



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:08 PM GMT

PDB ID : 4KOM  
Title : The structure of hemagglutinin from avian-origin H7N9 influenza virus in complex with avian receptor analog 3'SLNLN (NeuAc<#945;2-3Gal<#946;1-4GlcNAc<#946;1-3Gal<#946;1-4Glc)  
Authors : Shi, Y.; Zhang, W.; Wang, F.; Qi, J.; Song, H.; Wu, Y.; Gao, F.; Zhang, Y.; Fan, Z.; Gong, W.; Wang, D.; Shu, Y.; Wang, Y.; Yan, J.; Gao, G.F.  
Deposited on : 2013-05-12  
Resolution : 2.60 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 (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

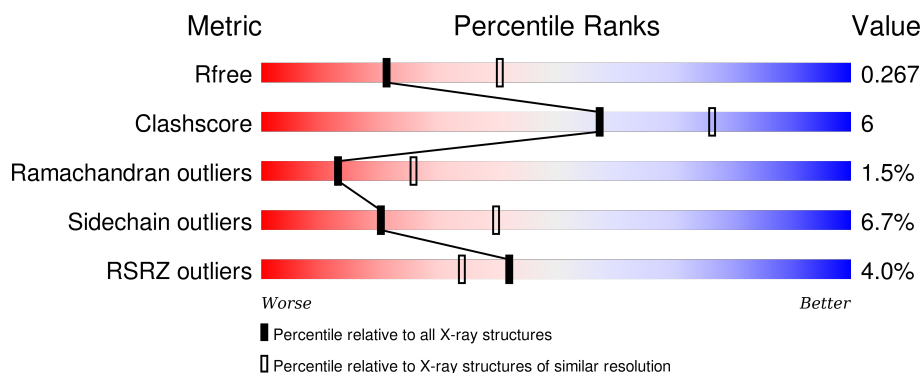
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


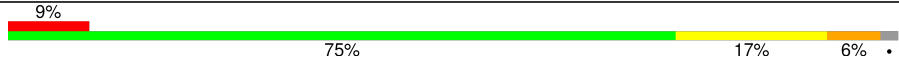
The reported resolution of this entry is 2.60 Å.

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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	314	
2	B	169	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3923 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2394	1487	433	459	15			

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	166	Total	C	N	O	S	0	0	0
			1345	828	234	276	7			

- Molecule 3 is SUGAR (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		

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	4	Total	C	N	O	0	0
			57	31	2	24		

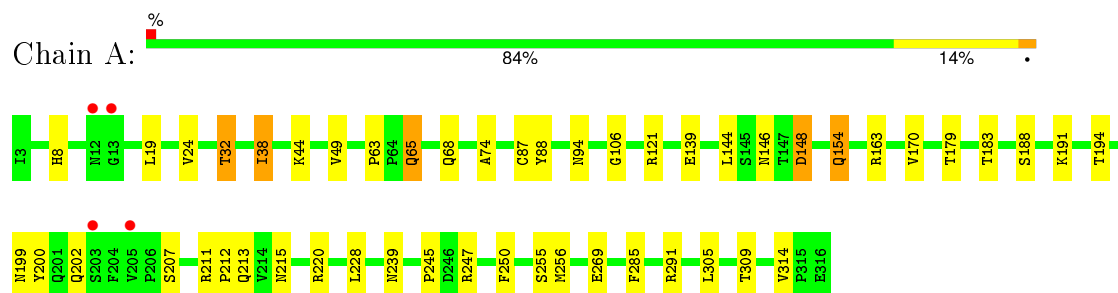
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	58	Total	O	0	0
			58	58		
5	B	27	Total	O	0	0
			27	27		

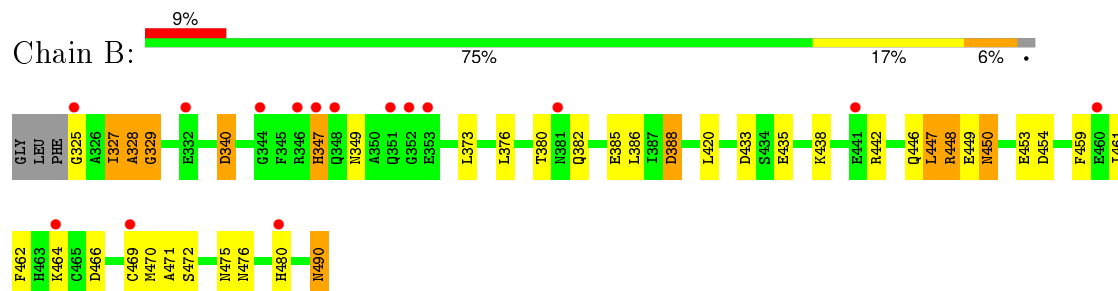
### 3 Residue-property plots [i](#)

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



#### • Molecule 2: Hemagglutinin HA2



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.06 Å   117.06 Å   296.43 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	39.08 – 2.60 39.07 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.08-2.60) 99.5 (39.07-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.47 (at 2.61 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.223 , 0.272 0.219 , 0.267	Depositor DCC
$R_{free}$ test set	1235 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	58.1	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 46.9	EDS
Estimated twinning fraction	0.007 for -1/3*h+1/3*k+1/3*l,-k,8/3*h+4/3*k+1/3*l 0.019 for -2/3*h-1/3*k-1/3*l,-1/3*h-2/3*k+1/3*l,-4/3*h+4/3*k+1/3*l 0.004 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k+1/3*l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 24233 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3923	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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

### 5.1 Standard geometry

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	0.24	0/2440	0.44	0/3298
2	B	0.23	0/1368	0.39	0/1844
All	All	0.24	0/3808	0.42	0/5142

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

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	2394	0	2348	26	0
2	B	1345	0	1241	21	0
3	A	28	0	26	0	0
3	B	14	0	13	0	0
4	A	57	0	49	3	0
5	A	58	0	0	0	0
5	B	27	0	0	0	0
All	All	3923	0	3677	45	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 6.

All (45) 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:B:380:THR:HG22	2:B:382:GLN:H	1.54	0.72
2:B:471:ALA:O	2:B:475:ASN:ND2	2.29	0.65
1:A:213:GLN:NE2	4:A:605:NAG:O7	2.28	0.64
2:B:325:GLY:N	2:B:433:ASP:OD1	2.35	0.60
1:A:44:LYS:HE2	1:A:269:GLU:HB2	1.83	0.60
1:A:291:ARG:HH21	2:B:388:ASP:HB3	1.65	0.60
2:B:327:ILE:O	2:B:329:GLY:N	2.38	0.56
2:B:490:ASN:OD1	2:B:490:ASN:N	2.38	0.55
2:B:349:ASN:HD22	2:B:466:ASP:HA	1.72	0.54
2:B:327:ILE:HG13	2:B:328:ALA:H	1.73	0.52
1:A:207:SER:O	1:A:211:ARG:NH2	2.33	0.52
2:B:453:GLU:HG2	2:B:459:PHE:HE2	1.74	0.51
1:A:32:THR:HG23	1:A:285:PHE:HD1	1.76	0.51
1:A:148:ASP:OD2	1:A:148:ASP:N	2.45	0.50
1:A:314:VAL:HG21	2:B:328:ALA:HB2	1.95	0.49
1:A:309:THR:HG22	2:B:373:LEU:HD11	1.94	0.48
1:A:121:ARG:HG3	1:A:146:ASN:HA	1.95	0.48
1:A:106:GLY:HA2	1:A:255:SER:HB3	1.95	0.48
2:B:347:HIS:ND1	2:B:470:MET:HG3	2.30	0.46
1:A:63:PRO:HB2	1:A:65:GLN:OE1	2.17	0.45
2:B:462:PHE:HB3	2:B:490:ASN:HB2	1.98	0.45
1:A:139:GLU:OE1	1:A:247:ARG:HD3	2.16	0.45
1:A:183:THR:HG22	1:A:188:SER:HA	1.98	0.45
2:B:450:ASN:N	2:B:450:ASN:OD1	2.50	0.44
4:A:604:GAL:O2	4:A:605:NAG:N2	2.50	0.44
2:B:446:GLN:NE2	2:B:476:ASN:HA	2.32	0.44
1:A:213:GLN:HE22	4:A:605:NAG:C7	2.25	0.44
1:A:163:ARG:HD3	1:A:250:PHE:CZ	2.52	0.44
1:A:179:THR:O	1:A:183:THR:HG23	2.18	0.44
1:A:38:ILE:HG13	1:A:38:ILE:O	2.16	0.44
1:A:170:VAL:O	1:A:245:PRO:HB3	2.18	0.44
1:A:87:CYS:O	1:A:215:ASN:ND2	2.49	0.44
1:A:32:THR:HG22	1:A:305:LEU:HB2	1.99	0.44
1:A:191:LYS:HA	1:A:239:ASN:HD21	1.84	0.43
2:B:340:ASP:OD1	2:B:340:ASP:N	2.52	0.43
2:B:435:GLU:HA	2:B:438:LYS:HD3	2.01	0.42
1:A:154:GLN:OE1	1:A:239:ASN:HB3	2.20	0.42
2:B:469:CYS:O	2:B:472:SER:OG	2.25	0.42
2:B:376:LEU:HD22	2:B:420:LEU:HD21	2.01	0.42
1:A:212:PRO:O	1:A:220:ARG:NH2	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:447:LEU:H	2:B:447:LEU:HG	1.72	0.42
2:B:327:ILE:HG23	2:B:328:ALA:N	2.34	0.41
1:A:200:TYR:CE2	1:A:202:GLN:HB2	2.55	0.41
1:A:87:CYS:SG	1:A:88:TYR:N	2.93	0.41
1:A:49:VAL:HG23	1:A:74:ALA:HB2	2.02	0.41

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	312/314 (99%)	292 (94%)	18 (6%)	2 (1%)	30	56
2	B	164/169 (97%)	143 (87%)	16 (10%)	5 (3%)	5	8
All	All	476/483 (99%)	435 (91%)	34 (7%)	7 (2%)	13	26

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	328	ALA
2	B	327	ILE
1	A	199	ASN
1	A	154	GLN
2	B	448	ARG
2	B	464	LYS
2	B	329	GLY

### 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	263/263 (100%)	250 (95%)	13 (5%)	31	57
2	B	142/144 (99%)	128 (90%)	14 (10%)	10	18
All	All	405/407 (100%)	378 (93%)	27 (7%)	20	40

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	19	LEU
1	A	24	VAL
1	A	32	THR
1	A	38	ILE
1	A	65	GLN
1	A	68	GLN
1	A	94	ASN
1	A	144	LEU
1	A	148	ASP
1	A	194	THR
1	A	228	LEU
1	A	256	MET
2	B	340	ASP
2	B	347	HIS
2	B	385	GLU
2	B	386	LEU
2	B	388	ASP
2	B	442	ARG
2	B	447	LEU
2	B	448	ARG
2	B	449	GLU
2	B	450	ASN
2	B	454	ASP
2	B	461	ILE
2	B	480	HIS
2	B	490	ASN

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 ⓘ

4 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	SIA	A	603	4	16,20,21	1.72	4 (25%)	18,28,31	2.55	5 (27%)
4	GAL	A	604	4	12,12,12	0.56	0	17,17,17	0.57	0
4	NAG	A	605	4	14,14,15	0.58	0	15,19,21	0.89	1 (6%)
4	GAL	A	606	4	11,11,12	0.66	0	14,15,17	1.26	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	SIA	A	603	4	-	0/14/34/38	0/1/1/1
4	GAL	A	604	4	-	0/2/22/22	0/1/1/1
4	NAG	A	605	4	-	0/6/23/26	0/1/1/1
4	GAL	A	606	4	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	SIA	C7-C6	-3.42	1.48	1.52
4	A	603	SIA	C3-C4	-2.01	1.49	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	SIA	O6-C6	2.46	1.48	1.43
4	A	603	SIA	C10-N5	3.35	1.47	1.34

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	SIA	O6-C2-C3	-8.74	93.06	109.86
4	A	603	SIA	C8-C7-C6	-2.60	107.78	113.01
4	A	603	SIA	C6-C5-N5	2.03	114.60	111.07
4	A	605	NAG	C4-C3-C2	2.17	114.60	111.23
4	A	603	SIA	O9-C9-C8	2.77	117.11	111.10
4	A	603	SIA	C3-C4-C5	2.94	114.75	111.47
4	A	606	GAL	C1-C2-C3	3.83	114.08	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	604	GAL	1	0
4	A	605	NAG	3	0

## 5.6 Ligand geometry

3 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	601	1	14,14,15	0.41	0	15,19,21	1.29	1 (6%)
3	NAG	A	602	1	14,14,15	0.46	0	15,19,21	0.99	2 (13%)
3	NAG	B	501	2	14,14,15	0.46	0	15,19,21	0.68	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	601	1	-	0/6/23/26	0/1/1/1
3	NAG	A	602	1	-	0/6/23/26	0/1/1/1
3	NAG	B	501	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	NAG	C2-N2-C7	-2.15	120.28	123.04
3	A	602	NAG	C1-O5-C5	2.30	115.16	112.25
3	A	601	NAG	C1-O5-C5	3.84	117.13	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

### 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	314/314 (100%)	-0.17	4 (1%) 79 75	36, 62, 103, 162	0
2	B	166/169 (98%)	0.38	15 (9%) 12 8	32, 100, 155, 186	0
All	All	480/483 (99%)	0.02	19 (3%) 42 34	32, 69, 135, 186	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	480	HIS	5.1
2	B	352	GLY	4.1
2	B	353	GLU	3.7
2	B	325	GLY	3.5
2	B	351	GLN	3.0
1	A	12	ASN	2.8
2	B	332	GLU	2.7
2	B	344	GLY	2.7
2	B	347	HIS	2.6
1	A	205	VAL	2.5
2	B	460	GLU	2.4
1	A	203	SER	2.4
1	A	13	GLY	2.3
2	B	381	ASN	2.2
2	B	464	LYS	2.1
2	B	348	GLN	2.1
2	B	441	GLU	2.0
2	B	346	ARG	2.0
2	B	469	CYS	2.0

### 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	SIA	A	603	20/21	0.95	0.18	0.24	66,72,81,83	0
4	NAG	A	605	14/15	0.90	0.29	-	105,113,125,125	0
4	GAL	A	606	11/12	0.92	0.16	-	74,85,92,93	0
4	GAL	A	604	12/12	0.61	0.33	-	140,152,162,164	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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	B	501	14/15	0.92	0.15	0.34	71,87,101,105	0
3	NAG	A	602	14/15	0.79	0.24	-	107,119,123,124	0
3	NAG	A	601	14/15	0.84	0.24	-	112,124,127,128	0

### 6.5 Other polymers

There are no such residues in this entry.