



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:49 AM UTC

PDB ID : 1FFQ / pdb_00001ffq
Title : CRYSTAL STRUCTURE OF CHITINASE A COMPLEXED WITH AL-
LOSAMIDIN
Authors : Papanikolau, Y.; Tavlas, G.; Vorgias, C.E.; Petratos, K.
Deposited on : 2000-07-26
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

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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

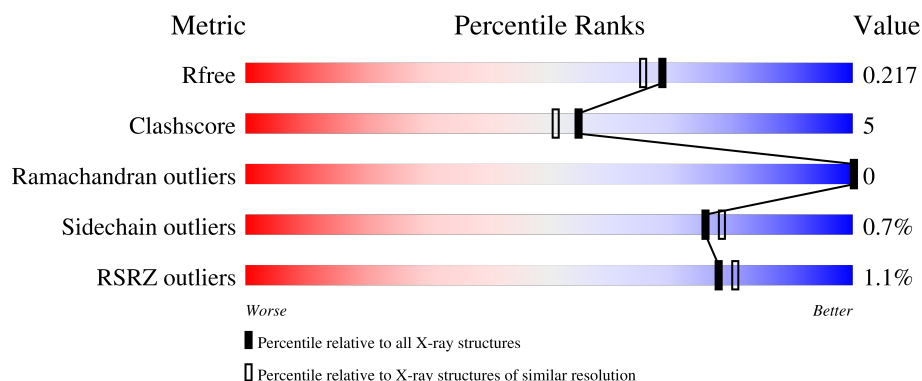
1 Overall quality at a glance

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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (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 ≥ 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	540	83% 16% .
2	B	2	100%

2 Entry composition [i](#)

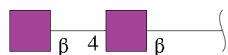
There are 4 unique types of molecules in this entry. The entry contains 4873 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CHITINASE A.

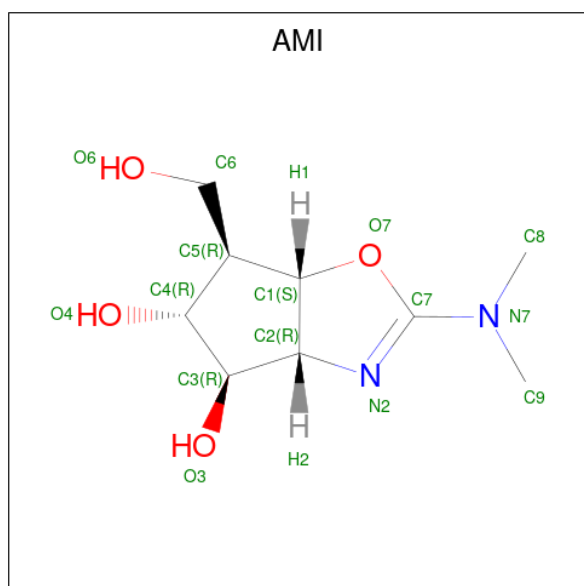
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	540	4170	2656	700	799	15	0	9	0

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-allopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-allopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0

- Molecule 3 is ALLOSAMIZOLINE (CCD ID: AMI) (formula: C₉H₁₆N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	9	2	4		

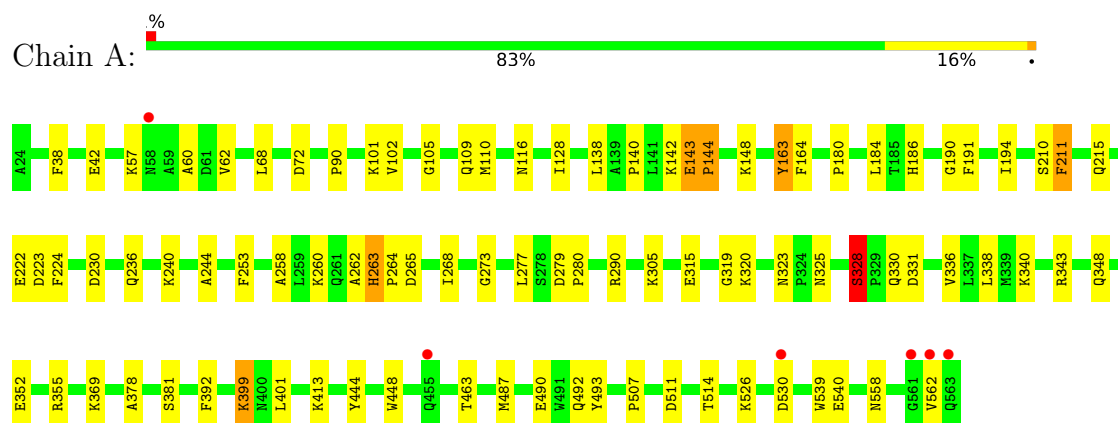
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	660	Total	O	0	0
			660	660		

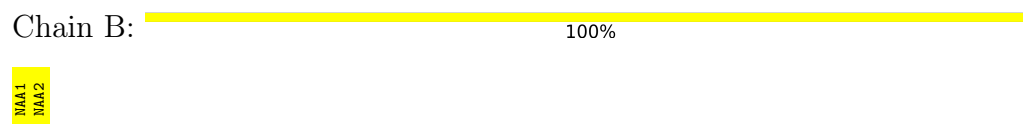
3 Residue-property plots

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: CHITINASE A



• Molecule 2: 2-acetamido-2-deoxy-beta-D-allopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-allopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	199.12Å 131.82Å 59.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.90 10.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.6 (10.00-1.90) 97.8 (10.00-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.02 (at 1.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.189 , 0.232 0.179 , 0.217	Depositor DCC
R_{free} test set	3145 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4873	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: AMI, NAA

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	0.80	1/4313 (0.0%)	1.62	51/5851 (0.9%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	HIS	CE1-NE2	5.75	1.38	1.32

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	265	ASP	CA-CB-CG	-8.28	104.32	112.60
1	A	90	PRO	CA-C-O	-7.90	112.33	121.34
1	A	263	HIS	CA-C-N	6.72	126.42	119.56
1	A	263	HIS	C-N-CA	6.72	126.42	119.56
1	A	143	GLU	CA-C-N	6.46	126.41	119.76
1	A	143	GLU	C-N-CA	6.46	126.41	119.76
1	A	338	LEU	CA-C-O	6.36	127.50	120.82
1	A	338	LEU	O-C-N	-6.31	115.57	122.07
1	A	72	ASP	CA-C-O	-6.28	113.89	121.05
1	A	211	PHE	CA-C-O	6.26	127.18	120.55
1	A	140	PRO	N-CA-CB	6.15	108.80	103.27
1	A	105	GLY	O-C-N	-6.11	115.40	122.91
1	A	163	TYR	CA-C-O	-6.07	114.28	120.71
1	A	279	ASP	CA-CB-CG	5.99	118.59	112.60
1	A	144	PRO	N-CA-CB	5.98	108.63	103.31
1	A	164	PHE	CA-CB-CG	5.83	119.62	113.80
1	A	264	PRO	N-CA-CB	5.66	109.14	103.48
1	A	331	ASP	O-C-N	-5.64	116.14	122.12
1	A	68	LEU	O-C-N	5.63	130.22	123.13
1	A	325	ASN	CA-C-O	5.62	125.56	119.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	562	VAL	CA-C-O	-5.54	115.40	121.28
1	A	180	PRO	N-CA-CB	5.54	106.28	102.35
1	A	109	GLN	OE1-CD-NE2	-5.47	117.13	122.60
1	A	230	ASP	CA-C-N	5.47	125.29	119.28
1	A	230	ASP	C-N-CA	5.47	125.29	119.28
1	A	558	ASN	OD1-CG-ND2	-5.42	117.17	122.60
1	A	413	LYS	CA-C-N	5.38	125.00	119.56
1	A	413	LYS	C-N-CA	5.38	125.00	119.56
1	A	116	ASN	OD1-CG-ND2	-5.29	117.31	122.60
1	A	253	PHE	CA-CB-CG	5.28	119.08	113.80
1	A	323	ASN	CA-C-N	5.26	125.72	120.04
1	A	323	ASN	C-N-CA	5.26	125.72	120.04
1	A	369	LYS	CA-C-N	5.26	127.38	120.60
1	A	369	LYS	C-N-CA	5.26	127.38	120.60
1	A	102	VAL	CA-C-N	-5.22	114.30	122.65
1	A	102	VAL	C-N-CA	-5.22	114.30	122.65
1	A	290	ARG	NE-CZ-NH2	5.21	123.89	119.20
1	A	392	PHE	CA-C-N	5.18	130.60	122.21
1	A	392	PHE	C-N-CA	5.18	130.60	122.21
1	A	444	TYR	CA-C-N	-5.17	116.11	122.15
1	A	444	TYR	C-N-CA	-5.17	116.11	122.15
1	A	315	GLU	CA-C-N	5.13	130.94	121.70
1	A	315	GLU	C-N-CA	5.13	130.94	121.70
1	A	184	LEU	CA-C-O	-5.11	115.13	121.11
1	A	355	ARG	CD-NE-CZ	-5.11	117.25	124.40
1	A	210	SER	N-CA-C	5.10	116.64	111.14
1	A	211	PHE	O-C-N	-5.10	116.72	122.12
1	A	60	ALA	O-C-N	5.09	129.02	123.01
1	A	244	ALA	O-C-N	-5.07	116.70	122.89
1	A	511	ASP	CA-CB-CG	5.03	117.63	112.60
1	A	328	SER	CA-C-O	5.02	125.12	120.50

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	4170	0	4052	40	0
2	B	28	0	25	0	0
3	A	15	0	15	2	0
4	A	660	0	0	9	0
All	All	4873	0	4092	40	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 5.

All (40) 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:487:MET:HE2	1:A:493[B]:TYR:CE2	1.33	1.56
1:A:487:MET:CE	1:A:493[B]:TYR:HE2	1.38	1.36
1:A:260[B]:LYS:HG2	1:A:268:ILE:HD12	1.61	0.81
1:A:142:LYS:HE2	1:A:262:ALA:HB1	1.77	0.67
1:A:42:GLU:OE2	1:A:57:LYS:HD2	1.97	0.65
1:A:487:MET:CE	1:A:493[B]:TYR:CE2	2.30	0.63
1:A:143:GLU:OE1	1:A:240:LYS:NZ	2.31	0.57
1:A:348:GLN:O	1:A:352:GLU:HG3	2.06	0.55
1:A:163:TYR:CZ	3:A:3:AMI:H81	2.43	0.53
1:A:492:GLN:HG2	4:A:1155:HOH:O	2.08	0.53
1:A:263:HIS:ND1	4:A:915:HOH:O	2.34	0.51
1:A:399:LYS:HE3	1:A:463:THR:HB	1.93	0.50
1:A:148:LYS:NZ	4:A:762:HOH:O	2.45	0.50
1:A:336:VAL:HG13	4:A:989:HOH:O	2.11	0.50
1:A:222:GLU:HG3	4:A:853:HOH:O	2.14	0.47
1:A:539:TRP:HA	1:A:540:GLU:HA	1.77	0.47
1:A:526:LYS:NZ	1:A:530:ASP:OD2	2.48	0.46
1:A:328:SER:HB2	4:A:979:HOH:O	2.15	0.46
1:A:138:LEU:HD13	1:A:258:ALA:HB2	1.98	0.46
1:A:343:ARG:HD2	1:A:381:SER:O	2.16	0.45
1:A:163:TYR:CE2	3:A:3:AMI:H81	2.52	0.45
1:A:101:LYS:NZ	4:A:681:HOH:O	2.48	0.44
1:A:305:LYS:HE3	4:A:728:HOH:O	2.17	0.44
1:A:490:GLU:OE2	1:A:507:PRO:HD2	2.17	0.44
1:A:336:VAL:HG22	1:A:378:ALA:HB2	2.00	0.44
1:A:110[A]:MET:HE2	1:A:128:ILE:CG2	2.48	0.43
1:A:223:ASP:O	1:A:224:PHE:HB2	2.19	0.43
1:A:38:PHE:CG	1:A:62:VAL:HG22	2.54	0.42
1:A:143:GLU:HB3	1:A:144:PRO:HD2	2.02	0.42
1:A:319:GLY:O	1:A:320:LYS:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:SER:OG	1:A:330:GLN:HB3	2.20	0.42
1:A:340:LYS:HG3	4:A:989:HOH:O	2.20	0.41
1:A:401:LEU:HD22	1:A:448:TRP:CE2	2.55	0.41
1:A:211:PHE:O	1:A:215:GLN:HG2	2.20	0.41
1:A:190:GLY:HA2	1:A:191:PHE:HA	1.69	0.41
1:A:194:ILE:HB	1:A:280:PRO:HG2	2.03	0.41
1:A:273:GLY:HA2	1:A:277:LEU:O	2.21	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	547/540 (101%)	531 (97%)	16 (3%)	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	439/430 (102%)	436 (99%)	3 (1%)	76	78

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	328	SER
1	A	399	LYS
1	A	514	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	109	GLN
1	A	201	ASN
1	A	263	HIS
1	A	330	GLN
1	A	481	GLN
1	A	492	GLN

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	$\# Z > 2$
2	NAA	B	1	2,3	14,14,15	1.82	2 (14%)	17,19,21	1.91	5 (29%)
2	NAA	B	2	2	14,14,15	1.30	1 (7%)	17,19,21	1.24	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
2	NAA	B	1	2,3	-	2/6/23/26	0/1/1/1
2	NAA	B	2	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAA	C1-C2	4.99	1.59	1.52
2	B	2	NAA	C1-C2	2.30	1.55	1.52
2	B	1	NAA	C3-C2	2.17	1.57	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAA	C8-C7-N2	4.45	123.50	116.12
2	B	1	NAA	O7-C7-C8	-3.49	115.83	122.05
2	B	1	NAA	C2-N2-C7	-2.98	118.90	122.90
2	B	1	NAA	O5-C1-C2	-2.49	107.44	111.29
2	B	2	NAA	C8-C7-N2	2.13	119.65	116.12
2	B	1	NAA	O4-C4-C5	-2.13	104.09	109.32

There are no chirality outliers.

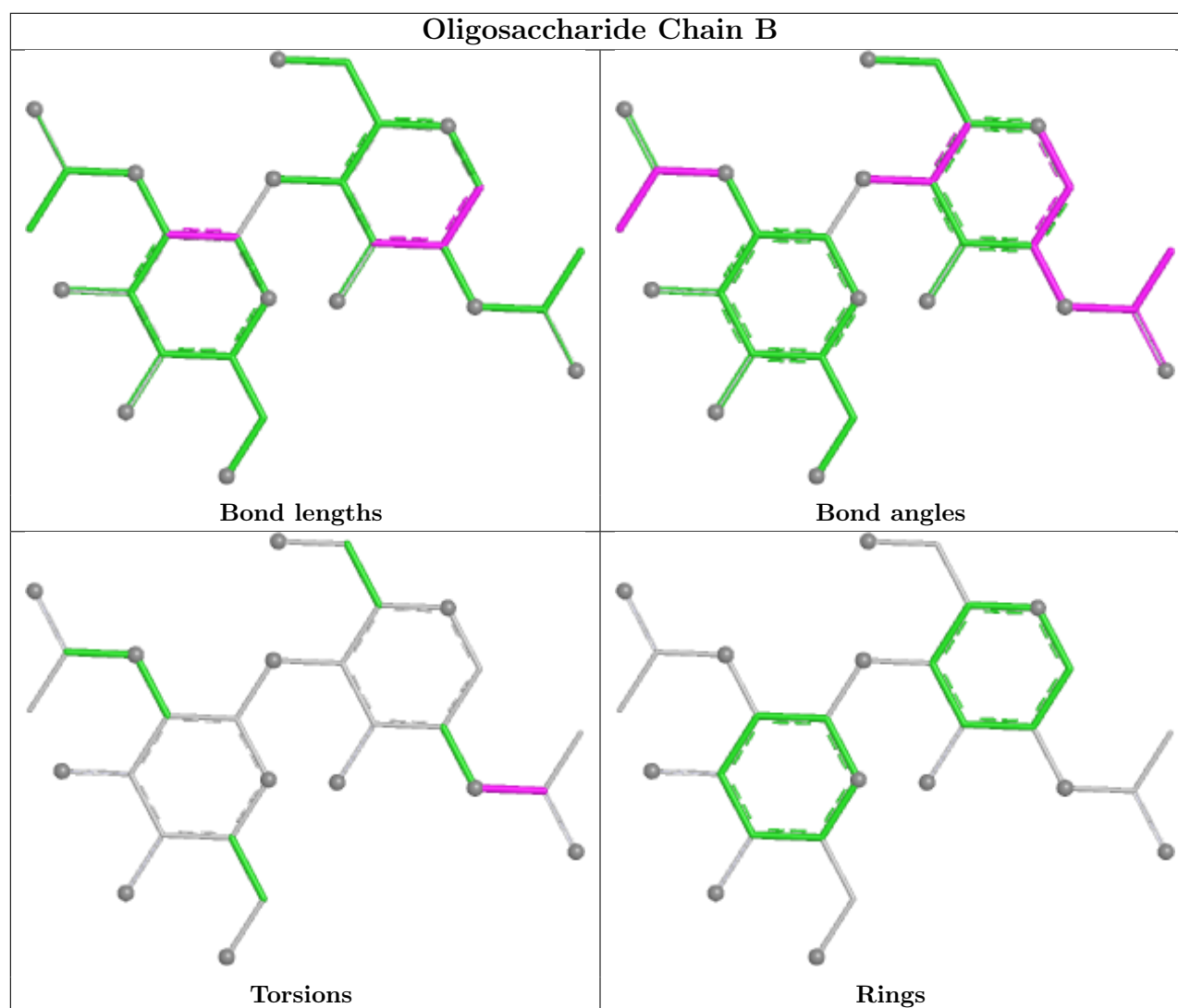
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAA	C8-C7-N2-C2
2	B	1	NAA	O7-C7-N2-C2

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](#)

1 ligand is 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	AMI	A	3	2	15,16,16	1.72	1 (6%)	15,24,24	4.25	4 (26%)

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	AMI	A	3	2	-	1/6/34/34	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3	AMI	C2-N2	-5.83	1.41	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3	AMI	O7-C7-N2	-14.92	110.06	117.78
3	A	3	AMI	C5-C4-C3	-4.93	97.80	103.86
3	A	3	AMI	O7-C1-C2	-2.36	100.78	104.12
3	A	3	AMI	O7-C1-C5	-2.21	107.92	112.31

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3	AMI	O7-C7-N7-C9

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3	AMI	2	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 [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, 95th 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 ²)	Q<0.9
1	A	540/540 (100%)	-0.23	6 (1%) 78 80	12, 25, 38, 58	9 (1%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	562	VAL	4.3
1	A	563	GLN	3.7
1	A	455	GLN	3.2
1	A	561	GLY	3.0
1	A	58	ASN	2.4
1	A	530	ASP	2.4

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

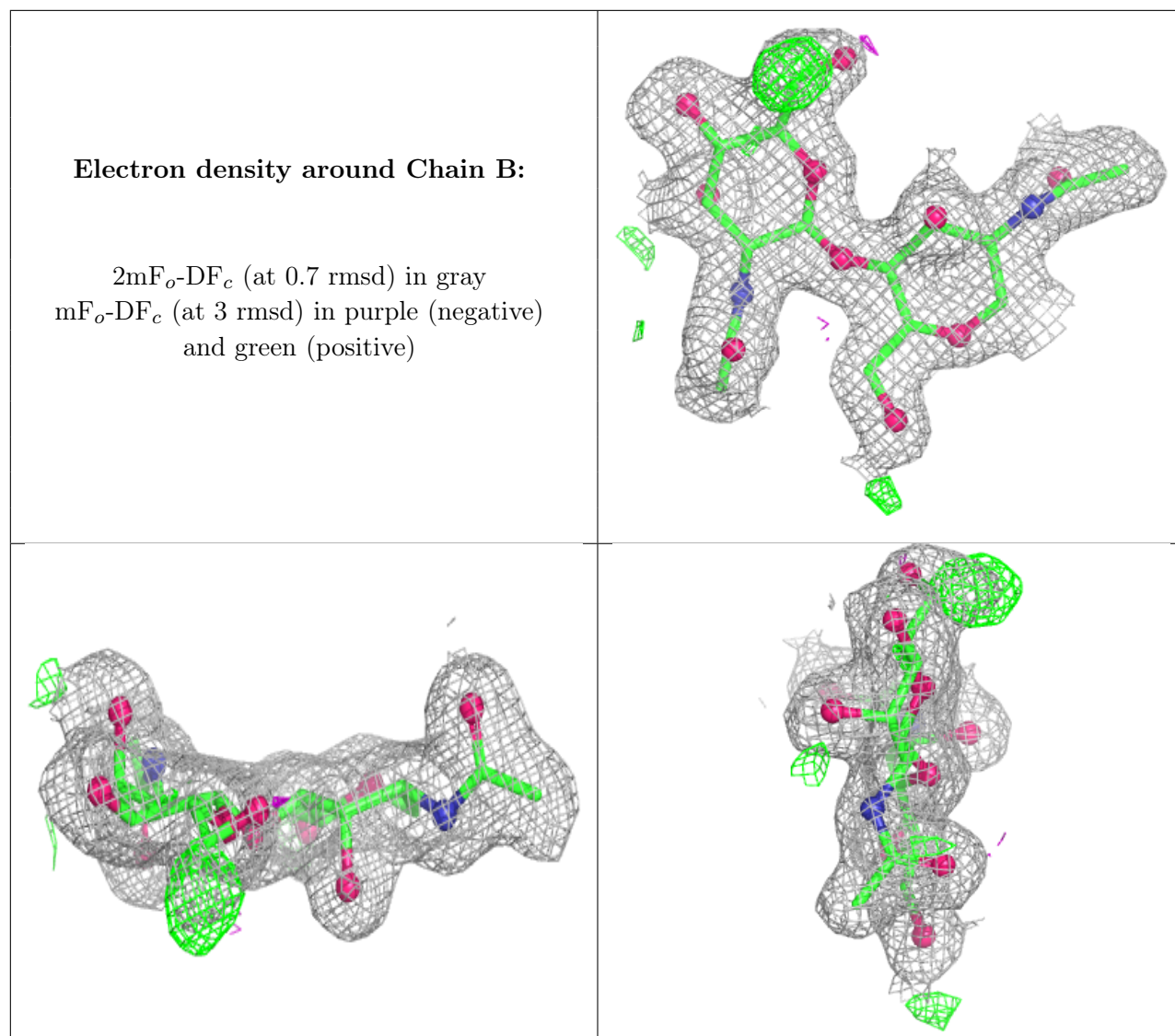
There are no non-standard protein/DNA/RNA residues in this entry.

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, 95th 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 ²)	Q<0.9
2	NAA	B	2	14/15	0.93	0.06	20,21,26,32	0
2	NAA	B	1	14/15	0.98	0.03	17,19,22,23	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, 95th 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 ²)	Q<0.9
3	AMI	A	3	15/15	0.97	0.05	15,18,21,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.