



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:33 AM GMT

PDB ID : 2HMG
Title : REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING
Authors : Weis, W.I.; Bruenger, A.T.; Skehel, J.J.; Wiley, D.C.
Deposited on : 1989-09-11
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

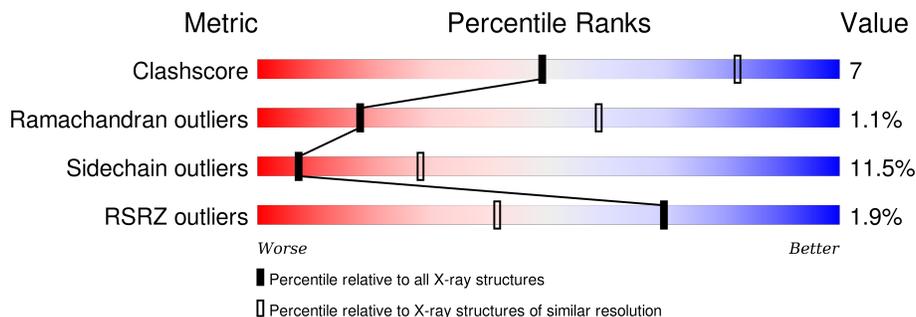
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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))
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 on the lower 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 $\leq 5\%$. 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	328	
1	C	328	
1	E	328	
2	B	175	
2	D	175	
2	F	175	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	329	-	-	-	X
3	NAG	A	348	-	-	-	X
3	NAG	C	329	-	-	-	X
3	NAG	C	348	-	-	-	X
3	NAG	E	329	-	-	-	X
3	NAG	E	348	-	-	-	X
4	NAG	C	340	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12189 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 (HA1 CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	328	2536	1583	445	495	13	0	0	0
1	C	328	2536	1583	445	495	13	0	0	0
1	E	328	2536	1583	445	495	13	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	146	ASP	GLY	CONFLICT	UNP P03437
C	146	ASP	GLY	CONFLICT	UNP P03437
E	146	ASP	GLY	CONFLICT	UNP P03437

- Molecule 2 is a protein called HEMAGGLUTININ (HA2 CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	175	1421	882	250	283	6	0	0	0
2	D	175	1421	882	250	283	6	0	0	0
2	F	175	1421	882	250	283	6	0	0	0

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	3	Total	C	N	O	0	0
			39	22	2	15		
4	C	3	Total	C	N	O	0	0
			39	22	2	15		
4	E	3	Total	C	N	O	0	0
			39	22	2	15		

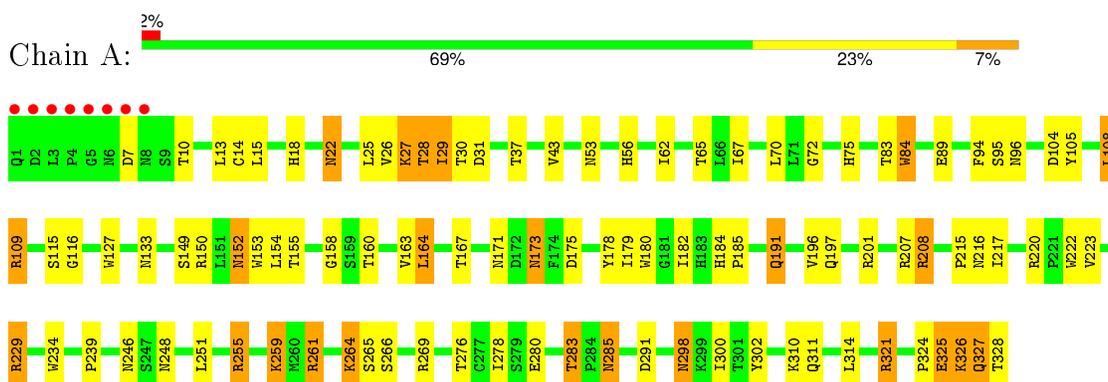
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	8	Total	O	0	0
			8	8		
5	B	3	Total	O	0	0
			3	3		
5	C	8	Total	O	0	0
			8	8		
5	D	3	Total	O	0	0
			3	3		
5	E	8	Total	O	0	0
			8	8		
5	F	3	Total	O	0	0
			3	3		

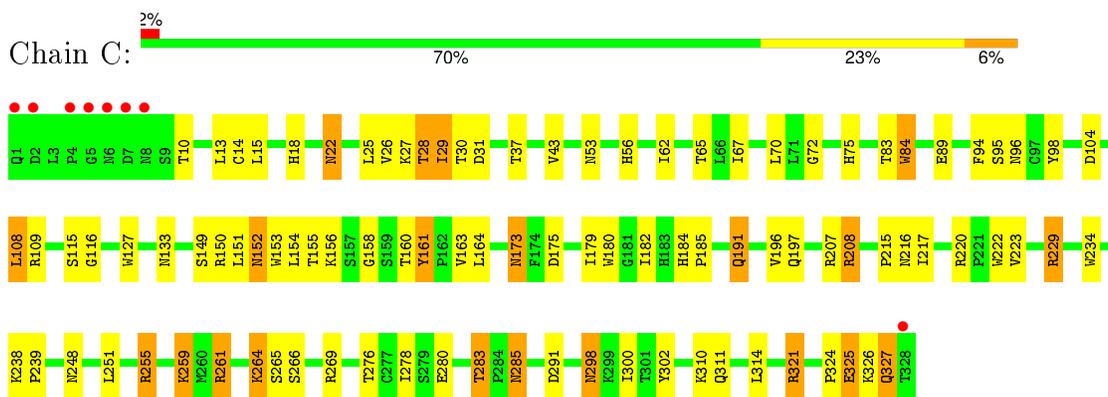
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

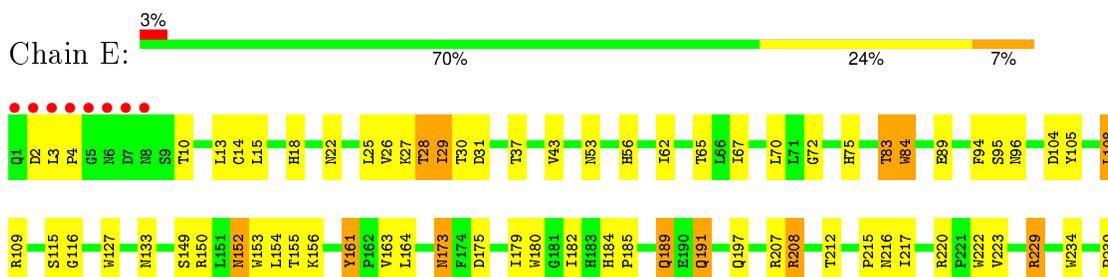
- Molecule 1: HEMAGGLUTININ (HA1 CHAIN)



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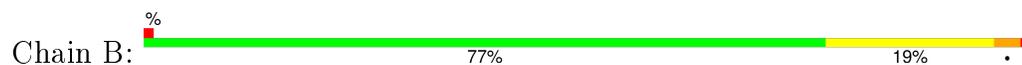


- Molecule 1: HEMAGGLUTININ (HA1 CHAIN)

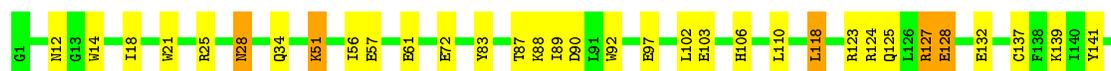




- Molecule 2: HEMAGGLUTININ (HA2 CHAIN)



- Molecule 2: HEMAGGLUTININ (HA2 CHAIN)



- Molecule 2: HEMAGGLUTININ (HA2 CHAIN)



4 Data and refinement statistics i

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	162.60Å 162.60Å 177.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00 7.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00) 79.4 (7.00-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.222 , (Not available) 0.206 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.3	EDS
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
L-test for twinning ¹	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 67242 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	12189	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	A	0.92	0/2593	1.47	35/3533 (1.0%)
1	C	0.89	0/2593	1.47	35/3533 (1.0%)
1	E	0.93	1/2593 (0.0%)	1.47	37/3533 (1.0%)
2	B	0.95	0/1445	1.49	18/1939 (0.9%)
2	D	0.96	0/1445	1.49	18/1939 (0.9%)
2	F	0.98	0/1445	1.50	25/1939 (1.3%)
All	All	0.93	1/12114 (0.0%)	1.48	168/16416 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	234	TRP	CG-CD2	-5.16	1.34	1.43

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	321	ARG	NE-CZ-NH1	-10.01	115.30	120.30
1	E	321	ARG	NE-CZ-NH1	-9.94	115.33	120.30
1	A	321	ARG	NE-CZ-NH1	-9.75	115.42	120.30
1	C	229	ARG	NE-CZ-NH1	-9.70	115.45	120.30
2	F	124	ARG	NE-CZ-NH1	-9.67	115.47	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	161	TYR	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	2536	0	2474	44	0
1	C	2536	0	2474	48	0
1	E	2536	0	2474	48	0
2	B	1421	0	1345	20	0
2	D	1421	0	1345	22	0
2	F	1421	0	1345	18	0
3	A	42	0	39	0	0
3	B	14	0	13	0	0
3	C	42	0	39	0	0
3	D	14	0	13	0	0
3	E	42	0	39	0	0
3	F	14	0	13	0	0
4	A	39	0	34	1	0
4	C	39	0	34	0	0
4	E	39	0	34	0	0
5	A	8	0	0	0	0
5	B	3	0	0	0	0
5	C	8	0	0	0	0
5	D	3	0	0	0	0
5	E	8	0	0	0	0
5	F	3	0	0	0	0
All	All	12189	0	11715	171	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 7.

The worst 5 of 171 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:C:325:GLU:HB2	2:D:12:ASN:ND2	2.04	0.72
2:D:25:ARG:HG2	2:D:34:GLN:HB3	1.72	0.70
2:B:51:LYS:HE3	2:B:103:GLU:OE2	1.93	0.69
1:E:29:ILE:HD11	2:F:102:LEU:HD23	1.75	0.69
2:D:51:LYS:HE3	2:D:103:GLU:OE2	1.92	0.69

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	326/328 (99%)	304 (93%)	18 (6%)	4 (1%)	16	56
1	C	326/328 (99%)	308 (94%)	14 (4%)	4 (1%)	16	56
1	E	326/328 (99%)	308 (94%)	16 (5%)	2 (1%)	30	72
2	B	173/175 (99%)	161 (93%)	10 (6%)	2 (1%)	16	56
2	D	173/175 (99%)	162 (94%)	9 (5%)	2 (1%)	16	56
2	F	173/175 (99%)	161 (93%)	10 (6%)	2 (1%)	16	56
All	All	1497/1509 (99%)	1404 (94%)	77 (5%)	16 (1%)	17	58

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	327	GLN
1	A	158	GLY
2	B	57	GLU
2	B	174	LYS
2	D	57	GLU

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	290/290 (100%)	250 (86%)	40 (14%)	4	20
1	C	290/290 (100%)	256 (88%)	34 (12%)	7	27
1	E	290/290 (100%)	252 (87%)	38 (13%)	5	22
2	B	149/149 (100%)	137 (92%)	12 (8%)	15	47
2	D	149/149 (100%)	136 (91%)	13 (9%)	13	43
2	F	149/149 (100%)	135 (91%)	14 (9%)	11	39
All	All	1317/1317 (100%)	1166 (88%)	151 (12%)	7	28

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	164	LEU
1	C	321	ARG
2	F	30	GLU
1	C	191	GLN
1	C	265	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	173	ASN
1	C	298	ASN
1	E	171	ASN
1	C	171	ASN
1	E	173	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

9 carbohydrates 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	339	1,4	14,14,15	0.75	1 (7%)	15,19,21	0.92	1 (6%)
4	NAG	A	340	4	14,14,15	0.68	0	15,19,21	1.03	1 (6%)
4	BMA	A	341	4	11,11,12	0.75	0	14,15,17	1.43	3 (21%)
4	NAG	C	339	1,4	14,14,15	0.74	1 (7%)	15,19,21	0.88	1 (6%)
4	NAG	C	340	4	14,14,15	0.54	0	15,19,21	1.00	2 (13%)
4	BMA	C	341	4	11,11,12	0.98	1 (9%)	14,15,17	1.46	2 (14%)
4	NAG	E	339	1,4	14,14,15	0.63	0	15,19,21	0.94	1 (6%)
4	NAG	E	340	4	14,14,15	0.55	0	15,19,21	0.92	0
4	BMA	E	341	4	11,11,12	0.56	0	14,15,17	1.11	1 (7%)

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	339	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	340	4	-	0/6/23/26	0/1/1/1
4	BMA	A	341	4	-	0/2/19/22	0/1/1/1
4	NAG	C	339	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	340	4	-	0/6/23/26	0/1/1/1
4	BMA	C	341	4	-	0/2/19/22	0/1/1/1
4	NAG	E	339	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	340	4	-	0/6/23/26	0/1/1/1
4	BMA	E	341	4	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	339	NAG	O5-C1	-2.11	1.40	1.43
4	A	339	NAG	O5-C1	-2.00	1.40	1.43
4	C	341	BMA	C2-C3	2.53	1.56	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	341	BMA	C2-C3-C4	-2.87	106.17	111.04
4	A	341	BMA	O5-C1-C2	-2.80	106.31	110.86
4	A	341	BMA	C1-C2-C3	-2.50	106.59	109.54
4	C	340	NAG	C3-C2-N2	-2.20	105.29	110.56
4	C	339	NAG	C3-C2-N2	-2.12	105.49	110.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	339	NAG	1	0

5.6 Ligand geometry

12 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
3	NAG	A	329	1	14,14,15	0.98	1 (7%)	15,19,21	0.69	0
3	NAG	A	334	1	14,14,15	0.74	0	15,19,21	1.07	1 (6%)
3	NAG	A	348	1	14,14,15	0.70	0	15,19,21	0.97	1 (6%)
3	NAG	B	401	2	14,14,15	0.60	0	15,19,21	1.03	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	329	1	14,14,15	0.81	0	15,19,21	0.70	0
3	NAG	C	334	1	14,14,15	0.64	0	15,19,21	1.08	1 (6%)
3	NAG	C	348	1	14,14,15	0.60	0	15,19,21	1.09	1 (6%)
3	NAG	D	401	2	14,14,15	0.79	1 (7%)	15,19,21	1.18	2 (13%)
3	NAG	E	329	1	14,14,15	1.14	1 (7%)	15,19,21	0.75	1 (6%)
3	NAG	E	334	1	14,14,15	0.70	0	15,19,21	1.10	1 (6%)
3	NAG	E	348	1	14,14,15	0.66	0	15,19,21	1.05	0
3	NAG	F	401	2	14,14,15	0.69	0	15,19,21	1.09	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	329	1	-	0/6/23/26	0/1/1/1
3	NAG	A	334	1	-	0/6/23/26	0/1/1/1
3	NAG	A	348	1	-	0/6/23/26	0/1/1/1
3	NAG	B	401	2	-	0/6/23/26	0/1/1/1
3	NAG	C	329	1	-	0/6/23/26	0/1/1/1
3	NAG	C	334	1	-	0/6/23/26	0/1/1/1
3	NAG	C	348	1	-	0/6/23/26	0/1/1/1
3	NAG	D	401	2	-	0/6/23/26	0/1/1/1
3	NAG	E	329	1	-	0/6/23/26	0/1/1/1
3	NAG	E	334	1	-	0/6/23/26	0/1/1/1
3	NAG	E	348	1	-	0/6/23/26	0/1/1/1
3	NAG	F	401	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	329	NAG	C1-C2	-3.22	1.48	1.52
3	A	329	NAG	C1-C2	-2.30	1.49	1.52
3	D	401	NAG	C1-C2	-2.05	1.49	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	NAG	C3-C4-C5	-2.41	106.00	110.20
3	D	401	NAG	C3-C4-C5	-2.39	106.03	110.20
3	A	348	NAG	C1-O5-C5	2.10	114.91	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	348	NAG	C1-O5-C5	2.12	114.93	112.25
3	E	329	NAG	C1-O5-C5	2.20	115.04	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	328/328 (100%)	-0.82	8 (2%) 62 32	4, 23, 55, 137	0
1	C	328/328 (100%)	-0.88	8 (2%) 62 32	4, 23, 50, 132	0
1	E	328/328 (100%)	-0.91	9 (2%) 58 28	5, 22, 48, 134	0
2	B	175/175 (100%)	-0.98	1 (0%) 90 73	2, 17, 48, 102	0
2	D	175/175 (100%)	-1.02	1 (0%) 90 73	3, 16, 42, 103	0
2	F	175/175 (100%)	-0.98	2 (1%) 82 58	2, 16, 42, 103	0
All	All	1509/1509 (100%)	-0.91	29 (1%) 70 41	2, 21, 51, 137	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	175	GLY	7.2
1	E	4	PRO	5.1
1	E	2	ASP	5.1
1	A	1	GLN	4.8
1	C	1	GLN	4.5

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	NAG	C	340	14/15	0.88	0.24	2.47	47,50,51,53	0
4	NAG	A	340	14/15	0.92	0.19	1.36	46,49,51,52	0
4	NAG	C	339	14/15	0.92	0.19	0.94	39,42,44,46	0
4	NAG	E	340	14/15	0.92	0.17	0.82	46,49,51,53	0
4	NAG	A	339	14/15	0.94	0.18	0.79	39,42,45,45	0
4	NAG	E	339	14/15	0.96	0.13	0.00	38,41,43,44	0
4	BMA	A	341	11/12	0.90	0.23	-	54,56,57,58	0
4	BMA	C	341	11/12	0.85	0.28	-	55,57,58,58	0
4	BMA	E	341	11/12	0.92	0.24	-	56,58,59,59	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	A	348	14/15	0.91	0.19	6.11	35,39,41,41	0
3	NAG	E	348	14/15	0.88	0.25	5.18	35,40,42,43	0
3	NAG	A	329	14/15	0.93	0.21	4.63	36,40,41,42	0
3	NAG	C	348	14/15	0.92	0.20	4.49	35,39,41,42	0
3	NAG	E	329	14/15	0.91	0.23	4.38	36,40,42,42	0
3	NAG	C	329	14/15	0.94	0.16	3.48	35,39,40,40	0
3	NAG	D	401	14/15	0.90	0.23	-	48,52,54,54	0
3	NAG	C	334	14/15	0.94	0.17	-	38,41,43,43	0
3	NAG	A	334	14/15	0.89	0.20	-	37,40,42,43	0
3	NAG	F	401	14/15	0.86	0.28	-	48,51,53,54	0
3	NAG	E	334	14/15	0.91	0.19	-	37,40,42,42	0
3	NAG	B	401	14/15	0.86	0.29	-	48,52,53,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.