



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 12, 2016 – 04:29 AM EDT

PDB ID : 4YY7  
Title : The structure of hemagglutinin from a H6N1 influenza virus (A/chicken/Taiwan/A2837/2013) in complex with avian receptor analog 3'SLNLN  
Authors : Wang, F.; Qi, J.; Bi, Y.; Zhang, W.; Wang, M.; Wang, M.; Liu, J.; Yan, J.; Shi, Y.; Gao, G.F.  
Deposited on : 2015-03-23  
Resolution : 2.99 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027107  
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) : rb-20027107

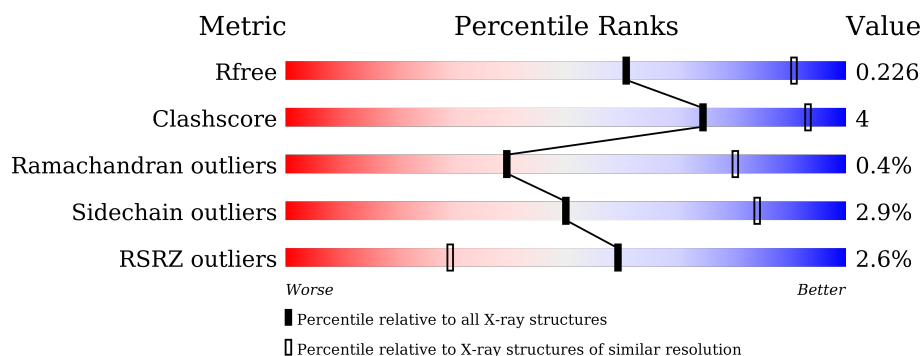
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.99 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))
$R_{free}$	91344	1578 (3.00-3.00)
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  $\geq 3$ , 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	325	<div> <div style="width: 100%;"></div> <div> <div style="width: 100%;"></div> <div>86%13%.</div> </div> </div>
1	C	325	<div> <div style="width: 100%;"></div> <div> <div style="width: 100%;"></div> <div>86%13%.</div> </div> </div>
2	B	164	<div> <div style="width: 100%;"></div> <div> <div style="width: 100%;"></div> <div>5%89%11%</div> </div> </div>
2	D	164	<div> <div style="width: 100%;"></div> <div> <div style="width: 100%;"></div> <div>6%94%6%</div> </div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7972 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.

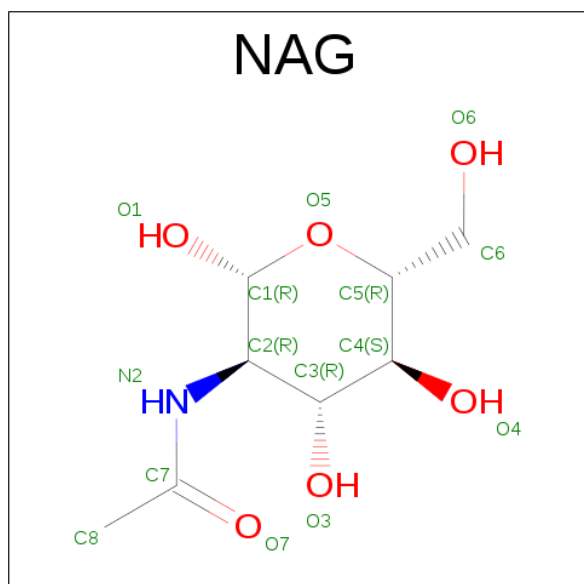
- Molecule 1 is a protein called HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	0	0
			2563	1625	436	489	13			
1	C	325	Total	C	N	O	S	0	0	0
			2563	1625	436	489	13			

- Molecule 2 is a protein called HA2.

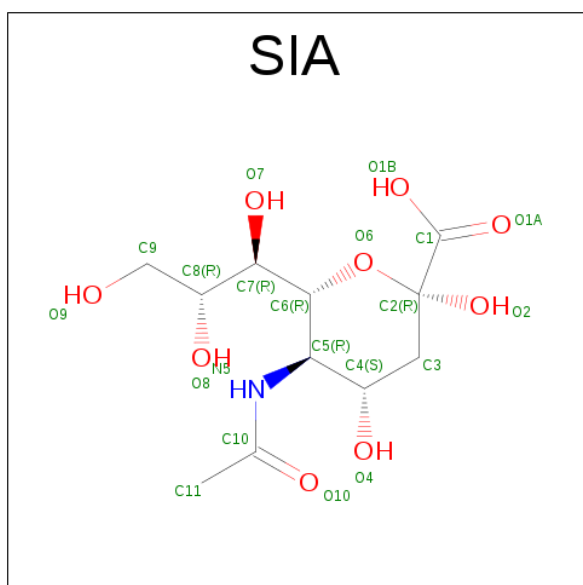
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	164	Total	C	N	O	S	0	0	0
			1321	825	229	260	7			
2	D	164	Total	C	N	O	S	0	0	0
			1321	825	229	260	7			

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



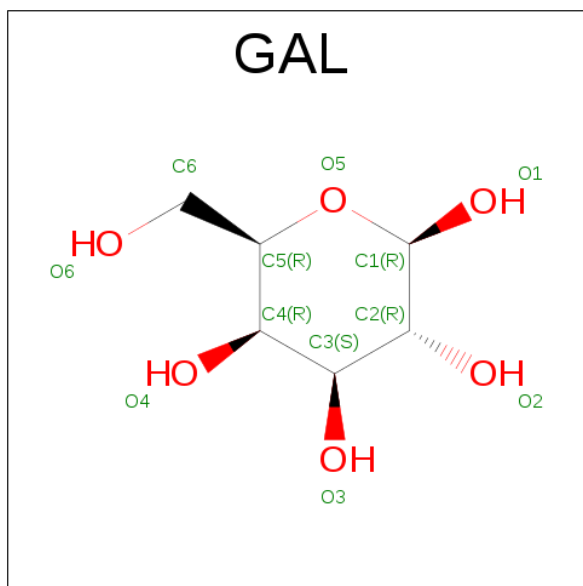
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			15	8	1	6		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			15	8	1	6		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is O-SIALIC ACID (three-letter code: SIA) (formula:  $C_{11}H_{19}NO_9$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			20	11	1	8		
4	C	1	Total	C	N	O	0	0
			20	11	1	8		

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

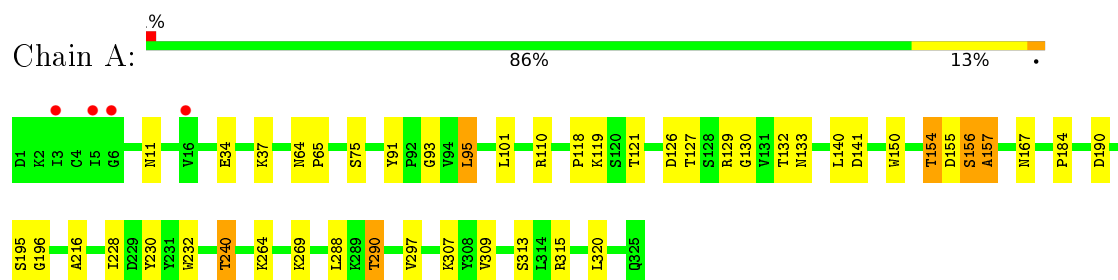


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	C	1	Total	C	O	0	0
			11	6	5		

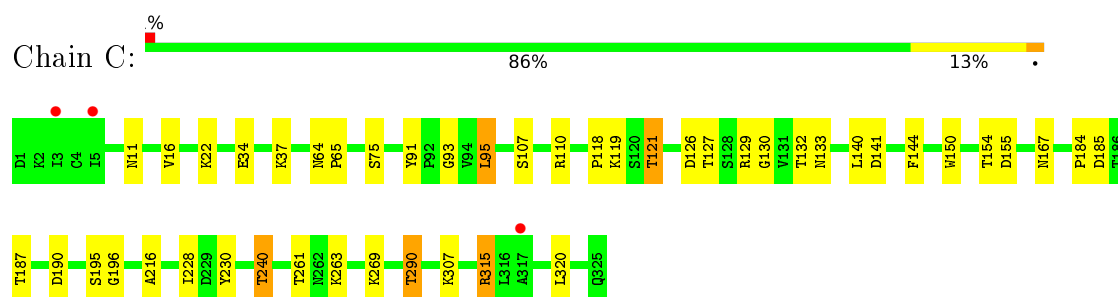
### 3 Residue-property plots [i](#)

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.

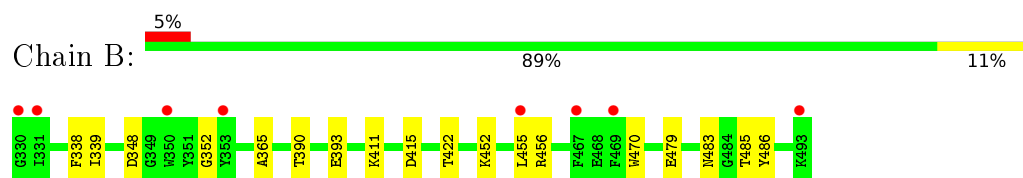
#### • Molecule 1: HA1



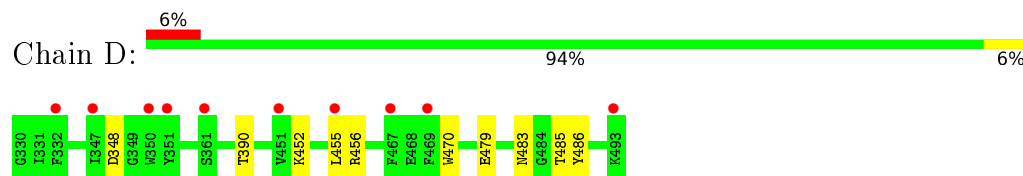
#### • Molecule 1: HA1



#### • Molecule 2: HA2



#### • Molecule 2: HA2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.77Å 96.77Å 132.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.45 – 2.99 45.45 – 2.99	Depositor EDS
% Data completeness (in resolution range)	98.7 (45.45-2.99) 98.7 (45.45-2.99)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.4_1496)	Depositor
R, $R_{free}$	0.199 , 0.226 0.200 , 0.226	Depositor DCC
$R_{free}$ test set	1386 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	79.0	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 29.8	EDS
Estimated twinning fraction	0.020 for -h,-k,l 0.449 for h,-h-k,-l 0.023 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 27698 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7972	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup> Theoretical 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: SIA, GAL, 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	0.26	0/2625	0.46	0/3571
1	C	0.26	0/2625	0.46	0/3571
2	B	0.29	0/1349	0.46	0/1818
2	D	0.29	0/1349	0.46	0/1818
All	All	0.27	0/7948	0.46	0/10778

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	A	2563	0	2508	23	0
1	C	2563	0	2508	23	0
2	B	1321	0	1229	13	0
2	D	1321	0	1229	8	0
3	A	57	0	52	1	0
3	B	14	0	13	3	0
3	C	57	0	52	3	0
3	D	14	0	13	3	0
4	A	20	0	17	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	20	0	17	0	0
5	A	11	0	9	0	0
5	C	11	0	9	0	0
All	All	7972	0	7656	63	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 4.

All (63) 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)
2:D:452:LYS:O	2:D:455:LEU:O	1.90	0.89
1:C:167:ASN:HA	1:C:240:THR:HB	1.59	0.83
2:D:485:THR:HG21	3:D:501:NAG:H82	1.68	0.76
1:A:167:ASN:HA	1:A:240:THR:HB	1.66	0.75
2:B:452:LYS:O	2:B:455:LEU:O	2.11	0.68
2:B:455:LEU:HD23	2:B:486:TYR:CE2	2.29	0.68
1:A:126:ASP:OD2	1:A:129:ARG:NH1	2.27	0.67
1:C:240:THR:HG21	3:C:602:NAG:H82	1.75	0.67
1:A:154:THR:O	1:A:156:SER:N	2.30	0.63
1:C:22:LYS:HD2	3:C:601:NAG:H82	1.82	0.60
1:C:130:GLY:HA3	1:C:150:TRP:HB3	1.83	0.59
2:B:485:THR:HG21	3:B:501:NAG:H82	1.83	0.59
1:C:16:VAL:HG12	1:C:315:ARG:HG2	1.88	0.55
2:D:479:GLU:HG2	3:D:501:NAG:O6	2.08	0.53
1:C:240:THR:CG2	3:C:602:NAG:H82	2.39	0.52
2:D:455:LEU:HD23	2:D:486:TYR:CE2	2.45	0.51
1:C:126:ASP:OD2	1:C:129:ARG:NH2	2.43	0.49
1:A:195:SER:OG	1:A:196:GLY:N	2.44	0.49
1:A:240:THR:HG21	3:A:402:NAG:H82	1.95	0.48
2:D:348:ASP:N	2:D:348:ASP:OD1	2.46	0.48
2:D:483:ASN:ND2	3:D:501:NAG:O7	2.48	0.47
2:B:348:ASP:OD1	2:B:348:ASP:N	2.47	0.47
1:C:11:ASN:N	1:C:11:ASN:OD1	2.48	0.46
1:A:307:LYS:HE3	2:B:390:THR:O	2.14	0.46
2:B:483:ASN:ND2	3:B:501:NAG:O7	2.49	0.46
1:A:93:GLY:HA3	1:A:228:ILE:O	2.16	0.45
1:A:91:TYR:HD2	1:A:132:THR:HG21	1.82	0.45
1:A:101:LEU:HB2	1:A:232:TRP:CE2	2.52	0.44
1:A:288:LEU:HD21	1:A:297:VAL:HG21	1.98	0.44
2:B:479:GLU:HG2	3:B:501:NAG:O6	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:SER:OG	1:A:157:ALA:N	2.51	0.44
1:A:130:GLY:HA3	1:A:150:TRP:HB3	1.99	0.43
1:C:34:GLU:HB2	1:C:290:THR:HG21	1.99	0.43
1:C:307:LYS:HE3	2:D:390:THR:O	2.18	0.43
1:C:95:LEU:HA	1:C:230:TYR:HB2	2.00	0.43
1:C:119:LYS:HD3	1:C:127:THR:HB	2.01	0.43
2:B:411:LYS:HG2	2:B:415:ASP:OD2	2.19	0.43
1:A:34:GLU:HB2	1:A:290:THR:HG21	2.00	0.42
1:A:184:PRO:HA	1:A:216:ALA:O	2.19	0.42
1:C:65:PRO:HG3	1:C:144:PHE:O	2.19	0.42
1:A:118:PRO:O	1:A:121:THR:OG1	2.28	0.42
1:A:95:LEU:HA	1:A:230:TYR:HB2	2.00	0.42
1:C:195:SER:OG	1:C:196:GLY:N	2.52	0.42
1:A:264:LYS:NZ	2:B:393:GLU:OE1	2.45	0.42
1:A:75:SER:OG	1:A:110:ARG:HD2	2.19	0.42
2:D:470:TRP:CE3	2:D:470:TRP:HA	2.54	0.41
1:C:185:ASP:OD1	1:C:187:THR:OG1	2.34	0.41
1:C:93:GLY:HA3	1:C:228:ILE:O	2.20	0.41
2:B:338:PHE:CE1	2:B:339:ILE:HG13	2.55	0.41
1:C:118:PRO:O	1:C:121:THR:OG1	2.29	0.41
1:A:11:ASN:N	1:A:11:ASN:OD1	2.43	0.41
1:C:133:ASN:HA	1:C:141:ASP:O	2.21	0.41
1:C:64:ASN:HA	1:C:65:PRO:HD3	1.90	0.41
1:A:119:LYS:HD3	1:A:127:THR:HB	2.03	0.41
1:C:184:PRO:HA	1:C:216:ALA:O	2.21	0.41
1:A:133:ASN:HA	1:A:141:ASP:O	2.21	0.41
2:B:352:GLY:HA3	2:B:365:ALA:HA	2.03	0.41
2:B:470:TRP:CE3	2:B:470:TRP:HA	2.55	0.41
1:A:309:VAL:CG2	2:B:422:THR:HA	2.51	0.40
1:C:91:TYR:HD2	1:C:132:THR:HG21	1.86	0.40
1:C:107:SER:O	1:C:261:THR:HG22	2.21	0.40
1:A:64:ASN:HA	1:A:65:PRO:HD3	1.90	0.40
1:C:75:SER:OG	1:C:110:ARG:HD2	2.20	0.40

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	323/325 (99%)	300 (93%)	20 (6%)	3 (1%)	21	64
1	C	323/325 (99%)	305 (94%)	17 (5%)	1 (0%)	46	84
2	B	162/164 (99%)	144 (89%)	18 (11%)	0	100	100
2	D	162/164 (99%)	146 (90%)	16 (10%)	0	100	100
All	All	970/978 (99%)	895 (92%)	71 (7%)	4 (0%)	39	80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	ASP
1	A	156	SER
1	C	155	ASP
1	A	157	ALA

### 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	285/285 (100%)	274 (96%)	11 (4%)	39	77
1	C	285/285 (100%)	273 (96%)	12 (4%)	36	76
2	B	139/139 (100%)	138 (99%)	1 (1%)	88	96
2	D	139/139 (100%)	138 (99%)	1 (1%)	88	96
All	All	848/848 (100%)	823 (97%)	25 (3%)	50	84

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LYS
1	A	95	LEU
1	A	140	LEU
1	A	154	THR
1	A	190	ASP
1	A	240	THR
1	A	269	LYS
1	A	290	THR
1	A	313	SER
1	A	315	ARG
1	A	320	LEU
2	B	456	ARG
1	C	37	LYS
1	C	95	LEU
1	C	121	THR
1	C	140	LEU
1	C	154	THR
1	C	190	ASP
1	C	240	THR
1	C	263	LYS
1	C	269	LYS
1	C	290	THR
1	C	315	ARG
1	C	320	LEU
2	D	456	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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

14 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	401	1	14,14,15	1.27	1 (7%)	15,19,21	0.81	1 (6%)
3	NAG	A	402	1,3	14,14,15	1.04	1 (7%)	15,19,21	1.51	1 (6%)
3	NAG	A	403	3	14,14,15	1.34	1 (7%)	15,19,21	0.95	1 (6%)
4	SIA	A	404	5	17,20,21	1.07	1 (5%)	18,28,31	2.57	7 (38%)
3	NAG	A	405	5	15,15,15	0.16	0	17,21,21	0.15	0
5	GAL	A	406	3,4	11,11,12	1.31	3 (27%)	15,15,17	1.32	2 (13%)
3	NAG	B	501	2	14,14,15	2.27	2 (14%)	15,19,21	1.35	1 (6%)
3	NAG	C	601	1	14,14,15	1.89	1 (7%)	15,19,21	1.59	1 (6%)
3	NAG	C	602	1,3	14,14,15	0.38	0	15,19,21	0.93	1 (6%)
3	NAG	C	603	3	14,14,15	0.61	0	15,19,21	0.53	0
4	SIA	C	604	5	17,20,21	0.55	0	18,28,31	2.70	4 (22%)
5	GAL	C	605	3,4	11,11,12	1.35	3 (27%)	15,15,17	1.49	2 (13%)
3	NAG	C	606	5	15,15,15	0.18	0	17,21,21	0.16	0
3	NAG	D	501	2	14,14,15	1.95	1 (7%)	15,19,21	1.55	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	401	1	-	0/6/23/26	0/1/1/1
3	NAG	A	402	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	403	3	-	0/6/23/26	0/1/1/1
4	SIA	A	404	5	-	0/14/34/38	0/1/1/1
3	NAG	A	405	5	-	0/6/26/26	0/1/1/1
5	GAL	A	406	3,4	-	0/2/19/22	0/1/1/1
3	NAG	B	501	2	-	0/6/23/26	0/1/1/1
3	NAG	C	601	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	602	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	603	3	-	0/6/23/26	0/1/1/1
4	SIA	C	604	5	-	0/14/34/38	0/1/1/1
5	GAL	C	605	3,4	-	0/2/19/22	0/1/1/1
3	NAG	C	606	5	-	0/6/26/26	0/1/1/1
3	NAG	D	501	2	-	0/6/23/26	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	404	SIA	C5-N5	-2.31	1.42	1.45
5	C	605	GAL	O3-C3	2.02	1.47	1.43
5	A	406	GAL	O3-C3	2.14	1.48	1.43
5	C	605	GAL	C2-C3	2.40	1.55	1.52
3	B	501	NAG	C1-C2	2.47	1.56	1.52
5	A	406	GAL	C1-C2	2.51	1.58	1.52
5	A	406	GAL	C2-C3	2.56	1.56	1.52
5	C	605	GAL	C1-C2	2.83	1.59	1.52
3	A	402	NAG	O5-C1	3.59	1.49	1.43
3	A	401	NAG	O5-C1	4.24	1.50	1.43
3	A	403	NAG	O5-C1	4.51	1.51	1.43
3	C	601	NAG	O5-C1	6.72	1.54	1.43
3	D	501	NAG	O5-C1	7.02	1.55	1.43
3	B	501	NAG	O5-C1	8.01	1.56	1.43

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	604	SIA	C7-C6-C5	-4.60	107.72	114.06
4	A	404	SIA	O9-C9-C8	-3.45	103.41	111.07
4	A	404	SIA	C7-C6-C5	-3.05	109.85	114.06
4	A	404	SIA	C4-C5-N5	-2.29	105.10	110.31
4	A	404	SIA	C6-C5-N5	-2.29	107.15	111.06
4	A	404	SIA	C8-C7-C6	-2.23	108.39	113.08
5	A	406	GAL	C1-O5-C5	2.02	115.11	112.14
4	C	604	SIA	C3-C4-C5	2.12	113.84	111.47
5	C	605	GAL	C1-O5-C5	2.57	115.92	112.14
3	A	403	NAG	C1-O5-C5	2.69	116.09	112.14
3	A	401	NAG	C1-O5-C5	2.74	116.17	112.14
4	A	404	SIA	O6-C2-C3	3.19	116.02	109.77
3	C	602	NAG	C1-O5-C5	3.22	116.88	112.14
4	C	604	SIA	O6-C2-C3	3.24	116.11	109.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	406	GAL	C1-C2-C3	3.42	113.70	109.55
5	C	605	GAL	C1-C2-C3	3.92	114.30	109.55
3	B	501	NAG	C1-O5-C5	4.42	118.64	112.14
3	A	402	NAG	C1-O5-C5	4.98	119.47	112.14
3	D	501	NAG	C1-O5-C5	5.32	119.96	112.14
3	C	601	NAG	C1-O5-C5	5.42	120.11	112.14
4	A	404	SIA	O6-C6-C5	7.86	121.36	108.48
4	C	604	SIA	O6-C6-C5	9.61	124.22	108.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	NAG	1	0
3	B	501	NAG	3	0
3	C	601	NAG	1	0
3	C	602	NAG	2	0
3	D	501	NAG	3	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 ⓘ

### 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	325/325 (100%)	0.14	4 (1%) 81 55	51, 76, 121, 180	0
1	C	325/325 (100%)	0.17	3 (0%) 85 64	50, 76, 124, 192	0
2	B	164/164 (100%)	0.43	8 (4%) 33 13	50, 115, 171, 207	0
2	D	164/164 (100%)	0.41	10 (6%) 25 9	49, 115, 177, 208	0
All	All	978/978 (100%)	0.24	25 (2%) 59 29	49, 83, 161, 208	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	455	LEU	5.8
2	D	467	PHE	4.9
2	B	455	LEU	4.9
2	D	351	TYR	3.8
2	B	467	PHE	3.8
2	D	493	LYS	3.3
2	D	469	PHE	3.2
1	C	5	ILE	3.2
1	C	3	ILE	3.1
1	A	5	ILE	2.9
2	D	451	VAL	2.9
1	A	3	ILE	2.7
2	B	493	LYS	2.7
2	B	469	PHE	2.6
2	D	347	ILE	2.6
2	B	353	TYR	2.4
2	D	350	TRP	2.4
1	A	6	GLY	2.3
2	B	330	GLY	2.3
2	B	350	TRP	2.3
1	A	16	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	361	SER	2.3
2	B	331	ILE	2.2
1	C	317	ALA	2.1
2	D	332	PHE	2.0

## 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](#)

There are no carbohydrates in this entry.

## 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, 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	SIA	C	604	20/21	0.88	0.24	0.84	100,106,113,114	0
3	NAG	D	501	14/15	0.73	0.20	0.05	143,149,154,154	0
4	SIA	A	404	20/21	0.89	0.20	-0.35	99,104,110,110	0
3	NAG	C	602	14/15	0.88	0.15	-0.67	90,96,100,101	0
3	NAG	B	501	14/15	0.77	0.18	-	148,154,157,158	0
5	GAL	C	605	11/12	0.96	0.14	-	79,82,87,88	0
3	NAG	C	601	14/15	0.75	0.26	-	139,143,145,145	0
3	NAG	A	405	15/15	0.93	0.14	-	130,133,136,136	0
3	NAG	A	403	14/15	0.82	0.20	-	120,124,127,131	0
3	NAG	C	603	14/15	0.89	0.21	-	124,129,132,136	0
3	NAG	C	606	15/15	0.93	0.12	-	126,130,134,134	0
3	NAG	A	401	14/15	0.77	0.28	-	157,162,164,166	0
5	GAL	A	406	11/12	0.95	0.14	-	82,86,89,91	0
3	NAG	A	402	14/15	0.91	0.14	-	88,100,107,107	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.