



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 13, 2024 – 01:23 pm BST

PDB ID : 3ZP2  
Title : INFLUENZA VIRUS (VN1194) H5 HA A138V mutant with LSTa  
Authors : Liu, J.; Stevens, D.J.; Gamblin, S.J.; Skehel, J.J.  
Deposited on : 2013-02-26  
Resolution : 2.50 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

<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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

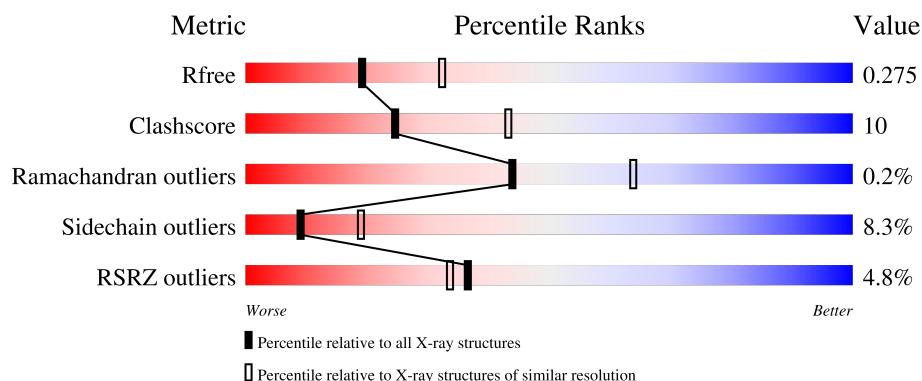
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


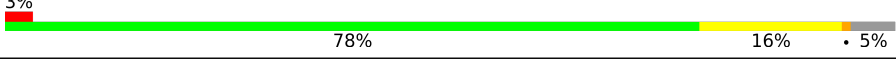

The reported resolution of this entry is 2.50 Å.

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))
$R_{free}$	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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	E	326	
2	F	166	
3	A	2	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4022 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 HAEMAGGLUTININ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	321	2551	1613	440	483	15	0	0	0

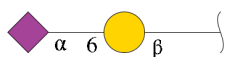
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	LYS	THR	conflict	UNP Q6DQ34
E	138	VAL	ALA	engineered mutation	UNP Q6DQ34

- Molecule 2 is a protein called HAEMAGGLUTININ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	158	1272	791	221	252	8	0	0	0

- Molecule 3 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	A	2	22	12	1	9	0	0	1

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	F	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

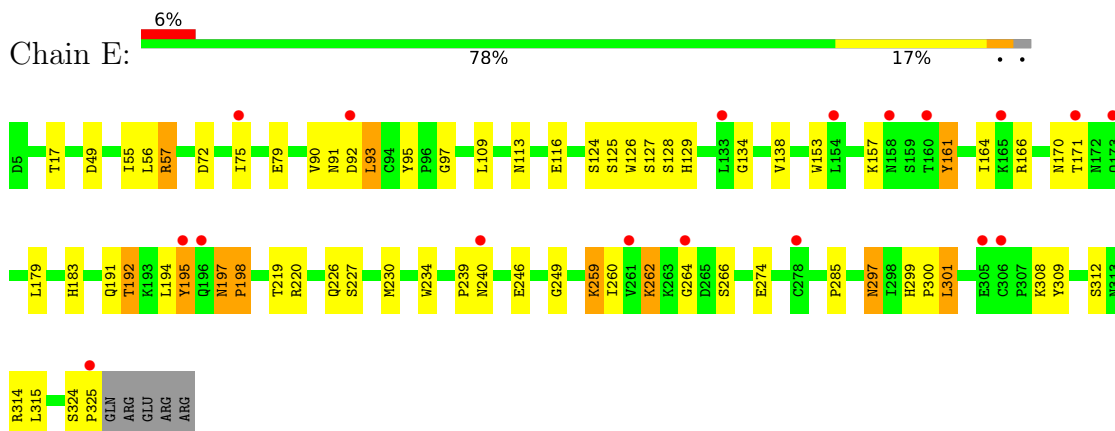
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	89	Total	O	0	0
			89	89		
5	F	60	Total	O	0	0
			60	60		

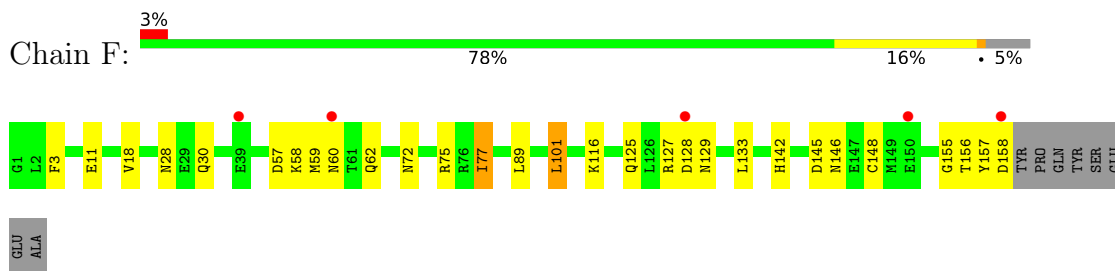
### 3 Residue-property plots [i](#)

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: HAEMAGGLUTININ



#### • Molecule 2: HAEMAGGLUTININ



#### • Molecule 3: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.18Å 101.18Å 449.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.50 30.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.50) 99.7 (30.00-2.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.61 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, $R_{free}$	0.233 , 0.279 0.235 , 0.275	Depositor DCC
$R_{free}$ test set	1574 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.4	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 40.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4022	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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: GAL, NAG, SIA

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	E	0.45	0/2613	0.62	0/3549
2	F	0.60	0/1296	0.76	1/1742 (0.1%)
All	All	0.51	0/3909	0.67	1/5291 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	129	ASN	N-CA-CB	-17.19	79.66	110.60

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	E	2551	0	2496	52	0
2	F	1272	0	1186	24	0
3	A	22	0	17	3	0
4	F	28	0	26	0	0
5	E	89	0	0	4	0
5	F	60	0	0	1	0
All	All	4022	0	3725	74	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 (74) 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:E:79:GLU:OE2	1:E:262:LYS:HE2	1.41	1.18
1:E:113:ASN:OD1	1:E:264:GLY:HA3	1.55	1.03
1:E:92:ASP:O	5:E:2051:HOH:O	1.92	0.86
1:E:299:HIS:HD2	1:E:301:LEU:H	1.22	0.85
1:E:79:GLU:OE2	1:E:262:LYS:CE	2.25	0.82
1:E:113:ASN:OD1	1:E:264:GLY:CA	2.31	0.78
2:F:125:GLN:HE22	2:F:155:GLY:HA2	1.50	0.77
2:F:77:ILE:H	2:F:77:ILE:HD13	1.53	0.73
1:E:95:TYR:CD2	1:E:230:MET:HG2	2.25	0.70
1:E:191:GLN:O	1:E:195:TYR:O	2.10	0.70
1:E:194:LEU:HD21	3:A:2:SIA:O10	1.94	0.68
1:E:192:THR:HA	1:E:195:TYR:O	1.95	0.65
1:E:197:ASN:OD1	1:E:197:ASN:N	2.30	0.64
1:E:299:HIS:CD2	1:E:300:PRO:HD2	2.32	0.63
2:F:142:HIS:HE1	2:F:157:TYR:OH	1.82	0.61
2:F:125:GLN:HE22	2:F:155:GLY:CA	2.12	0.61
1:E:161:TYR:CE1	1:E:249:GLY:HA2	2.37	0.59
1:E:72:ASP:O	1:E:75:ILE:HG12	2.04	0.58
1:E:194:LEU:CD2	3:A:2:SIA:O10	2.53	0.56
1:E:239:PRO:O	1:E:240:ASN:HB2	2.07	0.55
1:E:129:HIS:CD2	1:E:161:TYR:CE2	2.95	0.54
1:E:299:HIS:CD2	1:E:301:LEU:H	2.13	0.54
2:F:77:ILE:H	2:F:77:ILE:CD1	2.20	0.54
2:F:125:GLN:NE2	2:F:155:GLY:HA2	2.20	0.54
1:E:164:ILE:HG23	1:E:166:ARG:HG2	1.91	0.53
1:E:309:TYR:HD2	2:F:89:LEU:HD22	1.72	0.53
1:E:125:SER:OG	1:E:166:ARG:NH2	2.43	0.52
1:E:260:ILE:HG22	1:E:260:ILE:O	2.10	0.50
1:E:134:GLY:HA3	1:E:153:TRP:HB3	1.92	0.49
1:E:57:ARG:O	5:E:2038:HOH:O	2.20	0.49
2:F:142:HIS:CE1	2:F:157:TYR:OH	2.64	0.49
1:E:285:PRO:HD3	1:E:301:LEU:O	2.13	0.48
2:F:3:PHE:O	2:F:116:LYS:HD2	2.12	0.48
2:F:125:GLN:HE22	2:F:155:GLY:C	2.17	0.47
1:E:164:ILE:O	1:E:246:GLU:HA	2.15	0.47
2:F:156:THR:O	2:F:156:THR:OG1	2.30	0.47
1:E:183:HIS:NE2	3:A:2:SIA:O9	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:125:SER:O	1:E:126:TRP:HB2	2.15	0.47
1:E:116:GLU:O	1:E:259:LYS:HB2	2.15	0.46
1:E:164:ILE:CG2	1:E:166:ARG:HG2	2.46	0.46
2:F:59:MET:O	2:F:62:GLN:HG3	2.15	0.46
2:F:145:ASP:OD1	2:F:145:ASP:C	2.53	0.46
2:F:72:ASN:HD22	2:F:75:ARG:HH21	1.64	0.46
1:E:197:ASN:HA	1:E:198:PRO:HD3	1.80	0.45
1:E:90:VAL:HG23	1:E:91:ASN:N	2.31	0.45
2:F:125:GLN:NE2	2:F:155:GLY:C	2.71	0.44
1:E:113:ASN:OD1	1:E:264:GLY:C	2.56	0.44
1:E:95:TYR:HD2	1:E:230:MET:HG2	1.80	0.43
1:E:297:ASN:C	1:E:297:ASN:HD22	2.21	0.43
1:E:97:GLY:HA3	1:E:230:MET:O	2.18	0.43
1:E:124:SER:O	1:E:124:SER:OG	2.30	0.43
1:E:128:SER:HB2	1:E:129:HIS:CE1	2.52	0.43
1:E:192:THR:CA	1:E:195:TYR:O	2.64	0.43
2:F:30:GLN:HE22	2:F:145:ASP:HB2	1.82	0.43
1:E:126:TRP:CZ3	1:E:166:ARG:HG3	2.53	0.43
2:F:28:ASN:HD21	2:F:146:ASN:ND2	2.17	0.43
1:E:90:VAL:CG2	1:E:91:ASN:N	2.82	0.42
2:F:145:ASP:O	2:F:148:CYS:N	2.53	0.42
2:F:58:LYS:HD3	2:F:58:LYS:HA	1.89	0.42
1:E:170:ASN:ND2	1:E:239:PRO:HA	2.34	0.42
2:F:157:TYR:O	2:F:158:ASP:CB	2.68	0.41
2:F:101:LEU:HD13	5:F:2035:HOH:O	2.19	0.41
1:E:56:LEU:HD23	1:E:56:LEU:HA	1.82	0.41
1:E:324:SER:HA	1:E:325:PRO:HD3	1.94	0.41
1:E:129:HIS:CD2	1:E:161:TYR:CD2	3.09	0.41
1:E:314:ARG:NH2	5:E:2014:HOH:O	2.53	0.41
2:F:145:ASP:H	2:F:148:CYS:HB3	1.85	0.41
1:E:57:ARG:HG2	5:E:2039:HOH:O	2.21	0.41
1:E:308:LYS:HB3	2:F:62:GLN:NE2	2.36	0.40
1:E:92:ASP:O	1:E:93:LEU:C	2.58	0.40
1:E:129:HIS:HD2	1:E:161:TYR:CD2	2.39	0.40
1:E:179:LEU:HD23	1:E:234:TRP:HB3	2.03	0.40
1:E:129:HIS:HD2	1:E:161:TYR:CE2	2.39	0.40
2:F:145:ASP:O	2:F:148:CYS:HB3	2.21	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	E	319/326 (98%)	305 (96%)	13 (4%)	1 (0%)	37	56
2	F	156/166 (94%)	151 (97%)	5 (3%)	0	100	100
All	All	475/492 (96%)	456 (96%)	18 (4%)	1 (0%)	44	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	198	PRO

### 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	E	290/295 (98%)	264 (91%)	26 (9%)	8	16
2	F	134/141 (95%)	125 (93%)	9 (7%)	13	28
All	All	424/436 (97%)	389 (92%)	35 (8%)	9	19

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	17	THR
1	E	49	ASP
1	E	55	ILE
1	E	57	ARG
1	E	93	LEU

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Mol	Chain	Res	Type
1	E	109	LEU
1	E	127	SER
1	E	138	VAL
1	E	157	LYS
1	E	161	TYR
1	E	171	THR
1	E	192	THR
1	E	195	TYR
1	E	197	ASN
1	E	219	THR
1	E	220	ARG
1	E	226	GLN
1	E	227	SER
1	E	259	LYS
1	E	262	LYS
1	E	266	SER
1	E	274	GLU
1	E	297	ASN
1	E	301	LEU
1	E	312	SER
1	E	315	LEU
2	F	11	GLU
2	F	18	VAL
2	F	57	ASP
2	F	60	ASN
2	F	77	ILE
2	F	101	LEU
2	F	127	ARG
2	F	128	ASP
2	F	133	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	19	GLN
1	E	186	ASN
1	E	297	ASN
1	E	299	HIS
2	F	15	GLN
2	F	30	GLN
2	F	62	GLN
2	F	72	ASN

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Mol	Chain	Res	Type
2	F	125	GLN
2	F	142	HIS
2	F	146	ASN

### 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 ⓘ

2 monosaccharides 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	GAL	A	1	3	1,1,12	0.46	0	-		
3	SIA	A	2	3	20,20,21	0.63	0	24,28,31	1.60	5 (20%)

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	SIA	A	2	3	-	4/18/34/38	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	SIA	C6-O6-C2	4.88	121.77	111.34
3	A	2	SIA	C6-C5-N5	-3.16	105.67	110.91
3	A	2	SIA	C4-C5-N5	-3.02	104.40	110.38
3	A	2	SIA	O1B-C1-C2	2.29	119.57	113.03
3	A	2	SIA	O6-C2-C1	2.01	111.63	107.70

There are no chirality outliers.

All (4) torsion outliers are listed below:

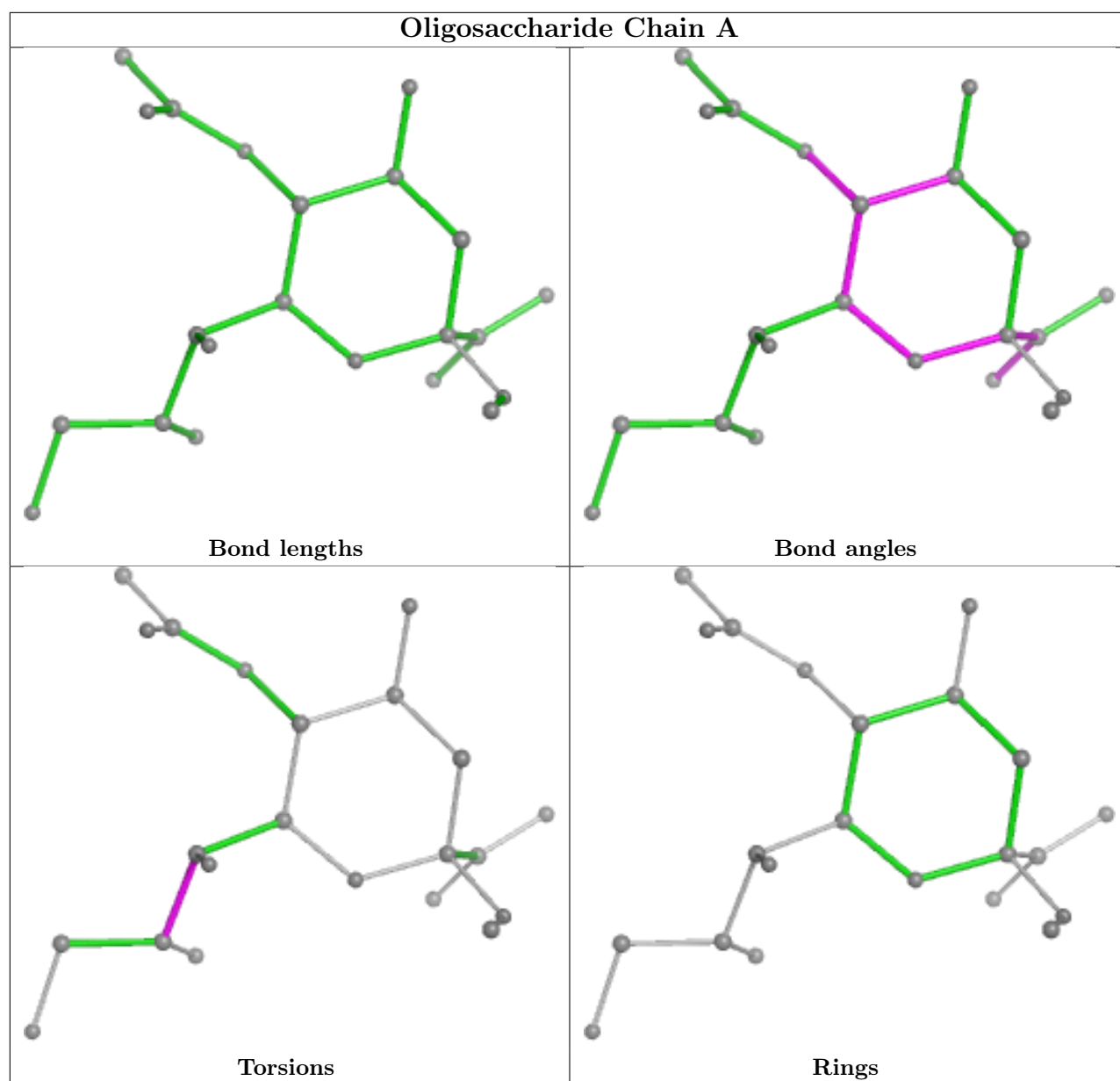
Mol	Chain	Res	Type	Atoms
3	A	2	SIA	C6-C7-C8-C9
3	A	2	SIA	O7-C7-C8-O8
3	A	2	SIA	C6-C7-C8-O8
3	A	2	SIA	O7-C7-C8-C9

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2	SIA	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 5.6 Ligand geometry [i](#)

2 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
4	NAG	F	411	1	14,14,15	0.42	0	17,19,21	0.81	0
4	NAG	F	421	1	14,14,15	0.43	0	17,19,21	1.09	1 (5%)

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	F	411	1	-	2/6/23/26	0/1/1/1
4	NAG	F	421	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(°)
4	F	421	NAG	O5-C1-C2	-2.02	108.10	111.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	411	NAG	O5-C5-C6-O6
4	F	411	NAG	C4-C5-C6-O6
4	F	421	NAG	C4-C5-C6-O6
4	F	421	NAG	O5-C5-C6-O6

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	E	321/326 (98%)	0.55	18 (5%) 31 29	26, 61, 80, 87	0
2	F	158/166 (95%)	0.11	5 (3%) 50 47	21, 41, 64, 85	0
All	All	479/492 (97%)	0.41	23 (4%) 36 34	21, 55, 79, 87	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	173	GLN	3.6
1	E	196	GLN	3.4
1	E	240	ASN	3.1
1	E	325	PRO	3.1
1	E	195	TYR	3.0
2	F	158	ASP	3.0
2	F	128	ASP	3.0
1	E	305	GLU	2.8
2	F	39	GLU	2.8
1	E	154	LEU	2.8
2	F	150	GLU	2.8
1	E	160	THR	2.7
1	E	278	CYS	2.5
1	E	165	LYS	2.5
1	E	306	CYS	2.4
1	E	92	ASP	2.3
1	E	75	ILE	2.2
1	E	171	THR	2.1
1	E	133	LEU	2.1
1	E	261	VAL	2.1
1	E	264	GLY	2.1
2	F	60	ASN	2.1
1	E	158	ASN	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](#)

SUGAR-RSR INFOmissingINFO

## 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( $\text{\AA}^2$ )	Q<0.9
4	NAG	F	421	14/15	0.67	0.18	88,89,91,91	0
4	NAG	F	411	14/15	0.82	0.12	84,85,85,86	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.