



wwPDB EM Map/Model Validation Report ⓘ

Jun 9, 2016 – 05:09 AM EDT

PDB ID : 5JNX
EMDB ID: : EMD8-8169
Title : The 6.6 Å cryo-EM structure of the full-length human NPC1 in complex with the cleaved glycoprotein of Ebola virus
Authors : Gong, X.; Qian, H.W.; Zhou, X.H.; Wu, J.P.; Wan, T.; Shi, Y.; Gao, F.; Zhou, Q.; Yan, N.
Deposited on : 2016-05-01
Resolution : 6.56 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027674

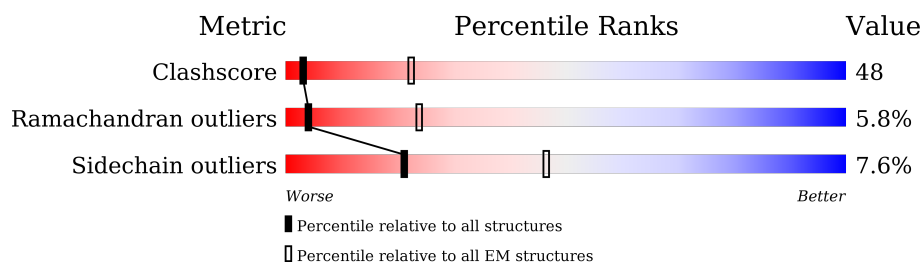
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.56 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1278	
2	C	158	
2	E	158	
2	G	158	
3	D	130	
3	F	130	
3	H	130	

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	A	1306	-	-	X	-
4	NAG	A	1307	-	-	X	-
4	NAG	A	1309	X	-	-	-
4	NAG	A	1312	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13749 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Niemann-Pick C1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1133	Total	C	N	O	S	1	0
			7695	4862	1315	1476	42		

- Molecule 2 is a protein called Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	158	Total	C	N	O	S	0	0
			1194	757	209	223	5		
2	E	158	Total	C	N	O	S	0	0
			1194	757	209	223	5		
2	G	158	Total	C	N	O	S	0	0
			1194	757	209	223	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	31	ARG	-	expression tag	UNP P87666
C	42	VAL	THR	engineered mutation	UNP P87666
E	31	ARG	-	expression tag	UNP P87666
E	42	VAL	THR	engineered mutation	UNP P87666
G	31	ARG	-	expression tag	UNP P87666
G	42	VAL	THR	engineered mutation	UNP P87666

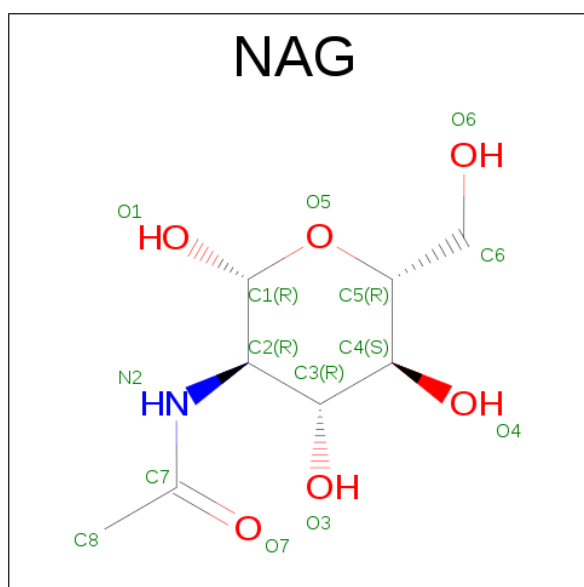
- Molecule 3 is a protein called Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	87	Total	C	N	O	S	0	0
			687	441	121	122	3		
3	F	87	Total	C	N	O	S	0	0
			687	441	121	122	3		
3	H	87	Total	C	N	O	S	0	0
			687	441	121	122	3		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	633	HIS	-	expression tag	UNP P87666
D	634	HIS	-	expression tag	UNP P87666
D	635	HIS	-	expression tag	UNP P87666
D	636	HIS	-	expression tag	UNP P87666
D	637	HIS	-	expression tag	UNP P87666
D	638	HIS	-	expression tag	UNP P87666
F	633	HIS	-	expression tag	UNP P87666
F	634	HIS	-	expression tag	UNP P87666
F	635	HIS	-	expression tag	UNP P87666
F	636	HIS	-	expression tag	UNP P87666
F	637	HIS	-	expression tag	UNP P87666
F	638	HIS	-	expression tag	UNP P87666
H	633	HIS	-	expression tag	UNP P87666
H	634	HIS	-	expression tag	UNP P87666
H	635	HIS	-	expression tag	UNP P87666
H	636	HIS	-	expression tag	UNP P87666
H	637	HIS	-	expression tag	UNP P87666
H	638	HIS	-	expression tag	UNP P87666

- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	

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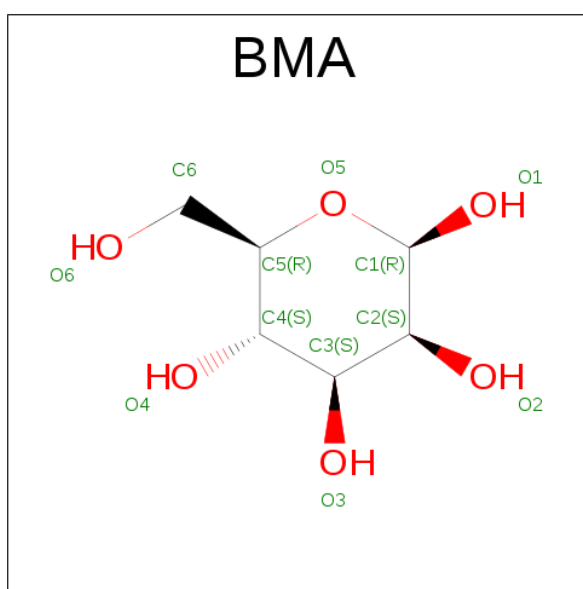
Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	A	1	Total	C	N	O	0
			294	168	21	105	
4	D	1	Total	C	N	O	0
			28	16	2	10	
4	D	1	Total	C	N	O	0
			28	16	2	10	

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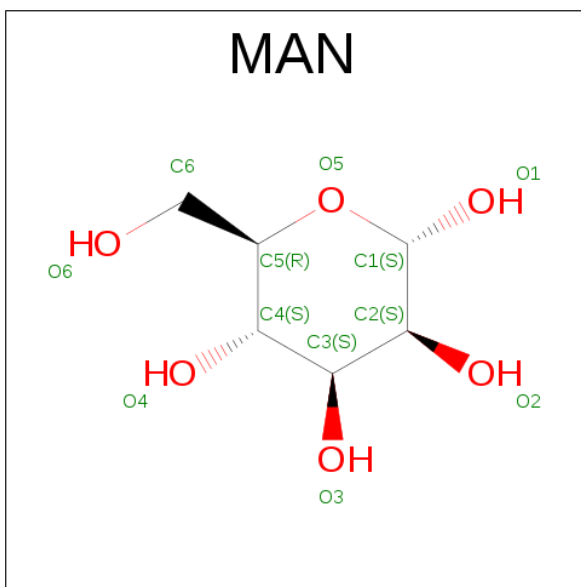
Mol	Chain	Residues	Atoms				AltConf
4	F	1	Total	C	N	O	0
			28	16	2	10	
4	F	1	Total	C	N	O	0
			28	16	2	10	
4	H	1	Total	C	N	O	0
			28	16	2	10	
4	H	1	Total	C	N	O	0
			28	16	2	10	

- Molecule 5 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).

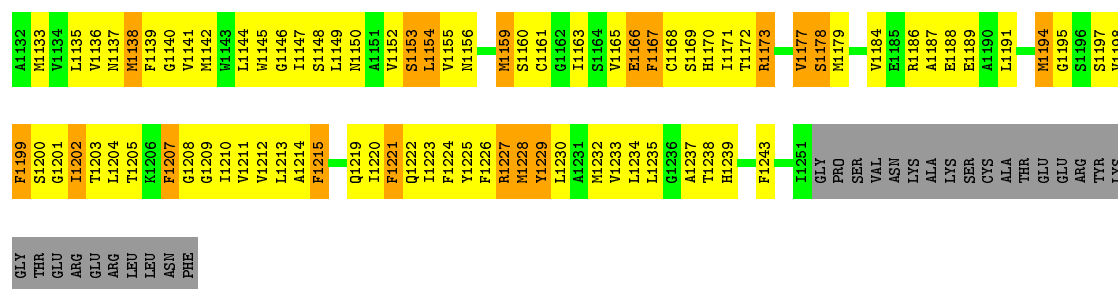


Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			22	12	10	
5	A	1	Total	C	O	0
			22	12	10	

- Molecule 6 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	C	O	0
			11	6	5	



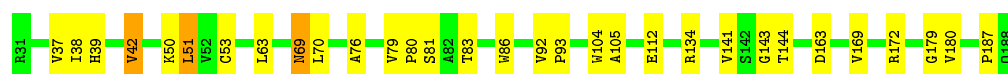
- Molecule 2: Envelope glycoprotein

Chain C: 86% 12% .



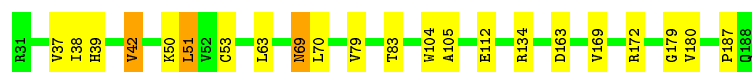
- Molecule 2: Envelope glycoprotein

Chain E: 80% 18% .



- Molecule 2: Envelope glycoprotein

Chain G: 86% 12% .



- Molecule 3: Envelope glycoprotein

Chain D: 52% 14% 33% .

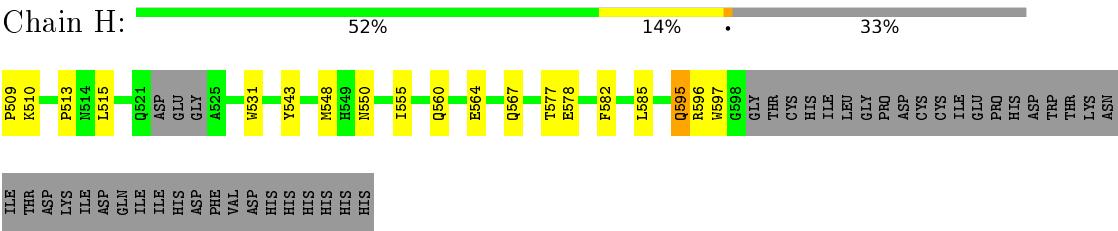


- Molecule 3: Envelope glycoprotein

Chain F: 52% 14% 33% .



- Molecule 3: Envelope glycoprotein



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	50223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	22500	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A	0.49	6/7843 (0.1%)	0.67	29/10748 (0.3%)
2	C	0.42	0/1223	0.59	1/1664 (0.1%)
2	E	0.44	0/1223	0.59	1/1664 (0.1%)
2	G	0.43	0/1223	0.59	1/1664 (0.1%)
3	D	0.42	0/702	0.62	0/952
3	F	0.42	0/702	0.62	0/952
3	H	0.42	0/702	0.62	0/952
All	All	0.47	6/13618 (0.0%)	0.64	32/18596 (0.2%)

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
1	A	0	2
2	C	0	1
2	E	0	1
2	G	0	1
All	All	0	5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	429	VAL	C-N	-5.49	1.23	1.34
1	A	166	PRO	N-CD	5.22	1.55	1.47
1	A	469	LEU	C-N	-5.20	1.22	1.34
1	A	424	PRO	N-CD	5.08	1.54	1.47
1	A	249	PRO	N-CD	5.07	1.54	1.47

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	602	SER	CB-CA-C	-9.99	91.12	110.10
1	A	755	PRO	CA-N-CD	-8.22	99.99	111.50
1	A	996	MET	C-N-CA	-6.63	105.12	121.70
1	A	887	PRO	N-CA-CB	6.58	111.20	103.30
1	A	836	PRO	N-CA-CB	6.46	111.06	103.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	602	SER	Peptide
1	A	603	PHE	Peptide
2	C	69	ASN	Sidechain
2	E	69	ASN	Sidechain
2	G	69	ASN	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7695	0	6476	1133	0
2	C	1194	0	1153	17	0
2	E	1194	0	1153	69	0
2	G	1194	0	1153	17	0
3	D	687	0	679	19	0
3	F	687	0	679	20	0
3	H	687	0	679	18	0
4	A	294	0	265	42	0
4	D	28	0	25	1	0
4	F	28	0	25	2	0
4	H	28	0	25	1	0
5	A	22	0	19	5	0
6	A	11	0	10	0	0
All	All	13749	0	12341	1252	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 48.

The worst 5 of 1252 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:724:LEU:HD22	1:A:1170:HIS:CE1	1.29	1.62
1:A:656:LEU:CD1	1:A:685:ILE:HG13	1.17	1.60
1:A:656:LEU:HD11	1:A:685:ILE:CG1	1.31	1.58
1:A:598:ASN:HD21	4:A:1310:NAG:C1	0.99	1.57
1:A:693:LEU:HD11	1:A:763:PHE:CE2	1.41	1.53

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 PDB entries followed by that with respect to all EM entries.

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	1126/1278 (88%)	897 (80%)	135 (12%)	94 (8%)	1	18
2	C	156/158 (99%)	142 (91%)	12 (8%)	2 (1%)	15	60
2	E	156/158 (99%)	141 (90%)	13 (8%)	2 (1%)	15	60
2	G	156/158 (99%)	142 (91%)	12 (8%)	2 (1%)	15	60
3	D	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	7	47
3	F	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	7	47
3	H	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	7	47
All	All	1843/2142 (86%)	1553 (84%)	184 (10%)	106 (6%)	4	27

5 of 106 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	LYS
1	A	256	PRO
1	A	350	PRO
1	A	372	ARG
1	A	374	THR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	643/1109 (58%)	558 (87%)	85 (13%)	5	28
2	C	126/130 (97%)	124 (98%)	2 (2%)	70	88
2	E	126/130 (97%)	124 (98%)	2 (2%)	70	88
2	G	126/130 (97%)	124 (98%)	2 (2%)	70	88
3	D	70/111 (63%)	69 (99%)	1 (1%)	74	89
3	F	70/111 (63%)	69 (99%)	1 (1%)	74	89
3	H	70/111 (63%)	69 (99%)	1 (1%)	74	89
All	All	1231/1832 (67%)	1137 (92%)	94 (8%)	21	53

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	730	GLU
1	A	1041	TYR
2	C	169	VAL
1	A	751	LEU
1	A	763	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	510	HIS
1	A	722	GLN
2	G	39	HIS
1	A	554	ASN
1	A	1046	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

30 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	$\# Z > 2$
4	NAG	A	1301	1,4	14,14,15	0.62	0	15,19,21	0.87	0
4	NAG	A	1302	4	14,14,15	0.55	0	15,19,21	0.73	1 (6%)
4	NAG	A	1303	1	14,14,15	0.29	0	15,19,21	0.52	0
4	NAG	A	1304	1,4	14,14,15	0.46	0	15,19,21	0.98	2 (13%)
4	NAG	A	1305	4	14,14,15	0.28	0	15,19,21	0.54	0
4	NAG	A	1306	1,4	14,14,15	0.29	0	15,19,21	0.52	0
4	NAG	A	1307	5,4	14,14,15	0.28	0	15,19,21	0.54	0
5	BMA	A	1308	4	11,11,12	0.26	0	15,15,17	0.58	0
4	NAG	A	1309	1	14,14,15	0.48	0	15,19,21	0.98	0
4	NAG	A	1310	1,4	14,14,15	0.34	0	15,19,21	1.47	2 (13%)
4	NAG	A	1311	4	14,14,15	0.63	0	15,19,21	1.10	2 (13%)
4	NAG	A	1312	1,4	14,14,15	0.27	0	15,19,21	0.53	0
4	NAG	A	1313	5,4	14,14,15	0.26	0	15,19,21	0.85	0
5	BMA	A	1314	4,6	11,11,12	0.28	0	15,15,17	0.63	0
6	MAN	A	1315	5	11,11,12	0.35	0	15,15,17	1.21	1 (6%)
4	NAG	A	1316	1	14,14,15	0.40	0	15,19,21	1.16	2 (13%)
4	NAG	A	1317	1	14,14,15	0.28	0	15,19,21	0.53	0
4	NAG	A	1318	4	14,14,15	0.38	0	15,19,21	1.15	2 (13%)
4	NAG	A	1319	1,4	14,14,15	0.37	0	15,19,21	1.15	2 (13%)
4	NAG	A	1320	1	14,14,15	0.29	0	15,19,21	0.54	0
4	NAG	A	1321	-	14,14,15	0.29	0	15,19,21	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1322	1	14,14,15	0.29	0	15,19,21	0.54	0
4	NAG	A	1323	1	14,14,15	0.27	0	15,19,21	0.54	0
4	NAG	A	1324	1	14,14,15	0.41	0	15,19,21	1.17	2 (13%)
4	NAG	D	701	3,4	14,14,15	0.68	0	15,19,21	0.70	0
4	NAG	D	702	4	14,14,15	0.29	0	15,19,21	0.47	0
4	NAG	F	701	3,4	14,14,15	0.69	0	15,19,21	0.70	0
4	NAG	F	702	4	14,14,15	0.29	0	15,19,21	0.47	0
4	NAG	H	701	3,4	14,14,15	0.67	0	15,19,21	0.69	0
4	NAG	H	702	4	14,14,15	0.29	0	15,19,21	0.47	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
4	NAG	A	1301	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1302	4	-	0/6/23/26	0/1/1/1
4	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1304	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1305	4	-	0/6/23/26	0/1/1/1
4	NAG	A	1306	1,4	-	2/6/23/26	0/1/1/1
4	NAG	A	1307	5,4	-	0/6/23/26	0/1/1/1
5	BMA	A	1308	4	-	0/2/19/22	0/1/1/1
4	NAG	A	1309	1	1/1/5/7	0/6/23/26	0/1/1/1
4	NAG	A	1310	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1311	4	-	0/6/23/26	0/1/1/1
4	NAG	A	1312	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1313	5,4	-	0/6/23/26	0/1/1/1
5	BMA	A	1314	4,6	-	0/2/19/22	0/1/1/1
6	MAN	A	1315	5	-	0/2/19/22	0/1/1/1
4	NAG	A	1316	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1317	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1318	4	-	0/6/23/26	0/1/1/1
4	NAG	A	1319	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1320	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1321	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1322	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1323	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1324	1	-	0/6/23/26	0/1/1/1
4	NAG	D	701	3,4	-	0/6/23/26	0/1/1/1
4	NAG	D	702	4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	F	701	3,4	-	0/6/23/26	0/1/1/1
4	NAG	F	702	4	-	0/6/23/26	0/1/1/1
4	NAG	H	701	3,4	-	0/6/23/26	0/1/1/1
4	NAG	H	702	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1310	NAG	O4-C4-C3	-3.37	102.75	110.36
4	A	1324	NAG	C2-N2-C7	-2.44	119.94	123.11
4	A	1318	NAG	C2-N2-C7	-2.39	119.99	123.11
4	A	1316	NAG	C2-N2-C7	-2.39	120.00	123.11
4	A	1319	NAG	C2-N2-C7	-2.38	120.00	123.11

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1309	NAG	C1

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1306	NAG	C8-C7-N2-C2
4	A	1306	NAG	O7-C7-N2-C2

There are no ring outliers.

18 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1303	NAG	1	0
4	A	1304	NAG	1	0
4	A	1305	NAG	1	0
4	A	1306	NAG	14	0
4	A	1307	NAG	12	0
5	A	1308	BMA	3	0
4	A	1310	NAG	3	0
4	A	1312	NAG	7	0
4	A	1313	NAG	6	0
5	A	1314	BMA	2	0
4	A	1317	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1319	NAG	3	0
4	A	1322	NAG	3	0
4	A	1323	NAG	1	0
4	A	1324	NAG	2	0
4	D	701	NAG	1	0
4	F	701	NAG	2	0
4	H	701	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.