



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 11:03 AM GMT

PDB ID : 1HGG  
Title : BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY  
Authors : Sauter, N.K.; Hanson, J.E.; Glick, G.D.; Brown, J.H.; Crowther, R.L.; Park, S.-J.; Skehel, J.J.; Wiley, D.C.  
Deposited on : 1991-11-01  
Resolution : 2.90 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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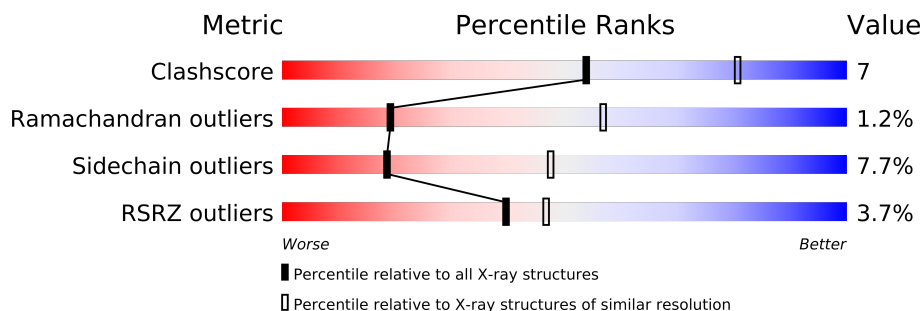
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.90 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	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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 that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	A	329	-	X
3	NAG	A	334	-	X
3	NAG	A	348	-	X
3	NAG	B	401	-	X
3	NAG	C	329	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	C	348	-	X
3	NAG	D	401	-	X
3	NAG	E	329	-	X
3	NAG	E	348	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15882 atoms, of which 3408 are hydrogens and 0 are deuterium.

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.

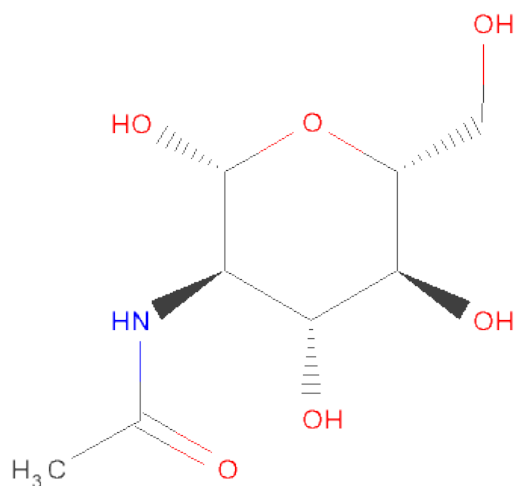
- Molecule 1 is a protein called HEMAGGLUTININ, CHAIN HA1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	328	Total	C	H	N	O	S	0	0	0
			3120	1581	588	445	493	13			
1	C	328	Total	C	H	N	O	S	0	0	0
			3120	1581	588	445	493	13			
1	E	328	Total	C	H	N	O	S	0	0	0
			3120	1581	588	445	493	13			

- Molecule 2 is a protein called HEMAGGLUTININ, CHAIN HA2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	175	Total	C	H	N	O	S	0	0	0
			1752	882	331	250	283	6			
2	D	175	Total	C	H	N	O	S	0	0	0
			1752	882	331	250	283	6			
2	F	175	Total	C	H	N	O	S	0	0	0
			1752	882	331	250	283	6			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	D	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	F	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	3	Total	C	H	N	O	0	0
			76	22	37	2	15		
4	C	3	Total	C	H	N	O	0	0
			76	22	37	2	15		
4	E	3	Total	C	H	N	O	0	0
			76	22	37	2	15		

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	3	Total	C	H	N	O	0	0
			81	23	38	1	19		
5	A	3	Total	C	H	N	O	0	0
			81	23	38	1	19		
5	C	3	Total	C	H	N	O	0	0
			81	23	38	1	19		
5	C	3	Total	C	H	N	O	0	0
			81	23	38	1	19		
5	E	3	Total	C	H	N	O	0	0
			81	23	38	1	19		
5	E	3	Total	C	H	N	O	0	0
			81	23	38	1	19		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	13	Total	H	O	0	0
			39	26	13		
6	B	11	Total	H	O	0	0
			33	22	11		
6	C	11	Total	H	O	0	0
			33	22	11		
6	D	13	Total	H	O	0	0
			39	26	13		
6	E	12	Total	H	O	0	0
			36	24	12		
6	F	12	Total	H	O	0	0
			36	24	12		

### 3 Residue-property plots

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.

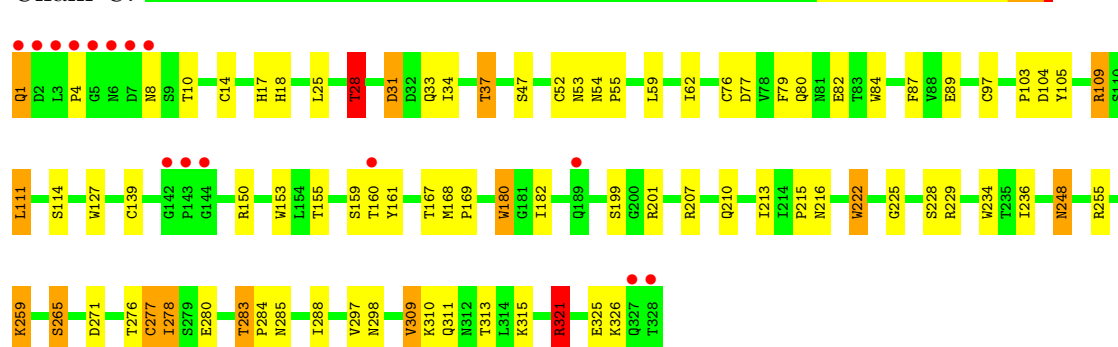
#### • Molecule 1: HEMAGGLUTININ, CHAIN HA1

Chain A:



#### • Molecule 1: HEMAGGLUTININ, CHAIN HA1

Chain C:



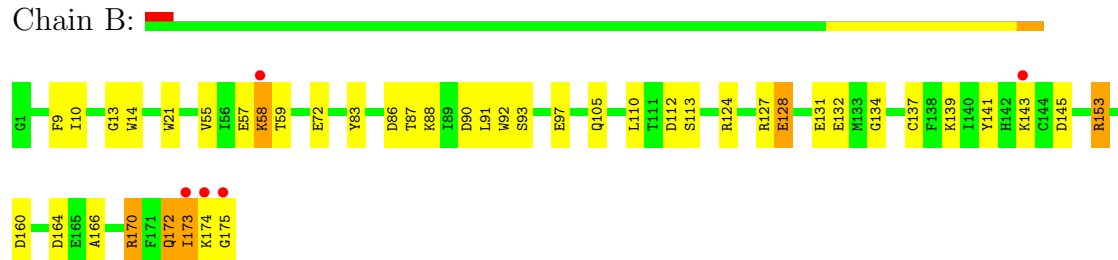
#### • Molecule 1: HEMAGGLUTININ, CHAIN HA1

Chain E:



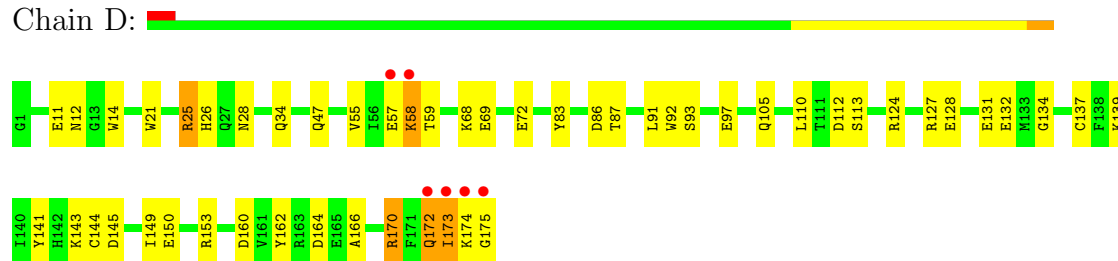
- Molecule 2: HEMAGGLUTININ, CHAIN HA2

Chain B:



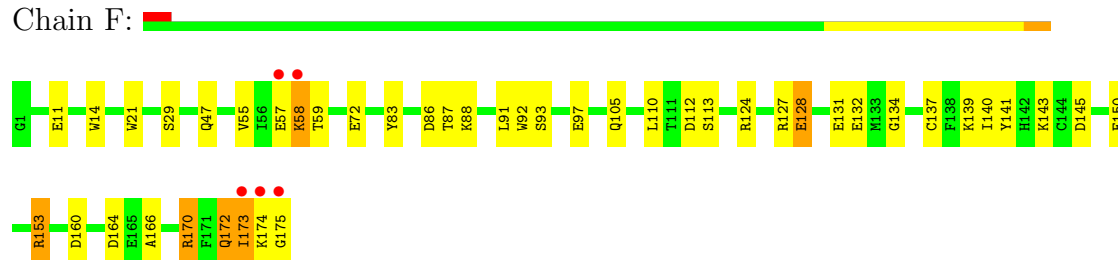
- Molecule 2: HEMAGGLUTININ, CHAIN HA2

Chain D:



- Molecule 2: HEMAGGLUTININ, CHAIN HA2

Chain F:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.70Å 162.70Å 177.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.90 18.81 – 2.91	Depositor EDS
% Data completeness (in resolution range)	(Not available) (7.00-2.90) 69.2 (18.81-2.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 2.93Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.229 , (Not available) 0.231 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	42.5	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 30.6	EDS
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 69831 reflections	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	15882	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, SIA, BGC, 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	0.91	2/2589 (0.1%)	1.47	38/3527 (1.1%)
1	C	0.89	1/2589 (0.0%)	1.45	33/3527 (0.9%)
1	E	0.92	1/2589 (0.0%)	1.48	36/3527 (1.0%)
2	B	0.92	0/1445	1.46	15/1939 (0.8%)
2	D	0.96	0/1445	1.49	20/1939 (1.0%)
2	F	0.95	0/1445	1.46	15/1939 (0.8%)
All	All	0.92	4/12102 (0.0%)	1.47	157/16398 (1.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	234	TRP	CG-CD2	-5.97	1.33	1.43
1	A	310	LYS	CD-CE	5.47	1.65	1.51
1	C	310	LYS	CD-CE	5.24	1.64	1.51
1	A	234	TRP	CG-CD2	-5.05	1.35	1.43

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	321	ARG	NE-CZ-NH2	-14.02	113.29	120.30
1	A	321	ARG	NE-CZ-NH2	-11.81	114.39	120.30
1	C	321	ARG	NE-CZ-NH2	-11.79	114.40	120.30
1	E	321	ARG	NE-CZ-NH1	10.92	125.76	120.30
1	C	321	ARG	NE-CZ-NH1	10.86	125.73	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2532	588	1889	38	0
1	C	2532	588	1889	40	0
1	E	2532	588	1889	40	0
2	B	1421	331	1015	26	0
2	D	1421	331	1015	28	0
2	F	1421	331	1015	28	0
3	A	42	42	0	0	0
3	B	14	14	0	0	0
3	C	42	42	0	0	0
3	D	14	14	0	0	0
3	E	42	42	0	0	0
3	F	14	14	0	0	0
4	A	39	37	0	1	0
4	C	39	37	0	2	0
4	E	39	37	0	1	0
5	A	86	76	0	1	0
5	C	86	76	0	1	0
5	E	86	76	0	1	0
6	A	13	26	0	1	0
6	B	11	22	0	1	0
6	C	11	22	0	2	0
6	D	13	26	0	1	0
6	E	12	24	0	3	0
6	F	12	24	0	1	0
All	All	12474	3408	8712	169	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 169 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:321:ARG:HH11	1:A:321:ARG:HG2	1.48	0.79
1:C:321:ARG:HH11	1:C:321:ARG:HG2	1.49	0.77
1:E:321:ARG:HG2	1:E:321:ARG:HH11	1.46	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:83:TYR:O	2:B:87:THR:HG23	1.93	0.68
2:D:83:TYR:O	2:D:87:THR:HG23	1.95	0.67

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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%)	17 (5%)	5 (2%)	15	50
1	C	326/328 (99%)	307 (94%)	16 (5%)	3 (1%)	25	66
1	E	326/328 (99%)	309 (95%)	16 (5%)	1 (0%)	50	85
2	B	173/175 (99%)	160 (92%)	10 (6%)	3 (2%)	14	45
2	D	173/175 (99%)	160 (92%)	10 (6%)	3 (2%)	14	45
2	F	173/175 (99%)	160 (92%)	10 (6%)	3 (2%)	14	45
All	All	1497/1509 (99%)	1400 (94%)	79 (5%)	18 (1%)	19	57

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	326	LYS
2	B	58	LYS
2	B	173	ILE
2	D	58	LYS

### 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 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	289/289 (100%)	259 (90%)	30 (10%)	10	29
1	C	289/289 (100%)	264 (91%)	25 (9%)	15	41
1	E	289/289 (100%)	259 (90%)	30 (10%)	10	29
2	B	149/149 (100%)	144 (97%)	5 (3%)	49	86
2	D	149/149 (100%)	144 (97%)	5 (3%)	49	86
2	F	149/149 (100%)	143 (96%)	6 (4%)	42	81
All	All	1314/1314 (100%)	1213 (92%)	101 (8%)	18	47

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	155	THR
1	C	280	GLU
1	E	326	LYS
1	C	160	THR
1	C	248	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	38	ASN
1	C	81	ASN
1	E	38	ASN
2	B	146	ASN
1	E	81	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

27 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	12,14,15	0.61	0	15,19,21	0.99	1 (6%)
4	NAG	A	340	4	12,14,15	0.80	0	15,19,21	1.10	2 (13%)
4	BMA	A	341	4	10,11,12	0.54	0	11,15,17	0.80	0
5	GAL	A	349	5	10,11,12	0.71	0	11,15,17	1.04	1 (9%)
5	BGC	A	350	5	12,12,12	1.27	1 (8%)	17,17,17	1.04	2 (11%)
5	SIA	A	351	5	20,20,21	3.93	2 (10%)	23,28,31	2.98	6 (26%)
5	GAL	A	352	5	10,11,12	0.76	0	11,15,17	0.98	1 (9%)
5	BGC	A	353	5	12,12,12	0.55	0	17,17,17	0.89	0
5	SIA	A	354	5	20,20,21	3.83	3 (15%)	23,28,31	3.19	5 (21%)
4	NAG	C	339	1,4	12,14,15	0.69	0	15,19,21	1.05	1 (6%)
4	NAG	C	340	4	12,14,15	0.52	0	15,19,21	1.12	3 (20%)
4	BMA	C	341	4	10,11,12	0.62	0	11,15,17	1.04	1 (9%)
5	GAL	C	349	5	10,11,12	0.82	0	11,15,17	1.07	1 (9%)
5	BGC	C	350	5	12,12,12	1.28	1 (8%)	17,17,17	0.96	1 (5%)
5	SIA	C	351	5	20,20,21	3.75	3 (15%)	23,28,31	2.87	4 (17%)
5	GAL	C	352	5	10,11,12	0.77	0	11,15,17	0.95	1 (9%)
5	BGC	C	353	5	12,12,12	0.57	0	17,17,17	0.79	0
5	SIA	C	354	5	20,20,21	3.95	3 (15%)	23,28,31	3.15	5 (21%)
4	NAG	E	339	1,4	12,14,15	0.82	0	15,19,21	0.97	1 (6%)
4	NAG	E	340	4	12,14,15	0.63	0	15,19,21	1.06	2 (13%)
4	BMA	E	341	4	10,11,12	0.82	0	11,15,17	1.98	2 (18%)
5	GAL	E	349	5	10,11,12	0.76	0	11,15,17	1.08	0
5	BGC	E	350	5	12,12,12	1.15	1 (8%)	17,17,17	1.02	1 (5%)
5	SIA	E	351	5	20,20,21	3.56	2 (10%)	23,28,31	2.96	5 (21%)
5	GAL	E	352	5	10,11,12	0.81	0	11,15,17	0.98	1 (9%)
5	BGC	E	353	5	12,12,12	0.47	0	17,17,17	0.76	0
5	SIA	E	354	5	20,20,21	4.00	3 (15%)	23,28,31	3.13	6 (26%)

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
5	GAL	A	349	5	-	0/2/19/22	0/1/1/1
5	BGC	A	350	5	-	0/2/22/22	0/1/1/1
5	SIA	A	351	5	-	0/15/34/38	0/1/1/1
5	GAL	A	352	5	-	0/2/19/22	0/1/1/1
5	BGC	A	353	5	-	0/2/22/22	0/1/1/1
5	SIA	A	354	5	-	0/15/34/38	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
5	GAL	C	349	5	-	0/2/19/22	0/1/1/1
5	BGC	C	350	5	-	0/2/22/22	0/1/1/1
5	SIA	C	351	5	-	0/15/34/38	0/1/1/1
5	GAL	C	352	5	-	0/2/19/22	0/1/1/1
5	BGC	C	353	5	-	0/2/22/22	0/1/1/1
5	SIA	C	354	5	-	0/15/34/38	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
5	GAL	E	349	5	-	0/2/19/22	0/1/1/1
5	BGC	E	350	5	-	0/2/22/22	0/1/1/1
5	SIA	E	351	5	-	0/15/34/38	0/1/1/1
5	GAL	E	352	5	-	0/2/19/22	0/1/1/1
5	BGC	E	353	5	-	0/2/22/22	0/1/1/1
5	SIA	E	354	5	-	0/15/34/38	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	354	SIA	O6-C2	17.37	1.44	1.28
5	C	354	SIA	O6-C2	17.18	1.44	1.28
5	A	351	SIA	O6-C2	17.02	1.43	1.28
5	A	354	SIA	O6-C2	16.68	1.43	1.28
5	C	351	SIA	O6-C2	16.14	1.43	1.28

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	354	SIA	O6-C2-C3	-13.96	106.67	124.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	354	SIA	O6-C2-C3	-13.77	106.92	124.91
5	E	354	SIA	O6-C2-C3	-13.43	107.37	124.91
5	A	351	SIA	O6-C2-C3	-12.84	108.13	124.91
5	E	351	SIA	O6-C2-C3	-12.79	108.20	124.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	12,14,15	0.80	1 (8%)	15,19,21	1.01	0
3	NAG	A	334	1	12,14,15	0.61	0	15,19,21	1.55	2 (13%)
3	NAG	A	348	1	12,14,15	0.73	0	15,19,21	1.43	2 (13%)
3	NAG	B	401	2	12,14,15	0.83	0	15,19,21	1.07	1 (6%)
3	NAG	C	329	1	12,14,15	0.71	0	15,19,21	0.99	0
3	NAG	C	334	1	12,14,15	0.69	0	15,19,21	1.73	2 (13%)
3	NAG	C	348	1	12,14,15	0.69	0	15,19,21	1.53	3 (20%)
3	NAG	D	401	2	12,14,15	0.92	0	15,19,21	1.11	0
3	NAG	E	329	1	12,14,15	0.72	0	15,19,21	0.96	0
3	NAG	E	334	1	12,14,15	0.60	0	15,19,21	1.65	2 (13%)
3	NAG	E	348	1	12,14,15	0.69	0	15,19,21	1.49	4 (26%)
3	NAG	F	401	2	12,14,15	1.00	1 (8%)	15,19,21	1.03	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
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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	401	NAG	C4-C5	2.05	1.57	1.53
3	A	329	NAG	C4-C5	2.02	1.57	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	334	NAG	O5-C5-C6	4.30	111.50	106.98
3	E	334	NAG	O5-C5-C6	4.23	111.42	106.98
3	A	334	NAG	O5-C5-C6	3.78	110.95	106.98
3	C	334	NAG	O5-C5-C4	-3.55	106.15	110.65
3	E	334	NAG	O5-C5-C4	-3.33	106.42	110.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	328/328 (100%)	-0.24	13 (3%) 36 43	6, 26, 52, 144	0
1	C	328/328 (100%)	-0.20	15 (4%) 31 38	6, 26, 51, 150	0
1	E	328/328 (100%)	-0.25	13 (3%) 36 43	6, 26, 52, 146	0
2	B	175/175 (100%)	-0.47	5 (2%) 49 58	3, 21, 51, 105	0
2	D	175/175 (100%)	-0.49	6 (3%) 43 51	3, 20, 50, 106	0
2	F	175/175 (100%)	-0.54	5 (2%) 49 58	2, 20, 50, 105	0
All	All	1509/1509 (100%)	-0.32	57 (3%) 39 45	2, 24, 52, 150	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	7	ASP	10.4
1	E	6	ASN	9.9
1	A	7	ASP	9.4
1	A	328	THR	9.1
1	C	7	ASP	8.2

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

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

### 6.3 Carbohydrates ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	SIA	E	354	20/21	0.36	8.61	0,42,44,44	37
5	BGC	E	353	12/12	0.45	5.35	0,0,49,50	23
5	GAL	E	352	11/12	0.35	4.55	0,0,47,48	21
5	BGC	A	350	12/12	0.46	4.16	0,0,67,68	23
5	SIA	A	354	20/21	0.36	3.69	0,41,44,44	37
5	SIA	C	354	20/21	0.35	2.93	0,41,44,44	37
5	BGC	C	353	12/12	0.39	2.65	0,0,49,50	23
5	BGC	E	350	12/12	0.33	2.64	0,0,67,68	23
5	GAL	A	352	11/12	0.38	2.06	0,0,47,48	21
5	BGC	A	353	12/12	0.35	1.90	0,0,49,50	23
5	SIA	E	351	20/21	0.21	1.45	0,35,41,42	37
5	SIA	A	351	20/21	0.21	1.40	0,35,41,42	37
5	GAL	C	352	11/12	0.34	1.35	0,0,47,48	21
5	GAL	E	349	11/12	0.20	0.45	0,0,51,53	21
5	GAL	A	349	11/12	0.20	0.45	0,0,51,53	21
4	NAG	C	340	14/15	0.22	0.38	0,0,57,60	0
5	SIA	C	351	20/21	0.19	0.36	0,35,41,42	37
5	BGC	C	350	12/12	0.39	0.17	0,0,67,68	23
4	NAG	C	339	14/15	0.17	-0.04	0,0,45,48	0
4	NAG	A	340	14/15	0.16	-0.09	0,0,57,59	0
4	NAG	E	340	14/15	0.18	-0.32	0,0,57,59	0
5	GAL	C	349	11/12	0.16	-0.43	0,0,51,53	21
4	NAG	A	339	14/15	0.13	-0.50	0,0,45,48	0
4	NAG	E	339	14/15	0.13	-0.76	0,0,44,48	0
4	BMA	E	341	11/12	0.21	-	0,0,65,68	0
4	BMA	C	341	11/12	0.34	-	0,0,70,72	0
4	BMA	A	341	11/12	0.28	-	0,0,64,65	0

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	E	348	14/15	0.30	11.06	0,0,49,50	0
3	NAG	E	329	14/15	0.28	10.93	0,0,50,50	0
3	NAG	C	329	14/15	0.29	7.42	0,0,49,50	0
3	NAG	B	401	14/15	0.36	5.58	0,0,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	A	329	14/15	0.27	5.26	0,0,49,50	0
3	NAG	D	401	14/15	0.36	4.75	0,0,61,62	0
3	NAG	A	348	14/15	0.24	2.76	0,0,50,51	0
3	NAG	C	348	14/15	0.24	2.03	0,0,49,51	0
3	NAG	A	334	14/15	0.21	2.03	0,0,44,45	0
3	NAG	E	334	14/15	0.21	1.59	0,0,44,46	0
3	NAG	C	334	14/15	0.22	1.31	0,0,44,46	0
3	NAG	F	401	14/15	0.27	1.13	0,0,61,61	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.