



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 13, 2023 – 08:21 PM JST

PDB ID : 5Y2M  
Title : Crystal structure of a group 2 HA binding antibody AF4H1K1 Fab in complex with the H4N6 duck isolate (H4-CZ/56) hemagglutinin  
Authors : Xiao, H.; Qi, J.; Gao, F.G.  
Deposited on : 2017-07-26  
Resolution : 3.80 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

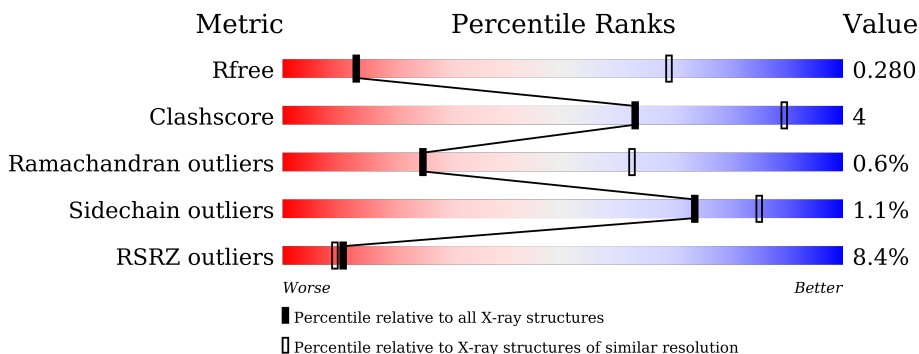
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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))
$R_{free}$	130704	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	327	 0% 89% 8% ..
1	B	327	 2% 87% 10% .
1	C	327	 2% 86% 11% ..
2	D	176	 6% 88% 10% .
2	E	176	 6% 90% 8% .
2	F	176	 6% 91% 7% .

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Mol	Chain	Length	Quality of chain
3	I	233	
3	K	233	
4	J	220	
4	L	220	

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
5	NAG	A	601	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18315 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
			Total	C	N	O	S			
1	A	319	2457	1538	437	470	12	0	0	0
1	B	319	2457	1538	437	470	12	0	0	0
1	C	319	2457	1538	437	470	12	0	0	0

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	172	1404	871	250	279	4	0	0	0
2	E	172	1404	871	250	279	4	0	0	0
2	F	172	1404	871	250	279	4	0	0	0

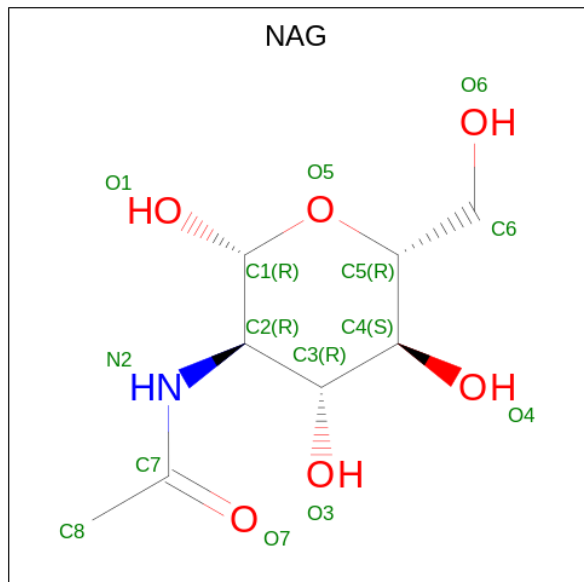
- Molecule 3 is a protein called a group 2 HA binding antibody AF4H1K1 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	I	224	1694	1077	286	325	6	0	0	0
3	K	224	1694	1077	286	325	6	0	0	0

- Molecule 4 is a protein called a group 2 HA binding antibody AF4H1K1 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	J	212	1630	1018	278	329	5	0	0	0
4	L	212	1630	1018	278	329	5	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).

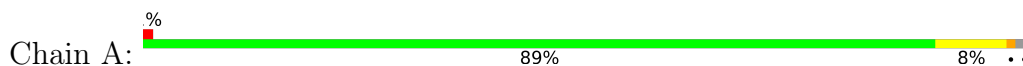


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		

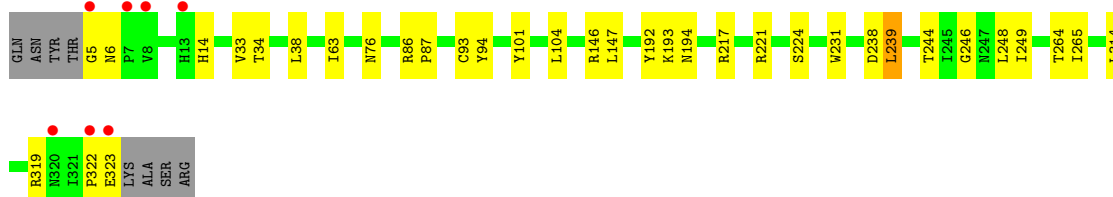
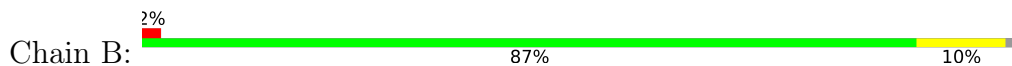
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

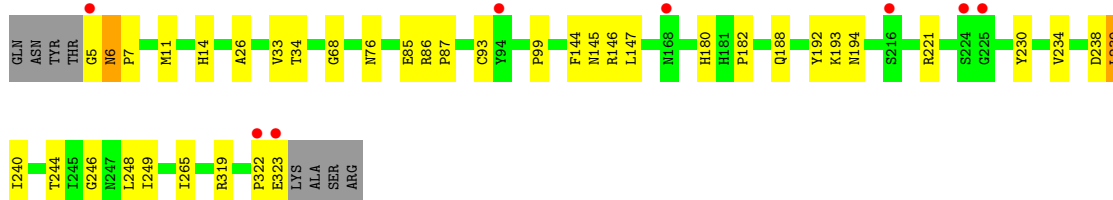
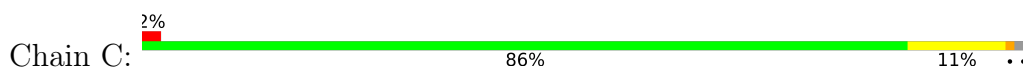
- Molecule 1: Hemagglutinin



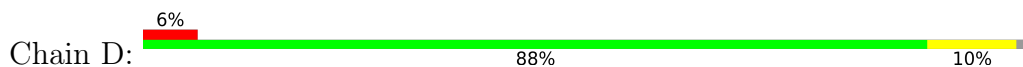
- Molecule 1: Hemagglutinin



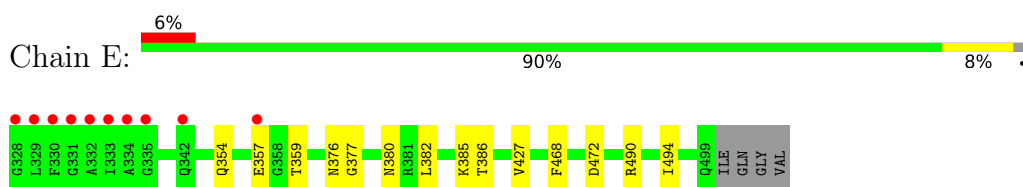
- Molecule 1: Hemagglutinin



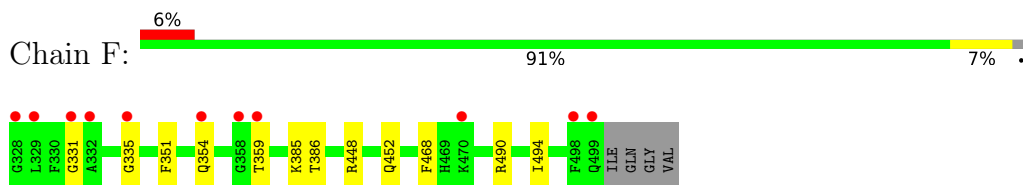
- Molecule 2: Hemagglutinin



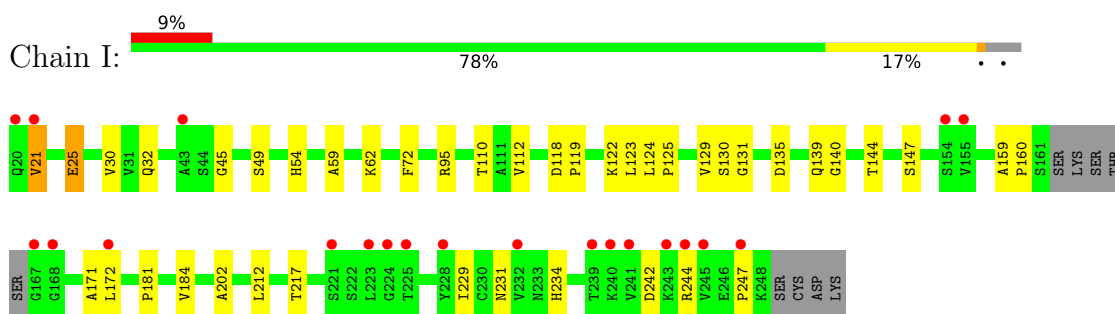
- Molecule 2: Hemagglutinin



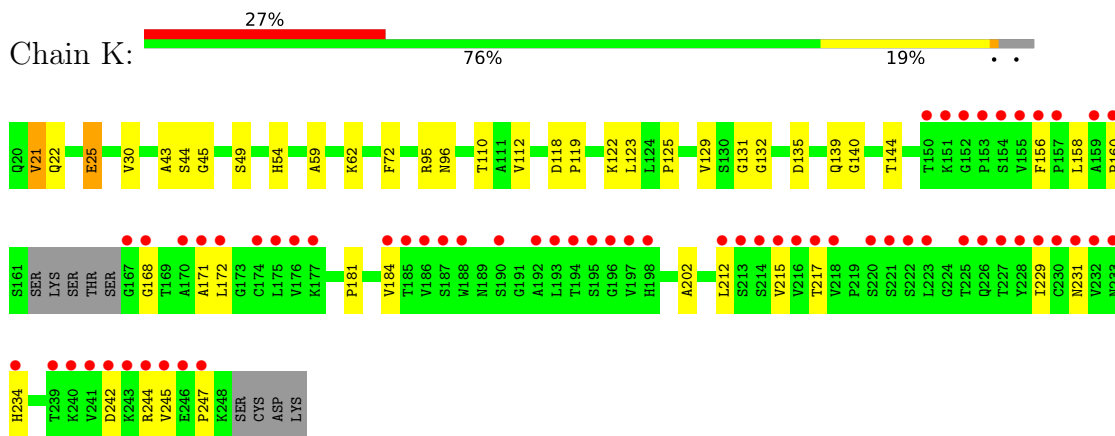
- Molecule 2: Hemagglutinin



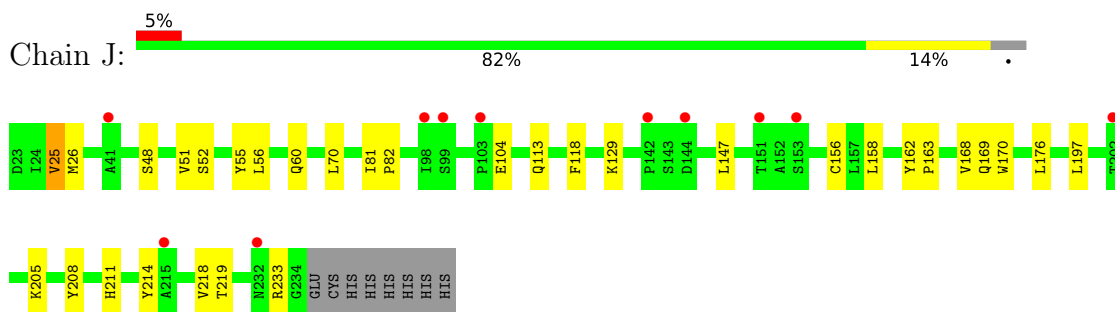
- Molecule 3: a group 2 HA binding antibody AF4H1K1 Fab heavy chain



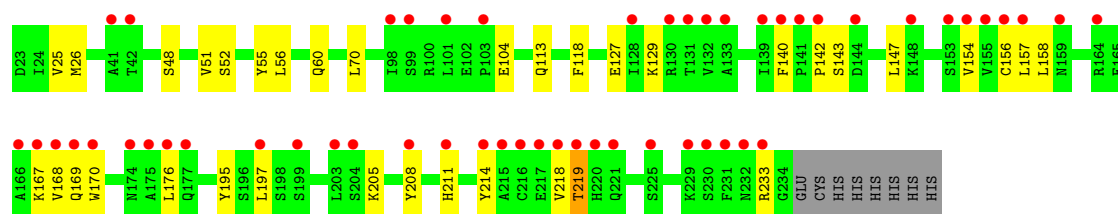
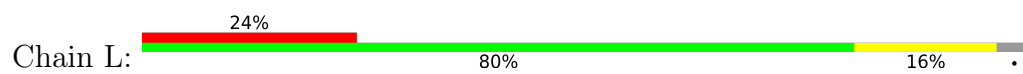
- Molecule 3: a group 2 HA binding antibody AF4H1K1 Fab heavy chain



- Molecule 4: a group 2 HA binding antibody AF4H1K1 Fab light chain



- Molecule 4: a group 2 HA binding antibody AF4H1K1 Fab light chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.17Å 140.94Å 138.10Å 90.00° 95.31° 90.00°	Depositor
Resolution (Å)	49.21 – 3.80 49.21 – 3.79	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.21-3.80) 99.5 (49.21-3.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 3.77Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.235 , 0.277 0.240 , 0.280	Depositor DCC
$R_{free}$ test set	2168 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	75.8	Xtrriage
Anisotropy	0.611	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 52.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	18315	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	98.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.25	0/2511	0.45	0/3418
1	B	0.25	0/2511	0.45	0/3418
1	C	0.24	0/2511	0.44	0/3418
2	D	0.28	0/1428	0.43	0/1922
2	E	0.27	0/1428	0.43	0/1922
2	F	0.28	0/1428	0.43	0/1922
3	I	0.24	0/1739	0.43	0/2372
3	K	0.24	0/1739	0.42	0/2372
4	J	0.23	0/1665	0.43	0/2258
4	L	0.24	0/1665	0.43	0/2258
All	All	0.25	0/18625	0.43	0/25280

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	2457	0	2402	16	0
1	B	2457	0	2402	21	0
1	C	2457	0	2402	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1404	0	1320	13	0
2	E	1404	0	1320	11	0
2	F	1404	0	1320	8	0
3	I	1694	0	1644	24	0
3	K	1694	0	1644	27	0
4	J	1630	0	1581	15	0
4	L	1630	0	1581	19	0
5	A	28	0	26	0	0
5	B	28	0	26	0	0
5	C	28	0	26	0	0
All	All	18315	0	17694	155	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.

The worst 5 of 155 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:B:244:THR:HG22	1:B:246:GLY:H	1.37	0.89
1:A:244:THR:HG22	1:A:246:GLY:H	1.40	0.86
1:C:244:THR:HG22	1:C:246:GLY:H	1.40	0.86
3:I:229:ILE:HG12	3:I:244:ARG:HG3	1.69	0.74
1:B:5:GLY:HA2	2:E:468:PHE:HA	1.68	0.74

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	317/327 (97%)	304 (96%)	11 (4%)	2 (1%)	25 62
1	B	317/327 (97%)	304 (96%)	11 (4%)	2 (1%)	25 62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	317/327 (97%)	304 (96%)	11 (4%)	2 (1%)	25	62
2	D	170/176 (97%)	161 (95%)	9 (5%)	0	100	100
2	E	170/176 (97%)	161 (95%)	9 (5%)	0	100	100
2	F	170/176 (97%)	160 (94%)	10 (6%)	0	100	100
3	I	220/233 (94%)	205 (93%)	14 (6%)	1 (0%)	29	66
3	K	220/233 (94%)	204 (93%)	14 (6%)	2 (1%)	17	54
4	J	210/220 (96%)	194 (92%)	13 (6%)	3 (1%)	11	46
4	L	210/220 (96%)	194 (92%)	13 (6%)	3 (1%)	11	46
All	All	2321/2415 (96%)	2191 (94%)	115 (5%)	15 (1%)	25	62

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	J	51	VAL
4	L	51	VAL
3	K	168	GLY
1	A	6	ASN
1	A	193	LYS

### 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	274/282 (97%)	272 (99%)	2 (1%)	84	91
1	B	274/282 (97%)	272 (99%)	2 (1%)	84	91
1	C	274/282 (97%)	272 (99%)	2 (1%)	84	91
2	D	147/150 (98%)	147 (100%)	0	100	100
2	E	147/150 (98%)	147 (100%)	0	100	100
2	F	147/150 (98%)	147 (100%)	0	100	100
3	I	187/196 (95%)	183 (98%)	4 (2%)	53	74
3	K	187/196 (95%)	183 (98%)	4 (2%)	53	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	J	184/192 (96%)	179 (97%)	5 (3%)	44	69
4	L	184/192 (96%)	180 (98%)	4 (2%)	52	72
All	All	2005/2072 (97%)	1982 (99%)	23 (1%)	73	85

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	J	219	THR
3	K	95	ARG
3	K	25	GLU
3	K	112	VAL
3	I	21	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
2	D	369	GLN
2	E	452	GLN
1	C	74	HIS

### 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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

6 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	$\# Z  > 2$
5	NAG	B	601	1	14,14,15	0.35	0	17,19,21	0.32	0
5	NAG	A	602	1	14,14,15	0.29	0	17,19,21	0.69	1 (5%)
5	NAG	B	602	1	14,14,15	0.29	0	17,19,21	0.48	0
5	NAG	C	602	1	14,14,15	0.22	0	17,19,21	0.43	0
5	NAG	A	601	1	14,14,15	0.28	0	17,19,21	0.36	0
5	NAG	C	601	1	14,14,15	0.40	0	17,19,21	0.31	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
5	NAG	B	601	1	-	2/6/23/26	0/1/1/1
5	NAG	A	602	1	-	2/6/23/26	0/1/1/1
5	NAG	B	602	1	-	2/6/23/26	0/1/1/1
5	NAG	C	602	1	-	2/6/23/26	0/1/1/1
5	NAG	A	601	1	-	1/6/23/26	0/1/1/1
5	NAG	C	601	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	NAG	C1-O5-C5	2.01	114.91	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	602	NAG	C8-C7-N2-C2
5	A	602	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
5	B	602	NAG	C8-C7-N2-C2
5	B	602	NAG	O7-C7-N2-C2
5	C	602	NAG	C8-C7-N2-C2

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, 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	319/327 (97%)	0.06	3 (0%) 84 79	33, 68, 102, 181	0
1	B	319/327 (97%)	0.14	7 (2%) 62 54	36, 71, 106, 205	0
1	C	319/327 (97%)	0.16	8 (2%) 57 49	41, 78, 110, 170	0
2	D	172/176 (97%)	0.40	10 (5%) 23 18	40, 90, 171, 309	0
2	E	172/176 (97%)	0.39	10 (5%) 23 18	45, 102, 173, 346	0
2	F	172/176 (97%)	0.35	11 (6%) 19 15	34, 110, 175, 299	0
3	I	224/233 (96%)	0.58	21 (9%) 8 7	41, 95, 171, 209	0
3	K	224/233 (96%)	1.36	62 (27%) 0 0	55, 101, 254, 347	0
4	J	212/220 (96%)	0.59	11 (5%) 27 24	55, 94, 148, 187	0
4	L	212/220 (96%)	1.42	53 (25%) 0 0	72, 143, 239, 296	0
All	All	2345/2415 (97%)	0.50	196 (8%) 11 9	33, 87, 191, 347	0

The worst 5 of 196 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	K	217	THR	11.0
3	K	175	LEU	9.7
3	K	193	LEU	9.4
3	K	215	VAL	9.3
3	K	214	SER	8.5

### 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](#)

There are no monosaccharides 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
5	NAG	A	601	14/15	0.65	0.41	102,123,129,129	0
5	NAG	B	602	14/15	0.78	0.33	67,77,82,93	0
5	NAG	A	602	14/15	0.79	0.29	65,78,151,153	0
5	NAG	C	601	14/15	0.79	0.37	104,123,130,132	0
5	NAG	C	602	14/15	0.82	0.37	63,69,78,86	0
5	NAG	B	601	14/15	0.83	0.34	114,125,131,132	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.