



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 09:46 am GMT

PDB ID : 4LKI  
Title : The structure of hemagglutinin L226Q mutant from a avian-origin H7N9 influenza virus (A/Anhui/1/2013)  
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 : 2013-07-07  
Resolution : 2.70 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

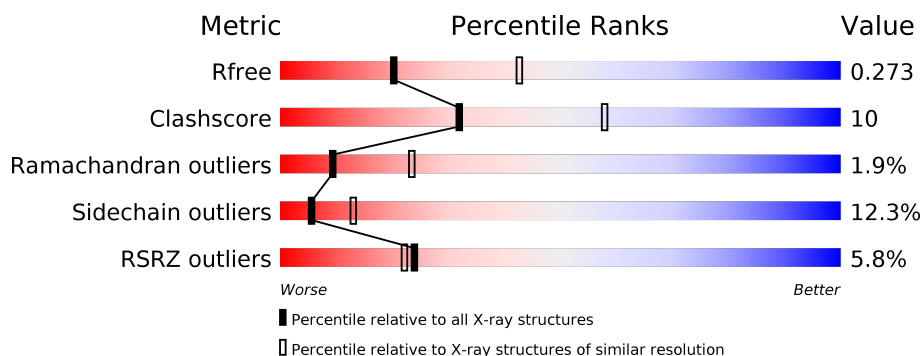
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	<div> <div>2%</div> <div>71%</div> <div>25%</div> <div>.</div> </div>
2	B	168	<div> <div>13%</div> <div>67%</div> <div>25%</div> <div>7%</div> <div>.</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3848 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2395	1486	434	460	15			

- Molecule 2 is a protein called hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	168	Total	C	N	O	S	0	0	0
			1364	843	236	278	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		

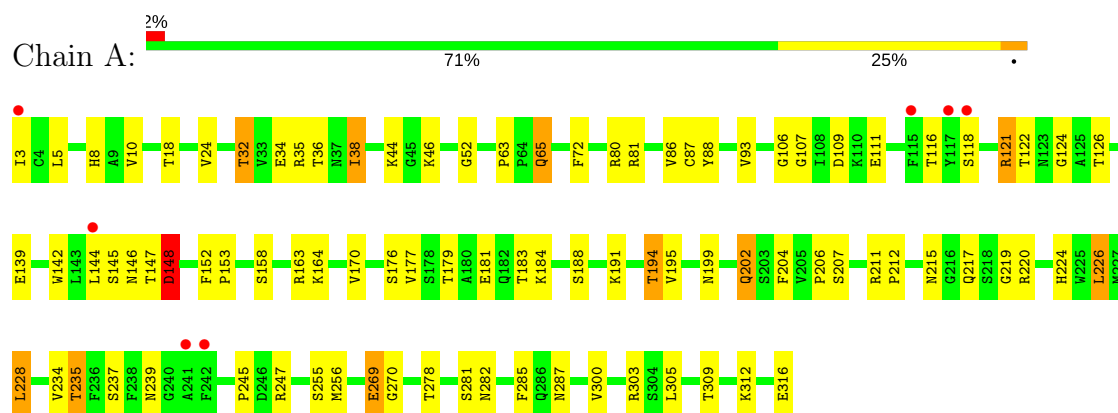
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	33	Total	O	0	0
			33	33		
4	B	14	Total	O	0	0
			14	14		

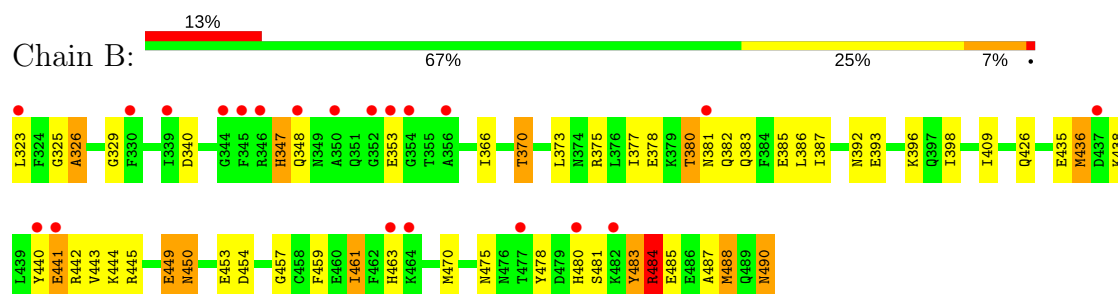
### 3 Residue-property plots [i](#)

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



#### • Molecule 2: hemagglutinin



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.09Å 116.09Å 295.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.59 – 2.70 47.59 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.59-2.70) 99.3 (47.59-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.238 , 0.277 0.233 , 0.273	Depositor DCC
$R_{free}$ test set	1093 reflections (5.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	68.1	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 54.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 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 0.006 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k+1/3*l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3848	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: 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	0.32	0/2441	0.51	0/3299
2	B	0.32	0/1388	0.49	0/1871
All	All	0.32	0/3829	0.50	0/5170

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	2395	0	2344	49	0
2	B	1364	0	1261	31	0
3	A	28	0	25	0	0
3	B	14	0	13	1	0
4	A	33	0	0	5	0
4	B	14	0	0	4	0
All	All	3848	0	3643	75	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 10.

All (75) 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)
3:B:501:NAG:H5	4:B:613:HOH:O	1.77	0.84
2:B:485:GLU:HA	2:B:488:MET:HB2	1.68	0.75
2:B:490:ASN:OD1	2:B:490:ASN:N	2.18	0.74
1:A:195:VAL:HB	4:A:732:HOH:O	1.87	0.74
1:A:3:ILE:HG13	2:B:347:HIS:HB3	1.74	0.70
2:B:383:GLN:NE2	2:B:385:GLU:OE2	2.25	0.70
1:A:158:SER:HB2	1:A:235:THR:HG23	1.74	0.69
2:B:441:GLU:O	2:B:445:ARG:NH1	2.26	0.69
1:A:207:SER:O	1:A:211:ARG:NH2	2.26	0.67
1:A:282:ASN:ND2	4:A:716:HOH:O	2.27	0.66
2:B:442:ARG:HH12	2:B:443:VAL:HG23	1.64	0.63
1:A:87:CYS:O	1:A:215:ASN:ND2	2.32	0.62
1:A:148:ASP:N	1:A:148:ASP:OD1	2.30	0.62
1:A:202:GLN:HB3	4:A:732:HOH:O	2.01	0.59
2:B:326:ALA:HB1	2:B:436:MET:HG2	1.86	0.58
1:A:111:GLU:OE2	1:A:163:ARG:NH1	2.37	0.57
1:A:212:PRO:O	1:A:220:ARG:NH2	2.36	0.57
2:B:463:HIS:HB3	2:B:487:ALA:HB2	1.85	0.57
1:A:194:THR:HG23	1:A:237:SER:HB2	1.88	0.56
2:B:348:GLN:NE2	2:B:353:GLU:OE1	2.38	0.56
1:A:124:GLY:HA3	1:A:142:TRP:HB3	1.87	0.55
1:A:46:LYS:HE3	4:A:722:HOH:O	2.06	0.55
1:A:183:THR:HG22	1:A:188:SER:HA	1.92	0.52
1:A:282:ASN:HB3	2:B:377:ILE:HG23	1.93	0.51
1:A:176:SER:OG	1:A:181:GLU:HB3	2.09	0.51
1:A:32:THR:HG23	1:A:285:PHE:HD2	1.76	0.51
2:B:347:HIS:CD2	2:B:470:MET:HG3	2.45	0.51
1:A:139:GLU:OE1	1:A:247:ARG:HD3	2.10	0.51
2:B:450:ASN:N	2:B:450:ASN:OD1	2.44	0.50
1:A:170:VAL:O	1:A:245:PRO:HB3	2.11	0.50
1:A:217:GLN:HG3	1:A:219:GLY:H	1.76	0.49
1:A:181:GLU:OE2	1:A:184:LYS:HD3	2.13	0.49
1:A:32:THR:HB	1:A:305:LEU:O	2.13	0.49
1:A:152:PHE:HA	1:A:153:PRO:HD3	1.69	0.49
2:B:409:ILE:HG22	4:B:603:HOH:O	2.13	0.48
1:A:87:CYS:SG	1:A:88:TYR:N	2.85	0.48
2:B:435:GLU:OE2	2:B:438:LYS:NZ	2.43	0.48
1:A:38:ILE:HG13	1:A:38:ILE:O	2.14	0.48
2:B:380:THR:C	2:B:382:GLN:H	2.16	0.48
1:A:109:ASP:OD2	1:A:163:ARG:NH2	2.33	0.47
2:B:453:GLU:HG2	2:B:459:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:LEU:HD21	1:A:234:VAL:HG21	1.98	0.46
2:B:325:GLY:O	2:B:329:GLY:HA3	2.15	0.46
2:B:461:ILE:HG13	2:B:461:ILE:H	1.58	0.46
1:A:3:ILE:O	2:B:459:PHE:N	2.37	0.46
1:A:52:GLY:O	1:A:80:ARG:HB2	2.16	0.46
1:A:270:GLY:HA3	1:A:278:THR:HG21	1.97	0.45
2:B:393:GLU:OE1	4:B:607:HOH:O	2.21	0.45
2:B:347:HIS:HD2	2:B:470:MET:HG3	1.79	0.45
1:A:34:GLU:HG2	1:A:281:SER:HB2	1.97	0.45
1:A:228:LEU:HA	1:A:228:LEU:HD23	1.79	0.45
1:A:191:LYS:O	1:A:206:PRO:HD2	2.18	0.44
1:A:287:ASN:ND2	1:A:300:VAL:O	2.42	0.44
2:B:323:LEU:HD21	4:B:602:HOH:O	2.17	0.44
2:B:444:LYS:HD2	2:B:453:GLU:OE1	2.18	0.44
1:A:44:LYS:HE2	1:A:269:GLU:HB2	1.99	0.43
1:A:63:PRO:HB2	1:A:65:GLN:OE1	2.17	0.43
1:A:3:ILE:N	2:B:459:PHE:O	2.51	0.43
2:B:398:ILE:HA	2:B:398:ILE:HD12	1.90	0.43
2:B:440:TYR:CE1	2:B:457:GLY:HA2	2.54	0.43
1:A:309:THR:HG22	2:B:373:LEU:HD11	2.00	0.42
2:B:366:ILE:O	2:B:370:THR:HB	2.19	0.42
1:A:191:LYS:HA	1:A:239:ASN:HD21	1.85	0.42
1:A:121:ARG:NH1	1:A:145:SER:O	2.53	0.41
1:A:148:ASP:O	1:A:184:LYS:NZ	2.51	0.41
2:B:481:SER:O	2:B:484:ARG:HB2	2.19	0.41
1:A:204:PHE:HE2	4:A:732:HOH:O	1.99	0.41
1:A:72:PHE:CE2	1:A:107:GLY:HA2	2.56	0.41
1:A:93:VAL:HG21	1:A:224:HIS:CE1	2.55	0.41
1:A:88:TYR:CE2	1:A:217:GLN:HG2	2.56	0.41
1:A:106:GLY:HA2	1:A:255:SER:HB3	2.02	0.41
1:A:35:ARG:HD3	1:A:303:ARG:HG3	2.03	0.41
1:A:18:THR:HB	2:B:426:GLN:OE1	2.21	0.41
2:B:387:ILE:HD12	2:B:387:ILE:HA	1.85	0.40
1:A:164:LYS:HD2	1:A:164:LYS:HA	1.85	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	312/314 (99%)	285 (91%)	25 (8%)	2 (1%)	28	56
2	B	166/168 (99%)	140 (84%)	19 (11%)	7 (4%)	3	7
All	All	478/482 (99%)	425 (89%)	44 (9%)	9 (2%)	9	23

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	484	ARG
1	A	199	ASN
2	B	441	GLU
2	B	478	TYR
2	B	483	TYR
1	A	148	ASP
2	B	381	ASN
2	B	326	ALA
2	B	449	GLU

### 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	263/263 (100%)	233 (89%)	30 (11%)	7	15
2	B	144/144 (100%)	124 (86%)	20 (14%)	4	10
All	All	407/407 (100%)	357 (88%)	50 (12%)	5	13

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	8	HIS
1	A	10	VAL
1	A	24	VAL
1	A	32	THR
1	A	36	THR
1	A	38	ILE
1	A	65	GLN
1	A	81	ARG
1	A	86	VAL
1	A	116	THR
1	A	118	SER
1	A	121	ARG
1	A	122	THR
1	A	126	THR
1	A	144	LEU
1	A	146	ASN
1	A	147	THR
1	A	148	ASP
1	A	177	VAL
1	A	179	THR
1	A	194	THR
1	A	202	GLN
1	A	226	LEU
1	A	228	LEU
1	A	235	THR
1	A	256	MET
1	A	269	GLU
1	A	312	LYS
1	A	316	GLU
2	B	340	ASP
2	B	347	HIS
2	B	370	THR
2	B	375	ARG
2	B	378	GLU
2	B	380	THR
2	B	386	LEU
2	B	392	ASN
2	B	396	LYS
2	B	436	MET
2	B	449	GLU
2	B	450	ASN

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Mol	Chain	Res	Type
2	B	454	ASP
2	B	461	ILE
2	B	475	ASN
2	B	480	HIS
2	B	483	TYR
2	B	484	ARG
2	B	488	MET
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 [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](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	0.42	0	15,19,21	1.49	1 (6%)
3	NAG	A	602	1	14,14,15	0.48	0	15,19,21	1.40	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	B	501	2	14,14,15	0.43	0	15,19,21	0.84	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	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 (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	NAG	C1-O5-C5	2.43	115.51	112.17
3	A	602	NAG	O5-C1-C2	2.50	114.96	111.47
3	A	602	NAG	C1-O5-C5	4.38	118.20	112.17
3	A	601	NAG	C1-O5-C5	4.70	118.64	112.17

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
3	B	501	NAG	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 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%)	0.05	7 (2%) 62 63	47, 78, 127, 161	0
2	B	168/168 (100%)	0.72	21 (12%) 4 3	44, 102, 165, 205	0
All	All	482/482 (100%)	0.29	28 (5%) 24 22	44, 86, 150, 205	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	441	GLU	5.0
2	B	323	LEU	4.5
2	B	381	ASN	4.2
2	B	344	GLY	4.1
2	B	348	GLN	3.9
1	A	3	ILE	3.8
2	B	354	GLY	3.8
2	B	339	ILE	3.4
2	B	346	ARG	3.3
2	B	353	GLU	3.2
1	A	115	PHE	3.0
1	A	144	LEU	2.9
1	A	118	SER	2.8
2	B	345	PHE	2.6
2	B	352	GLY	2.5
2	B	477	THR	2.5
2	B	482	LYS	2.5
1	A	241	ALA	2.5
2	B	480	HIS	2.5
2	B	464	LYS	2.4
1	A	117	TYR	2.4
2	B	350	ALA	2.4
2	B	356	ALA	2.4
1	A	242	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	437	ASP	2.3
2	B	330	PHE	2.2
2	B	440	TYR	2.2
2	B	463	HIS	2.1

## 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
3	NAG	B	501	14/15	0.91	0.21	0.37	91,96,105,106	0
3	NAG	A	601	14/15	0.84	0.17	-	119,133,138,139	0
3	NAG	A	602	14/15	0.69	0.27	-	155,168,171,171	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.