



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 07:37 PM EDT

PDB ID : 3OM0
Title : Crystal structure of the GluK5 (KA2) ATD crystallographic dimer at 1.4 Angstrom resolution
Authors : Kumar, J.; Mayer, M.L.
Deposited on : 2010-08-26
Resolution : 1.40 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

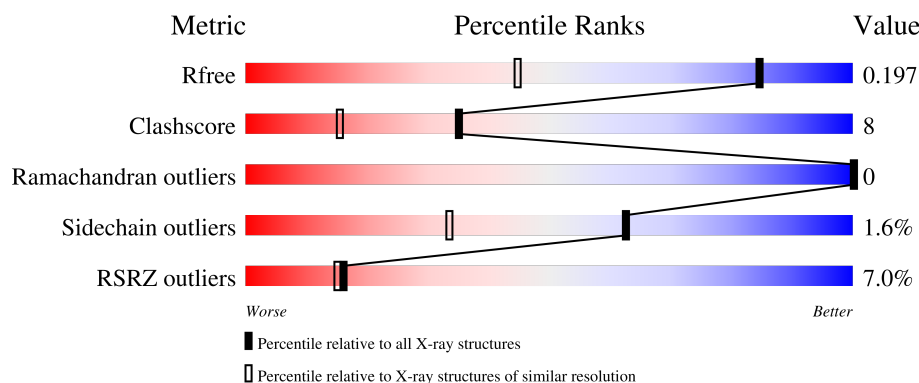
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


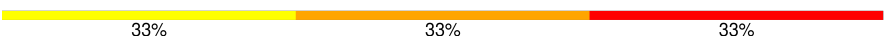
The reported resolution of this entry is 1.40 Å.

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	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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	393	
2	B	3	

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
2	BMA	B	3	X	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6771 atoms, of which 3189 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.

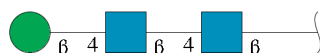
- Molecule 1 is a protein called Glutamate receptor, ionotropic kainate 5.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	369	6106	1914	3077	522	575	18	0	31	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	388	LEU	-	expression tag	UNP Q63273
A	389	GLU	-	expression tag	UNP Q63273
A	390	LEU	-	expression tag	UNP Q63273
A	391	VAL	-	expression tag	UNP Q63273
A	392	PRO	-	expression tag	UNP Q63273
A	393	ARG	-	expression tag	UNP Q63273

- Molecule 2 is an oligosaccharide called 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	H	N	O				
2	B	3	71	22	33	2	14		0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



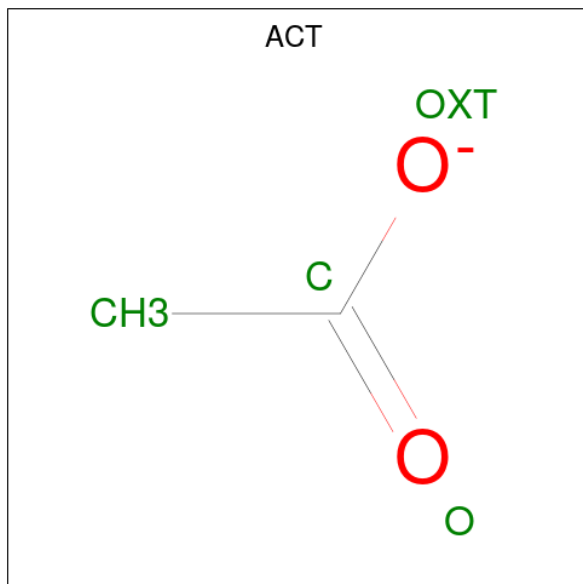
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			7	2	3	2		

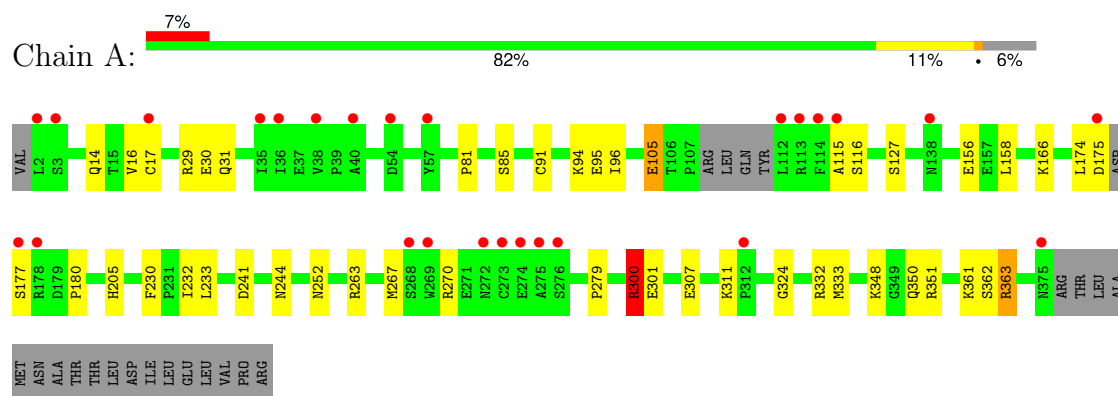
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	434	Total	O	0	16
			437	437		

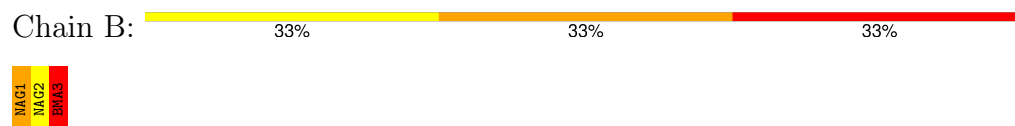
3 Residue-property plots [i](#)

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: Glutamate receptor, ionotropic kainate 5



- Molecule 2: 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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	66.31Å 101.99Å 116.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.89 – 1.40 31.88 – 1.40	Depositor EDS
% Data completeness (in resolution range)	98.6 (31.89-1.40) 98.6 (31.88-1.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.175 , 0.196 0.174 , 0.197	Depositor DCC
R_{free} test set	3885 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 51.5	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	0.97	EDS
Total number of atoms	6771	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, BMA, ACT

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	0.67	0/3189	0.78	5/4316 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	300[A]	ARG	NE-CZ-NH2	-7.86	116.37	120.30
1	A	300[B]	ARG	NE-CZ-NH2	-7.86	116.37	120.30
1	A	300[A]	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	A	300[B]	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	A	351	ARG	NE-CZ-NH1	5.54	123.07	120.30

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	3029	3077	3048	50	0
2	B	38	33	32	2	0
3	A	56	52	52	0	0
4	A	18	24	24	3	0
5	A	4	3	3	1	0
6	A	437	0	0	14	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3582	3189	3159	52	1

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 8.

All (52) 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:241:ASP:HA	1:A:363:ARG:HD2	1.56	0.88
1:A:363:ARG:N	1:A:363:ARG:HD3	1.99	0.76
1:A:205[B]:HIS:HB2	1:A:233:LEU:HD11	1.74	0.70
1:A:14:GLN:HB3	2:B:3:BMA:H2	1.74	0.69
1:A:115:ALA:HB1	1:A:332[A]:ARG:HH22	1.62	0.63
1:A:232[A]:ILE:HD11	6:A:793:HOH:O	2.00	0.62
1:A:333[B]:MET:HE2	6:A:414:HOH:O	2.00	0.61
1:A:333[B]:MET:CE	6:A:414:HOH:O	2.48	0.60
1:A:205[A]:HIS:HB2	1:A:233:LEU:HD11	1.83	0.60
1:A:230:PHE:CZ	1:A:361:LYS:HG2	2.37	0.59
1:A:81:PRO:HA	1:A:105:GLU:OE2	2.03	0.59
1:A:311:LYS:HB2	6:A:833:HOH:O	2.03	0.58
1:A:361:LYS:NZ	6:A:788:HOH:O	2.37	0.58
1:A:300[A]:ARG:CG	1:A:300[A]:ARG:HH11	2.21	0.54
1:A:115:ALA:HB1	1:A:332[A]:ARG:NH2	2.24	0.52
1:A:362:SER:HB2	1:A:363:ARG:HH11	1.75	0.51
1:A:174:LEU:HD21	1:A:180:PRO:HB3	1.92	0.51
1:A:174:LEU:O	1:A:177:SER:HA	2.12	0.49
1:A:94:LYS:HD3	5:A:404:ACT:OXT	2.13	0.48
1:A:332[A]:ARG:HD3	6:A:426[A]:HOH:O	2.13	0.48
1:A:29[A]:ARG:NH1	1:A:30:GLU:HG3	2.29	0.47
1:A:363:ARG:N	1:A:363:ARG:CD	2.72	0.47
1:A:332[A]:ARG:CZ	6:A:799:HOH:O	2.63	0.47
1:A:175:ASP:C	1:A:175:ASP:OD2	2.52	0.47
1:A:232[A]:ILE:HG22	1:A:279:PRO:O	2.15	0.47
1:A:362:SER:HB2	1:A:363:ARG:NH1	2.29	0.47
1:A:166:LYS:HG2	6:A:423:HOH:O	2.14	0.46
1:A:363:ARG:HD3	1:A:363:ARG:H	1.79	0.45
1:A:252:ASN:OD1	4:A:401:GOL:H31	2.17	0.45
1:A:332[A]:ARG:NH2	6:A:799:HOH:O	2.50	0.45
1:A:31:GLN:HG2	6:A:545:HOH:O	2.17	0.44
1:A:348:LYS:HE3	1:A:350:GLN:OE1	2.16	0.44
1:A:174:LEU:CD2	1:A:180:PRO:HB3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1:NAG:H82	2:B:1:NAG:C3	2.48	0.44
1:A:105:GLU:OE2	6:A:422:HOH:O	2.21	0.43
1:A:127[B]:SER:OG	1:A:158[B]:LEU:HB2	2.18	0.43
1:A:16:VAL:HG23	1:A:17:CYS:N	2.33	0.43
1:A:205[B]:HIS:HB2	1:A:233:LEU:CD1	2.47	0.42
1:A:230:PHE:CE2	1:A:361:LYS:HE2	2.54	0.42
1:A:267:MET:HA	1:A:270:ARG:HG2	2.02	0.42
4:A:402:GOL:H11	6:A:835:HOH:O	2.19	0.42
1:A:300[A]:ARG:HH11	1:A:300[A]:ARG:HG2	1.85	0.41
1:A:85[A]:SER:OG	1:A:105:GLU:HG2	2.20	0.41
1:A:232[A]:ILE:HB	1:A:279:PRO:HB2	2.01	0.41
1:A:244:ASN:HA	4:A:403:GOL:C1	2.50	0.41
1:A:307[A]:GLU:CD	1:A:307[A]:GLU:H	2.21	0.41
1:A:116:SER:HA	6:A:687:HOH:O	2.20	0.41
1:A:301:GLU:HG2	6:A:414:HOH:O	2.20	0.41
1:A:363:ARG:CD	1:A:363:ARG:H	2.34	0.41
1:A:91:CYS:HB3	1:A:96:ILE:O	2.21	0.41
1:A:95:GLU:O	1:A:324:GLY:HA3	2.20	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:794:HOH:O	6:A:806:HOH:O[5_445]	2.18	0.02

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	396/393 (101%)	387 (98%)	9 (2%)	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	355/346 (103%)	349 (98%)	6 (2%)	60 31

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	GLU
1	A	156	GLU
1	A	263	ARG
1	A	300[A]	ARG
1	A	300[B]	ARG
1	A	363	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	293	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](#)

3 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	NAG	B	1	2,1	13,13,15	1.13	1 (7%)	15,17,21	1.16	1 (6%)
2	NAG	B	2	2	14,14,15	0.65	0	17,19,21	1.14	1 (5%)
2	BMA	B	3	2	11,11,12	0.60	0	15,15,17	0.89	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
2	NAG	B	1	2,1	-	3/6/19/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	BMA	B	3	2	3/3/5/5	1/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	C1-C2	2.89	1.54	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C4-C3-C2	3.00	115.41	111.02
2	B	3	BMA	C1-C2-C3	2.31	113.01	109.64
2	B	1	NAG	O7-C7-N2	2.02	125.56	121.98

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	3	BMA	C5
2	B	3	BMA	C3
2	B	3	BMA	C2

All (6) torsion outliers are listed below:

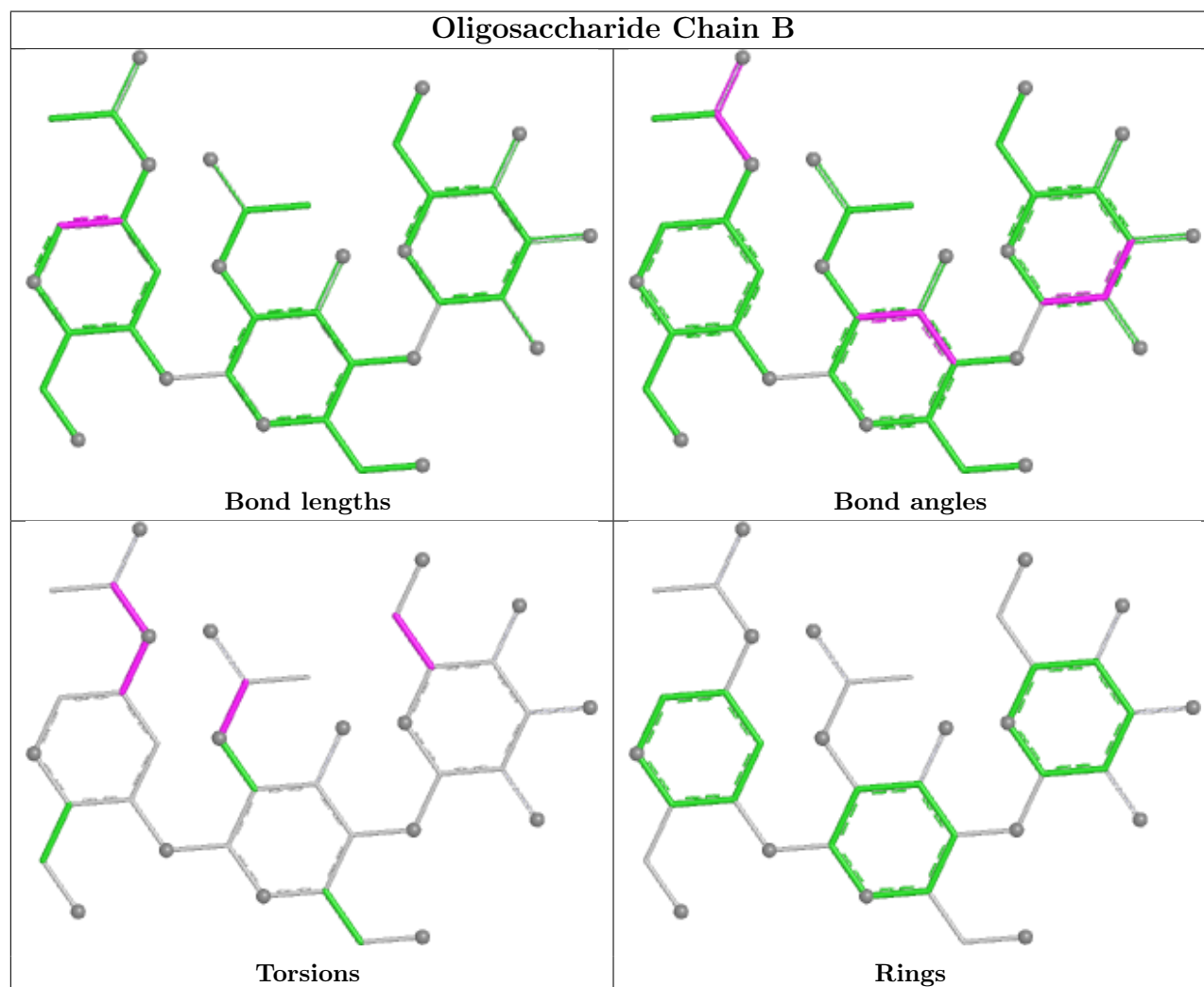
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O7-C7-N2-C2
2	B	2	NAG	C8-C7-N2-C2
2	B	1	NAG	C3-C2-N2-C7
2	B	3	BMA	O5-C5-C6-O6
2	B	2	NAG	O7-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	3	BMA	1	0
2	B	1	NAG	1	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

8 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	398	1	14,14,15	0.39	0	17,19,21	0.91	0
4	GOL	A	401	-	5,5,5	0.49	0	5,5,5	1.11	0
5	ACT	A	404	-	3,3,3	1.13	0	3,3,3	0.61	0
3	NAG	A	399	1	14,14,15	0.71	1 (7%)	17,19,21	1.97	5 (29%)
3	NAG	A	397	1	14,14,15	0.56	0	17,19,21	1.45	3 (17%)
3	NAG	A	400	1	14,14,15	0.46	0	17,19,21	1.31	4 (23%)
4	GOL	A	402	-	5,5,5	0.33	0	5,5,5	0.47	0
4	GOL	A	403	-	5,5,5	0.36	0	5,5,5	0.54	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	A	398	1	-	0/6/23/26	0/1/1/1
4	GOL	A	401	-	-	0/4/4/4	-
3	NAG	A	399	1	-	2/6/23/26	0/1/1/1
3	NAG	A	397	1	-	0/6/23/26	0/1/1/1
3	NAG	A	400	1	-	0/6/23/26	0/1/1/1
4	GOL	A	402	-	-	4/4/4/4	-
4	GOL	A	403	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	399	NAG	C1-C2	2.11	1.55	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	399	NAG	O5-C1-C2	-5.09	103.41	111.29
3	A	399	NAG	O5-C5-C6	3.42	114.33	107.66
3	A	400	NAG	C1-O5-C5	3.23	116.52	112.19
3	A	399	NAG	C1-C2-N2	2.83	114.89	110.43
3	A	397	NAG	C2-N2-C7	2.69	126.50	122.90
3	A	397	NAG	O7-C7-C8	-2.62	117.38	122.05
3	A	399	NAG	O7-C7-N2	2.44	126.29	121.98
3	A	400	NAG	O5-C5-C4	-2.25	105.35	110.83
3	A	397	NAG	O5-C5-C4	-2.14	105.62	110.83
3	A	400	NAG	C4-C3-C2	2.13	114.14	111.02
3	A	400	NAG	C2-N2-C7	-2.06	120.14	122.90
3	A	399	NAG	O7-C7-C8	-2.06	118.39	122.05

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	402	GOL	O1-C1-C2-C3
4	A	403	GOL	O1-C1-C2-O2
4	A	403	GOL	O1-C1-C2-C3
3	A	399	NAG	C4-C5-C6-O6
3	A	399	NAG	O5-C5-C6-O6
4	A	402	GOL	C1-C2-C3-O3
4	A	402	GOL	O1-C1-C2-O2
4	A	402	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	GOL	1	0
5	A	404	ACT	1	0
4	A	402	GOL	1	0
4	A	403	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	369/393 (93%)	0.08	26 (7%) 16 15	12, 22, 67, 204	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	LEU	10.6
1	A	112	LEU	9.0
1	A	177	SER	7.1
1	A	275	ALA	5.8
1	A	178	ARG	5.6
1	A	3	SER	5.4
1	A	35	ILE	5.4
1	A	175	ASP	5.2
1	A	57[A]	TYR	5.2
1	A	114	PHE	5.0
1	A	38	VAL	4.0
1	A	17	CYS	3.5
1	A	273	CYS	3.3
1	A	375	ASN	3.3
1	A	274	GLU	3.1
1	A	138	ASN	2.8
1	A	36	ILE	2.8
1	A	276	SER	2.8
1	A	115	ALA	2.8
1	A	54	ASP	2.8
1	A	312	PRO	2.6
1	A	113	ARG	2.5
1	A	272	ASN	2.5
1	A	40	ALA	2.3
1	A	269	TRP	2.2
1	A	268	SER	2.0

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

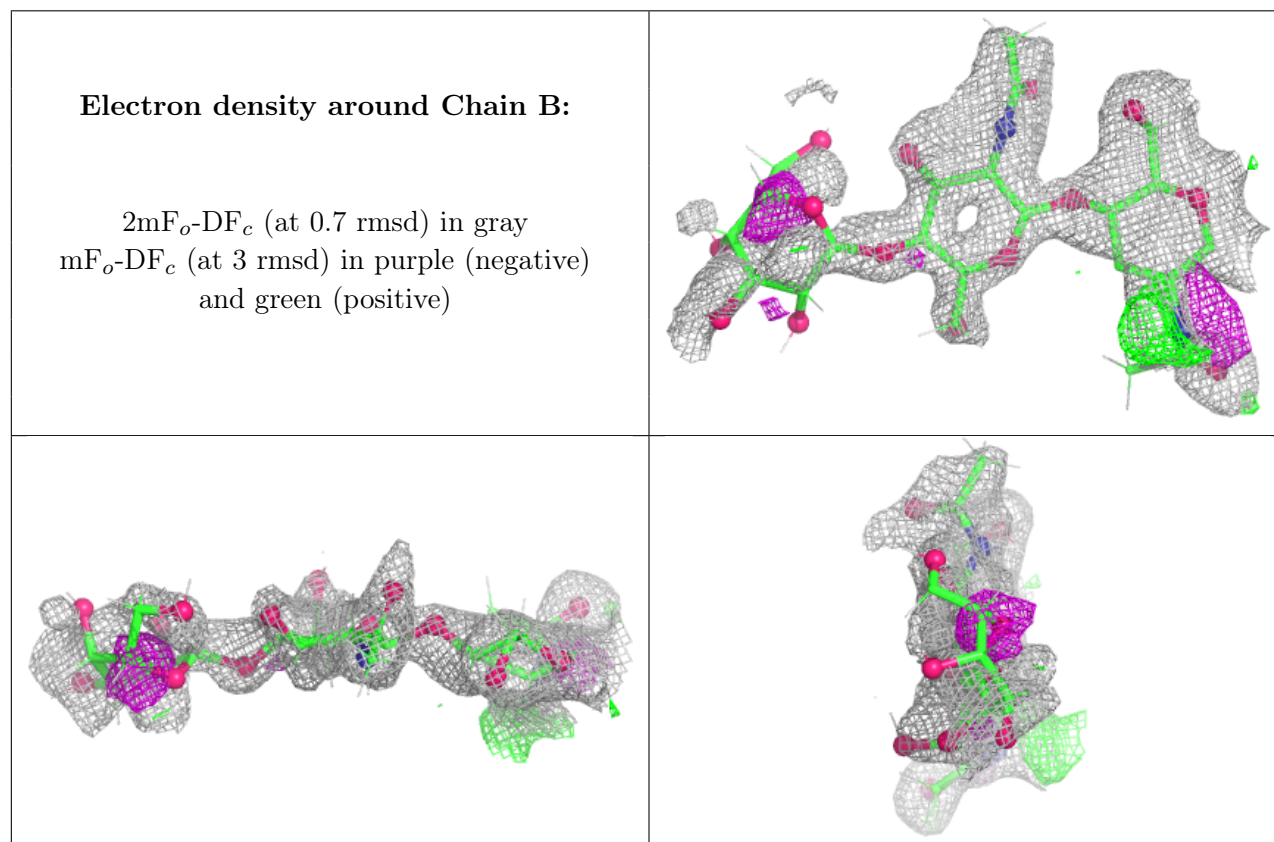
There are no non-standard protein/DNA/RNA residues in this entry.

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, 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(\AA^2)	Q<0.9
2	BMA	B	3	11/12	0.27	0.58	74,87,100,105	0
2	NAG	B	2	14/15	0.78	0.35	42,68,82,89	0
2	NAG	B	1	13/15	0.79	0.21	30,58,86,86	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
4	GOL	A	402	6/6	0.71	0.23	38,55,66,68	0
4	GOL	A	401	6/6	0.76	0.25	30,50,61,61	0
3	NAG	A	399	14/15	0.78	0.16	28,42,65,71	0
5	ACT	A	404	4/4	0.78	0.26	28,34,37,38	0
4	GOL	A	403	6/6	0.88	0.19	20,32,45,54	0
3	NAG	A	398	14/15	0.88	0.12	24,32,42,51	0
3	NAG	A	400	14/15	0.90	0.14	31,47,89,89	0
3	NAG	A	397	14/15	0.92	0.11	22,31,40,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.