



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 01:07 pm GMT

PDB ID : 4ASR  
Title : Crystal structure of ANCE in complex with Thr6-Bradykinin  
Authors : Akif, M.; Masuyer, G.; Sturrock, E.D.; Isaac, R.E.; Acharya, K.R.  
Deposited on : 2012-05-02  
Resolution : 1.90 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>.

---

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 : 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

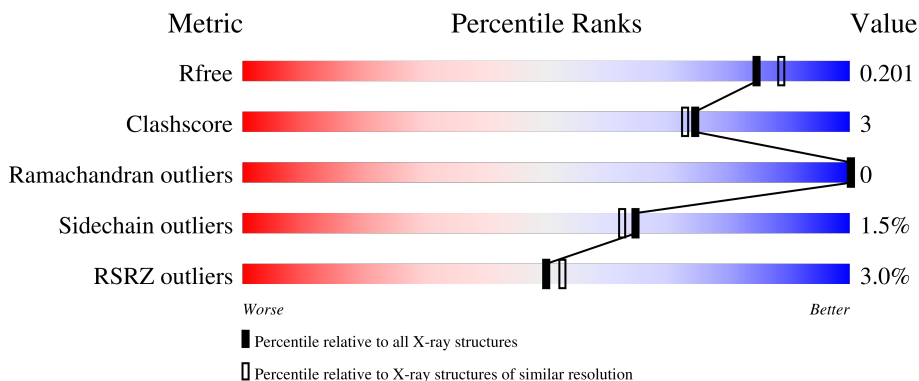
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	598	 3% 91% 9%
2	P	9	 33% 11% 56%
3	B	6	 67% 33%

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
3	MAN	B	6	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5600 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 ANGIOTENSIN-CONVERTING ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	598	4887	3127	807	933	20	0	2	0

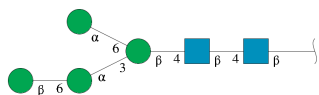
- Molecule 2 is a protein called BRADYKININ.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	P	4	26	16	7	3	0	0	1

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	6	THR	SER	engineered mutation	UNP ?

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	B	6	72	40	2	30	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

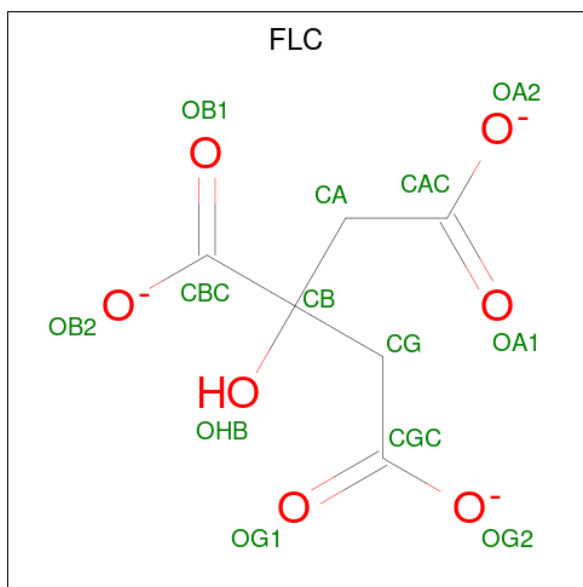
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- 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	14	8	1	5	0	0
5	A	1	14	8	1	5	0	0

- Molecule 6 is CITRATE ANION (three-letter code: FLC) (formula:  $C_6H_5O_7$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	6	7		

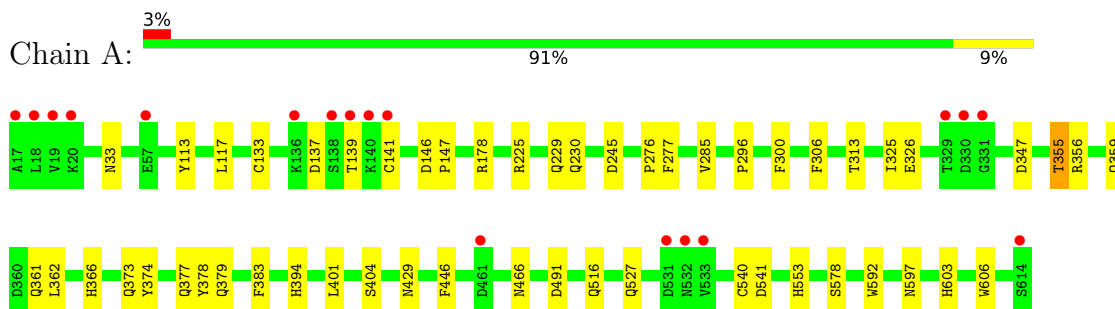
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	572	Total	O	0	0
			572	572		
7	P	1	Total	O	0	0
			1	1		

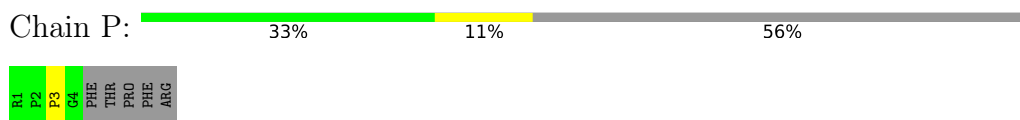
### 3 Residue-property plots [i](#)

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.

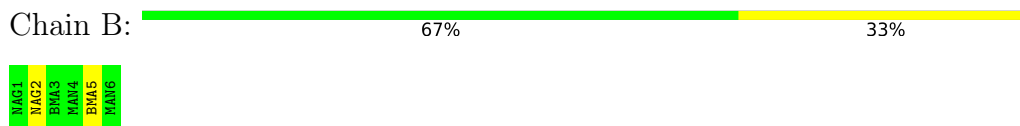
- Molecule 1: ANGIOTENSIN-CONVERTING ENZYME



- Molecule 2: BRADYKININ



- Molecule 3: beta-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.29Å 173.29Å 101.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	86.65 – 1.90 32.60 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.2 (86.65-1.90) 84.6 (32.60-1.90)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.54 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.183 , 0.200 0.183 , 0.201	Depositor DCC
$R_{free}$ test set	3821 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.5	Xtriage
Anisotropy	0.852	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 48.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.009 for $-2/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+4/3^*l,-1/3^*h+1/3^*k+1/3^*l$ 0.007 for $-h,1/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+1/3^*l$ 0.007 for $-1/3^*h+1/3^*k+4/3^*l,-k,2/3^*h+1/3^*k+1/3^*l$ 0.008 for $-h,2/3^*h+1/3^*k+4/3^*l,1/3^*h+2/3^*k-1/3^*l$ 0.013 for $-1/3^*h-2/3^*k+4/3^*l,-2/3^*h-1/3^*k-4/3^*l,1/3^*h-1/3^*k-1/3^*l$ 0.011 for $1/3^*h+2/3^*k-4/3^*l,-k,-2/3^*h-1/3^*k-1/3^*l$ 0.016 for $h,-h-k,-l$	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5600	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: MAN, NAG, FLC, BMA, ZN

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	0.34	0/5019	0.45	0/6800
2	P	1.06	1/27 (3.7%)	0.90	0/37
All	All	0.35	1/5046 (0.0%)	0.46	0/6837

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	3	PRO	C-N	-5.09	1.23	1.33

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	4887	0	4688	31	0
2	P	26	0	29	0	0
3	B	72	0	61	0	0
4	A	1	0	0	0	0
5	A	28	0	26	0	0
6	A	13	0	5	0	0
7	A	572	0	0	1	0
7	P	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5600	0	4809	31	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 3.

All (31) 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:A:325:ILE:O	1:A:355:THR:HG23	1.76	0.85
1:A:277:PHE:H	1:A:429:ASN:HD21	1.29	0.78
1:A:377:GLN:HE22	1:A:553:HIS:HD2	1.31	0.75
1:A:285:VAL:H	1:A:359:GLN:HE21	1.46	0.63
1:A:313:THR:H	1:A:373:GLN:HE22	1.46	0.62
1:A:377:GLN:HE22	1:A:553:HIS:CD2	2.19	0.57
1:A:516:GLN:NE2	1:A:578:SER:H	2.05	0.55
1:A:347:ASP:H	1:A:379:GLN:HE22	1.53	0.55
1:A:300:PHE:HE1	1:A:355:THR:HG21	1.71	0.54
1:A:276:PRO:HB3	1:A:592:TRP:CH2	2.43	0.53
1:A:466:ASN:ND2	1:A:491:ASP:H	2.06	0.52
1:A:147:PRO:HB3	1:A:356:ARG:HD3	1.91	0.52
1:A:133:CYS:HA	1:A:141:CYS:HA	1.91	0.52
1:A:33:ASN:HD22	1:A:383:PHE:HB3	1.79	0.48
1:A:285:VAL:H	1:A:359:GLN:NE2	2.12	0.46
1:A:296:PRO:HG2	1:A:326:GLU:HG2	1.98	0.45
1:A:230:GLN:NE2	1:A:597:ASN:HD22	2.15	0.45
1:A:306:PHE:CD1	1:A:401:LEU:HD13	2.52	0.45
1:A:466:ASN:HD21	1:A:491:ASP:H	1.66	0.44
1:A:404:SER:HB2	1:A:541:ASP:HA	2.00	0.43
1:A:527:GLN:HE21	1:A:541:ASP:H	1.67	0.43
1:A:362:LEU:O	1:A:366:HIS:HD2	2.02	0.43
1:A:146:ASP:HA	1:A:147:PRO:HA	1.77	0.43
1:A:137:ASP:OD1	1:A:139:THR:HG22	2.19	0.42
1:A:285:VAL:HG22	1:A:359:GLN:HE21	1.84	0.42
1:A:527:GLN:NE2	1:A:541:ASP:H	2.18	0.42
1:A:229:GLN:HE22	1:A:606:TRP:HH2	1.68	0.41
1:A:355:THR:HA	1:A:361:GLN:OE1	2.20	0.41
1:A:113:TYR:CE2	1:A:117:LEU:HD11	2.54	0.41
1:A:603:HIS:HE1	7:A:2318:HOH:O	2.04	0.41
1:A:225:ARG:O	1:A:229:GLN:HG2	2.20	0.40

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	598/598 (100%)	592 (99%)	6 (1%)	0	100	100
2	P	2/9 (22%)	2 (100%)	0	0	100	100
All	All	600/607 (99%)	594 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	522/520 (100%)	514 (98%)	8 (2%)	65	62
2	P	3/8 (38%)	3 (100%)	0	100	100
All	All	525/528 (99%)	517 (98%)	8 (2%)	65	62

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	178	ARG
1	A	245	ASP
1	A	355	THR
1	A	374	TYR
1	A	378	TYR
1	A	394	HIS
1	A	446	PHE
1	A	540	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	229	GLN
1	A	230	GLN
1	A	359	GLN
1	A	366	HIS
1	A	373	GLN
1	A	377	GLN
1	A	379	GLN
1	A	380	HIS
1	A	381	GLN
1	A	429	ASN
1	A	466	ASN
1	A	516	GLN
1	A	527	GLN
1	A	553	HIS
1	A	601	ASN
1	A	603	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](#)

6 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	NAG	B	1	3,1	14,14,15	0.49	0	17,19,21	0.59	0
3	NAG	B	2	3	14,14,15	0.49	0	17,19,21	1.25	2 (11%)
3	BMA	B	3	3	11,11,12	0.62	0	15,15,17	0.86	0
3	MAN	B	4	3	11,11,12	0.61	0	15,15,17	0.70	0
3	BMA	B	5	3	11,11,12	0.56	0	15,15,17	1.21	2 (13%)
3	MAN	B	6	3	11,11,12	0.62	0	15,15,17	0.86	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	B	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	B	2	3	-	3/6/23/26	0/1/1/1
3	BMA	B	3	3	-	1/2/19/22	0/1/1/1
3	MAN	B	4	3	-	2/2/19/22	0/1/1/1
3	BMA	B	5	3	-	2/2/19/22	0/1/1/1
3	MAN	B	6	3	-	0/2/19/22	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	5	BMA	C1-O5-C5	3.51	116.95	112.19
3	B	2	NAG	C2-N2-C7	3.19	127.45	122.90
3	B	2	NAG	C1-O5-C5	2.24	115.23	112.19
3	B	5	BMA	C1-C2-C3	2.03	112.16	109.67

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	4	MAN	C4-C5-C6-O6
3	B	4	MAN	O5-C5-C6-O6
3	B	5	BMA	O5-C5-C6-O6
3	B	2	NAG	C4-C5-C6-O6
3	B	5	BMA	C4-C5-C6-O6
3	B	2	NAG	O5-C5-C6-O6
3	B	2	NAG	C3-C2-N2-C7

*Continued on next page...*

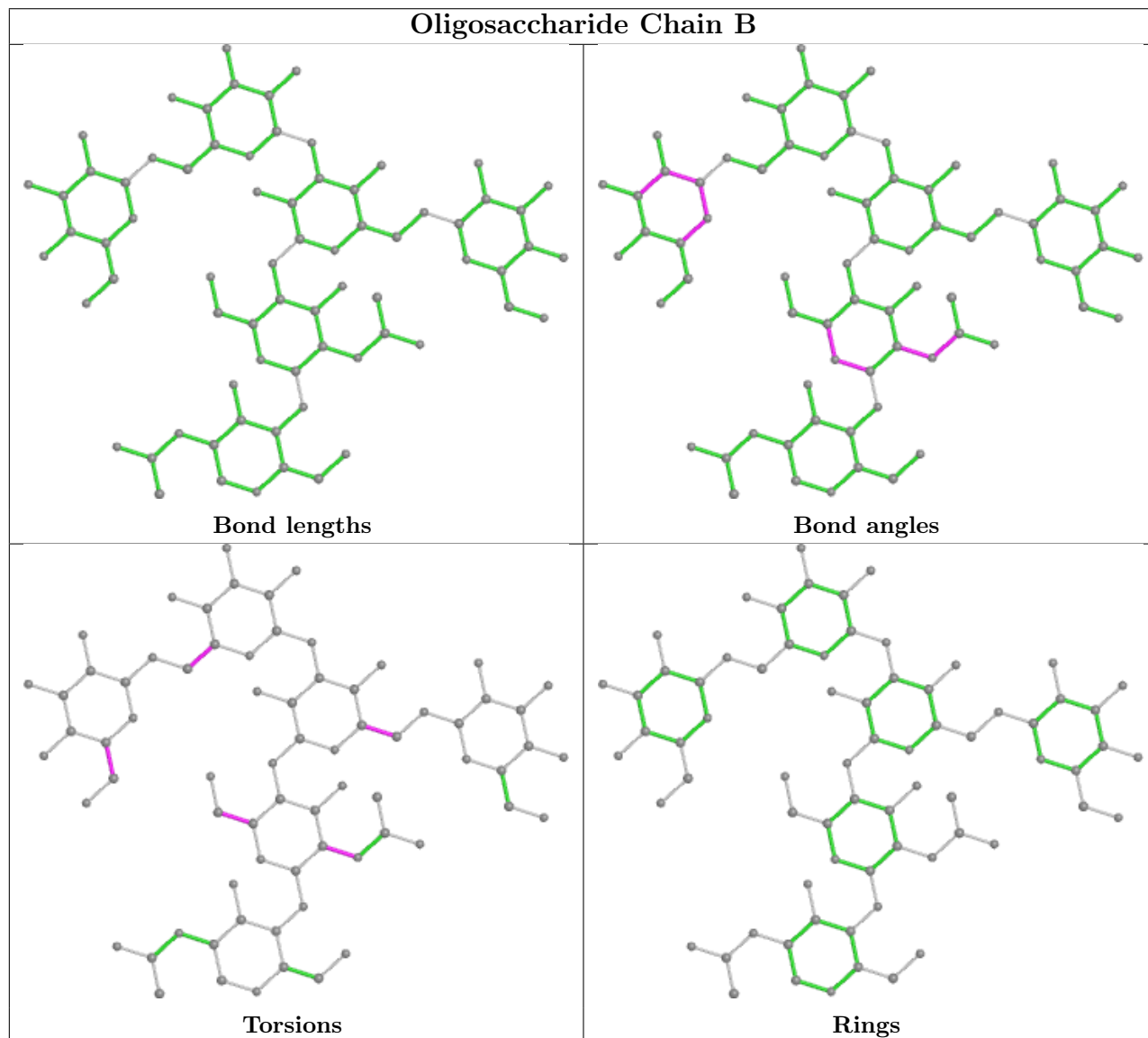
Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	3	BMA	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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
6	FLC	A	1624	-	12,12,12	1.00	0	17,17,17	1.30	2 (11%)
5	NAG	A	1623	-	14,14,15	0.51	0	17,19,21	0.86	0
5	NAG	A	1622	-	14,14,15	0.57	0	17,19,21	0.62	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
6	FLC	A	1624	-	-	13/16/16/16	-
5	NAG	A	1623	-	-	0/6/23/26	0/1/1/1
5	NAG	A	1622	-	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1624	FLC	OB2-CBC-CB	3.36	118.89	113.05
6	A	1624	FLC	OB1-CBC-CB	-2.06	119.34	122.25

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1624	FLC	CG-CB-CBC-OB1
6	A	1624	FLC	CG-CB-CBC-OB2
6	A	1624	FLC	OHB-CB-CBC-OB1
6	A	1624	FLC	OHB-CB-CBC-OB2
6	A	1624	FLC	CA-CB-CG-CGC
6	A	1624	FLC	CBC-CB-CG-CGC
6	A	1624	FLC	OHB-CB-CG-CGC
5	A	1622	NAG	O5-C5-C6-O6
6	A	1624	FLC	CAC-CA-CB-CBC
6	A	1624	FLC	CAC-CA-CB-CG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
5	A	1622	NAG	C4-C5-C6-O6
6	A	1624	FLC	CB-CA-CAC-OA2
6	A	1624	FLC	CB-CA-CAC-OA1
6	A	1624	FLC	CA-CB-CBC-OB2
6	A	1624	FLC	CAC-CA-CB-OHB

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	598/598 (100%)	-0.09	18 (3%) 50 53	15, 25, 36, 43	7 (1%)
2	P	4/9 (44%)	0.55	0 100 100	24, 24, 25, 28	0
All	All	602/607 (99%)	-0.09	18 (2%) 50 53	15, 25, 36, 43	7 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	139	THR	6.0
1	A	614	SER	4.1
1	A	17	ALA	3.7
1	A	531	ASP	3.3
1	A	136	LYS	3.3
1	A	329	THR	3.2
1	A	533	VAL	3.1
1	A	331	GLY	3.1
1	A	138	SER	2.9
1	A	18	LEU	2.9
1	A	20	LYS	2.9
1	A	141	CYS	2.9
1	A	57	GLU	2.7
1	A	19	VAL	2.7
1	A	140	LYS	2.6
1	A	330	ASP	2.3
1	A	461	ASP	2.0
1	A	532	ASN	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

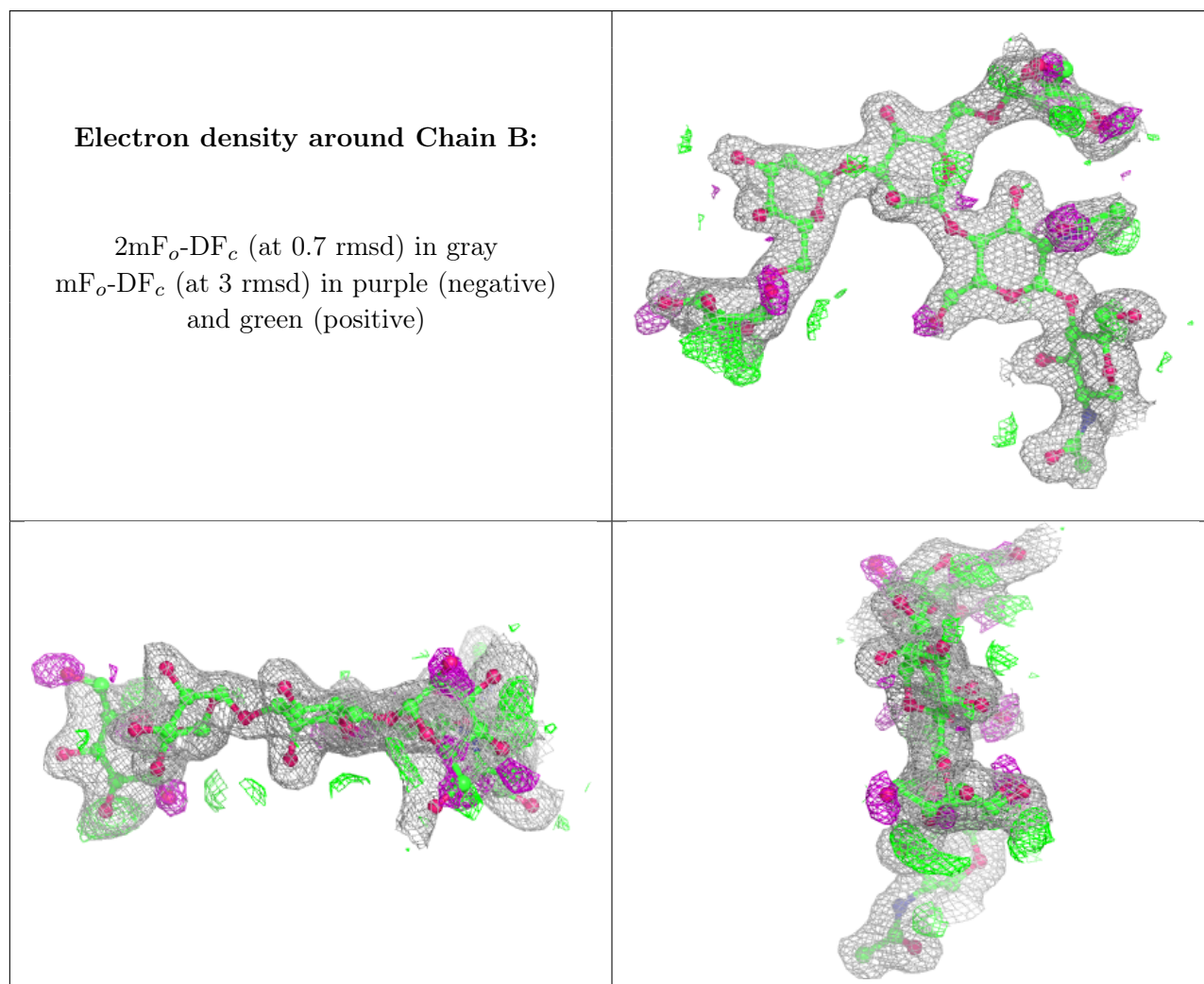
There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

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
3	MAN	B	6	11/12	0.69	0.41	50,51,52,52	0
3	BMA	B	5	11/12	0.78	0.24	50,51,51,52	0
3	MAN	B	4	11/12	0.86	0.21	45,46,48,49	0
3	BMA	B	3	11/12	0.90	0.24	40,43,45,48	0
3	NAG	B	2	14/15	0.91	0.15	29,32,34,36	0
3	NAG	B	1	14/15	0.97	0.07	20,22,23,26	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



## 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
6	FLC	A	1624	13/13	0.61	0.27	54,55,56,56	0
5	NAG	A	1622	14/15	0.65	0.38	24,26,27,27	14
5	NAG	A	1623	14/15	0.76	0.40	30,32,33,33	14
4	ZN	A	1615	1/1	0.99	0.07	21,21,21,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.