	14/15	0.98	0.05	90,106,117,117	0
11	NAG	G	631	14/15	0.98	0.05	51,73,99,102	0
11	NAG	G	617	14/15	0.99	0.04	45,54,74,79	0
11	NAG	G	618	14/15	0.99	0.03	35,46,52,54	0
11	NAG	G	629	14/15	0.99	0.04	42,51,62,69	0
11	NAG	G	630	14/15	0.99	0.03	50,61,67,79	0
11	NAG	G	613	14/15	0.99	0.04	56,71,86,112	0

6.5 Other polymers [i](#)

There are no such residues in this entry.