



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:43 PM UTC

PDB ID : 3RAR / pdb_00003rar
Title : X-ray structure of a bound phosphonate transition state analog and enantioselectivity of *Candida rugosa* lipase toward chiral carboxylic acids
Authors : Grochulski, P.; Kazlauskas, R.
Deposited on : 2011-03-28
Resolution : 2.19 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

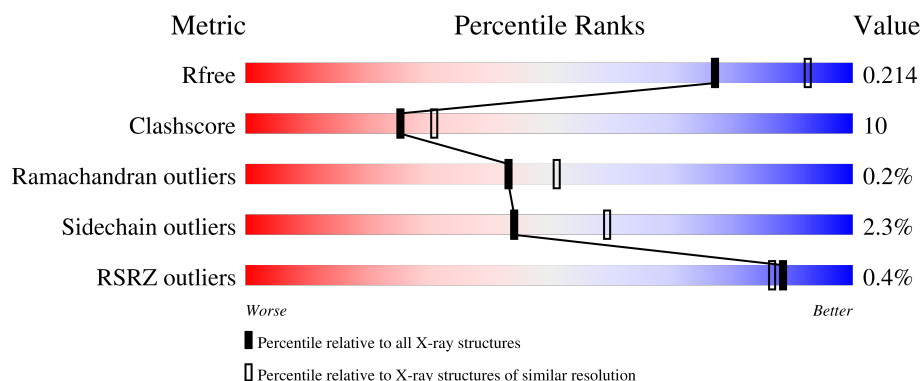
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

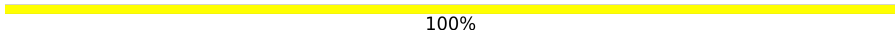
The reported resolution of this entry is 2.19 Å.

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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	534	 77% 21% .
2	B	2	 100%

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	NAG	B	1	X	-	-	-

2 Entry composition [i](#)

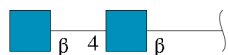
There are 6 unique types of molecules in this entry. The entry contains 4253 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lipase 1.

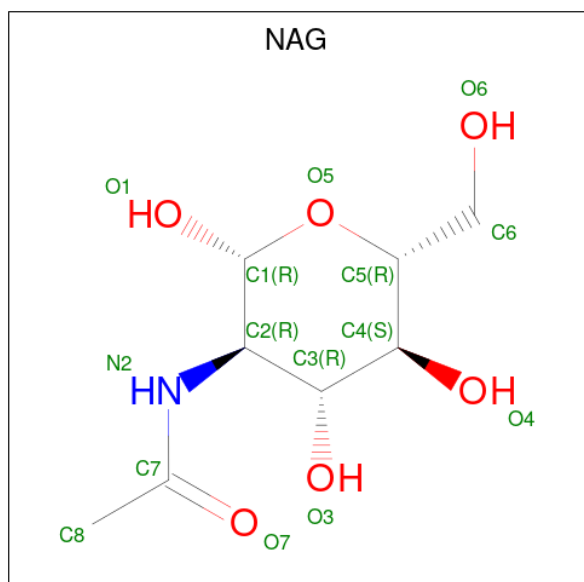
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	0	0
			4022	2556	659	788	19			

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



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

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

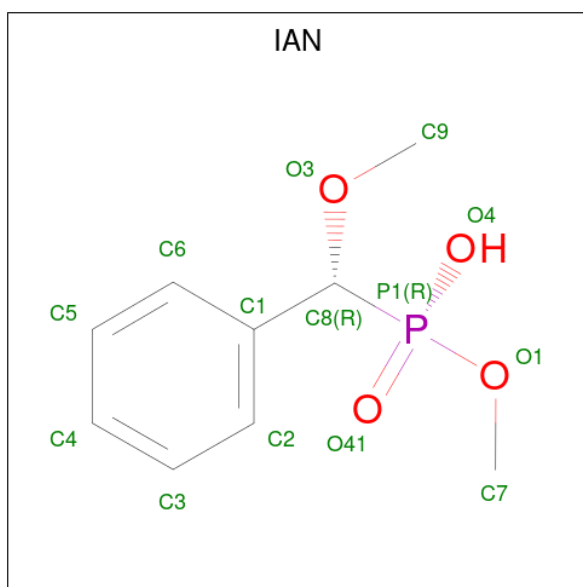


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Ca	0	0
			2	2		

- Molecule 5 is methyl hydrogen (R)-[(R)-methoxy(phenyl)methyl]phosphonate (CCD ID: IAN) (formula: C₉H₁₃O₄P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			13	9	3	1		

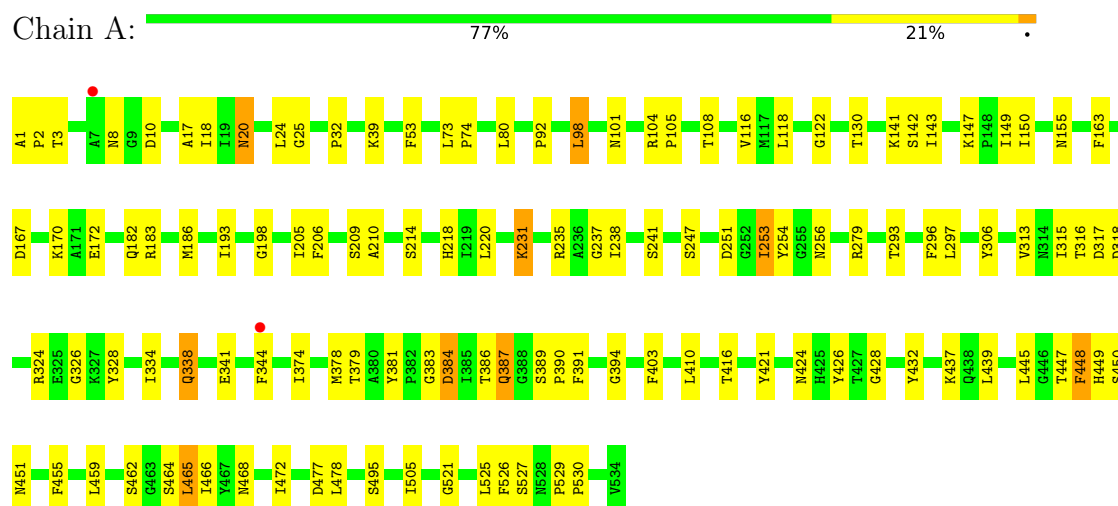
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	174	Total	O	0	0
			174	174		

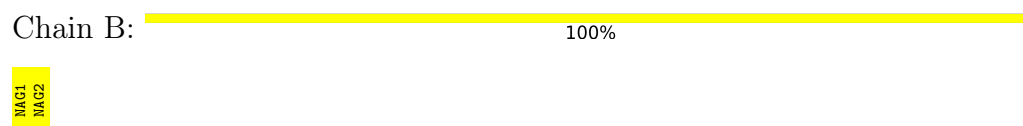
3 Residue-property plots

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: Lipase 1



• Molecule 2: 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	65.00Å 97.50Å 176.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.10 – 2.19 54.10 – 2.19	Depositor EDS
% Data completeness (in resolution range)	80.9 (54.10-2.19) 80.9 (54.10-2.19)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.48 (at 2.18Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.171 , 0.211 0.177 , 0.214	Depositor DCC
R_{free} test set	2343 reflections (9.87%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4253	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.57% 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: IAN, NAG, CA

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	0.39	0/4118	0.93	15/5601 (0.3%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	416	THR	N-CA-C	7.52	120.13	111.11
1	A	448	PHE	N-CA-C	7.47	120.39	110.53
1	A	381	TYR	CA-C-N	6.14	126.11	120.03
1	A	381	TYR	C-N-CA	6.14	126.11	120.03
1	A	315	ILE	N-CA-C	-6.12	97.18	106.42
1	A	316	THR	N-CA-C	5.82	119.86	112.87
1	A	293	THR	N-CA-C	-5.79	102.12	110.40
1	A	403	PHE	N-CA-C	5.75	118.01	111.11
1	A	253	ILE	N-CA-C	5.73	115.92	110.53
1	A	526	PHE	N-CA-C	5.65	119.49	112.59
1	A	527	SER	N-CA-C	-5.54	105.24	111.28
1	A	338	GLN	N-CA-C	-5.15	101.31	109.96
1	A	437	LYS	N-CA-C	-5.14	104.47	111.56
1	A	247	SER	N-CA-C	5.12	117.91	109.72
1	A	379	THR	N-CA-C	-5.08	105.39	112.45

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	4022	0	3892	77	0
2	B	28	0	25	0	0
3	A	14	0	13	1	0
4	A	2	0	0	0	0
5	A	13	0	12	0	0
6	A	174	0	0	1	0
All	All	4253	0	3942	77	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 (77) 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:167:ASP:H	1:A:256:ASN:HD21	1.10	0.98
1:A:424:ASN:HD21	1:A:495:SER:H	1.18	0.89
1:A:183:ARG:HH11	1:A:218:HIS:HD1	1.35	0.73
1:A:167:ASP:H	1:A:256:ASN:ND2	1.88	0.66
1:A:130:THR:HG23	1:A:155:ASN:HD22	1.63	0.63
1:A:1:ALA:HB3	1:A:2:PRO:HD3	1.80	0.62
1:A:130:THR:HG23	1:A:155:ASN:ND2	2.15	0.62
1:A:24:LEU:O	1:A:53:PHE:HB3	2.01	0.60
1:A:149:ILE:C	1:A:149:ILE:HD12	2.26	0.60
1:A:39:LYS:HE3	1:A:279:ARG:CZ	2.31	0.59
1:A:186:MET:HE1	1:A:218:HIS:CD2	2.37	0.59
1:A:220:LEU:HD23	1:A:328:TYR:HB3	1.85	0.58
1:A:338:GLN:HE21	1:A:451:ASN:HD21	1.52	0.58
1:A:338:GLN:NE2	1:A:451:ASN:HD21	2.02	0.57
1:A:182:GLN:HE22	1:A:214:SER:HB3	1.69	0.57
1:A:466:ILE:HG13	1:A:505:ILE:HD11	1.86	0.56
1:A:209:SER:HA	1:A:241:SER:O	2.09	0.53
1:A:39:LYS:HE3	1:A:279:ARG:NH2	2.24	0.52
1:A:317:ASP:CG	1:A:318:ASP:H	2.17	0.52
1:A:116:VAL:HG21	1:A:193:ILE:HG12	1.92	0.52
1:A:105:PRO:HB3	1:A:143:ILE:HD11	1.92	0.51
1:A:424:ASN:ND2	1:A:495:SER:H	1.98	0.51
1:A:389:SER:HA	1:A:390:PRO:C	2.36	0.51
1:A:73:LEU:HB3	1:A:74:PRO:HD3	1.93	0.50
1:A:20:ASN:C	1:A:20:ASN:HD22	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:PHE:CB	1:A:238:ILE:HB	2.42	0.49
1:A:170:LYS:HD2	1:A:251:ASP:OD1	2.12	0.49
1:A:326:GLY:HA2	1:A:328:TYR:CE1	2.49	0.48
1:A:383:GLY:O	1:A:384:ASP:C	2.56	0.48
1:A:25:GLY:H	1:A:101:ASN:ND2	2.11	0.48
1:A:426:TYR:CZ	1:A:428:GLY:HA3	2.49	0.48
1:A:521:GLY:O	1:A:525:LEU:HB2	2.13	0.48
1:A:445:LEU:HB3	1:A:448:PHE:HB3	1.97	0.47
1:A:80:LEU:O	1:A:80:LEU:HD13	2.15	0.47
1:A:104:ARG:HD2	1:A:108:THR:HB	1.96	0.47
1:A:39:LYS:HG3	1:A:279:ARG:NH2	2.29	0.47
1:A:296:PHE:CE1	1:A:297:LEU:HG	2.50	0.47
1:A:186:MET:HE1	1:A:218:HIS:CG	2.51	0.46
1:A:374:ILE:O	1:A:378:MET:HG3	2.15	0.46
1:A:17:ALA:O	1:A:18:ILE:HB	2.16	0.46
1:A:8:ASN:HD21	1:A:10:ASP:CG	2.24	0.46
1:A:338:GLN:O	1:A:341:GLU:HG2	2.16	0.46
1:A:1:ALA:O	1:A:3:THR:HG23	2.15	0.46
1:A:92:PRO:HA	6:A:691:HOH:O	2.16	0.45
1:A:167:ASP:N	1:A:256:ASN:HD21	1.94	0.45
1:A:313:VAL:HG12	3:A:991:NAG:O5	2.17	0.45
1:A:32:PRO:HD3	1:A:98:LEU:HD22	1.97	0.45
1:A:317:ASP:CG	1:A:318:ASP:N	2.73	0.45
1:A:122:GLY:HA2	1:A:210:ALA:HB3	1.99	0.45
1:A:253:ILE:HG23	1:A:254:TYR:N	2.32	0.45
1:A:462:SER:O	1:A:465:LEU:HB2	2.17	0.45
1:A:182:GLN:NE2	1:A:218:HIS:NE2	2.63	0.45
1:A:334:ILE:HG12	1:A:432:TYR:HB2	1.99	0.45
1:A:529:PRO:HB2	1:A:530:PRO:HD3	2.00	0.44
1:A:464:SER:O	1:A:468:ASN:HB2	2.17	0.44
1:A:389:SER:HA	1:A:391:PHE:N	2.33	0.44
1:A:25:GLY:H	1:A:101:ASN:HD22	1.66	0.44
1:A:142:SER:HB2	1:A:147:LYS:O	2.17	0.43
1:A:206:PHE:HB2	1:A:238:ILE:HB	1.99	0.43
1:A:477:ASP:O	1:A:478:LEU:HB2	2.17	0.43
1:A:39:LYS:HG3	1:A:279:ARG:HH21	1.83	0.43
1:A:324:ARG:HD3	1:A:421:TYR:OH	2.18	0.43
1:A:455:PHE:HA	1:A:459:LEU:O	2.19	0.43
1:A:172:GLU:CD	1:A:279:ARG:HH22	2.25	0.42
1:A:318:ASP:C	1:A:318:ASP:OD2	2.61	0.42
1:A:118:LEU:C	1:A:118:LEU:HD23	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:GLN:HE21	1:A:387:GLN:HB2	1.57	0.42
1:A:449:HIS:O	1:A:450:SER:OG	2.32	0.42
1:A:150:ILE:HD12	1:A:198:GLY:CA	2.50	0.42
1:A:231:LYS:O	1:A:231:LYS:HD3	2.20	0.41
1:A:386:THR:HA	1:A:394:GLY:O	2.21	0.41
1:A:338:GLN:HE21	1:A:447:THR:HG22	1.85	0.41
1:A:468:ASN:O	1:A:472:ILE:HG13	2.21	0.41
1:A:20:ASN:C	1:A:20:ASN:ND2	2.78	0.41
1:A:205:ILE:O	1:A:237:GLY:HA2	2.20	0.41
1:A:163:PHE:HB2	1:A:306:TYR:HB3	2.03	0.41
1:A:296:PHE:CD1	1:A:297:LEU:HG	2.56	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	532/534 (100%)	502 (94%)	29 (6%)	1 (0%)	43 51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	ASP

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	431/431 (100%)	421 (98%)	10 (2%)	44 59

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	98	LEU
1	A	141	LYS
1	A	231	LYS
1	A	235	ARG
1	A	344	PHE
1	A	387	GLN
1	A	410	LEU
1	A	439	LEU
1	A	465	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	155	ASN
1	A	182	GLN
1	A	187	GLN
1	A	222	ASN
1	A	240	GLN
1	A	256	ASN
1	A	330	ASN
1	A	338	GLN
1	A	339	ASN
1	A	364	GLN
1	A	387	GLN
1	A	424	ASN
1	A	456	GLN
1	A	500	ASN
1	A	528	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$
2	NAG	B	1	1,2	14,14,15	0.84	1 (7%)	17,19,21	1.07	3 (17%)
2	NAG	B	2	2	14,14,15	0.54	0	17,19,21	0.75	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	NAG	B	1	1,2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	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	2.26	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C2-N2-C7	-2.38	119.72	122.90
2	B	1	NAG	C2-N2-C7	-2.26	119.87	122.90
2	B	1	NAG	C1-O5-C5	2.12	115.03	112.19
2	B	1	NAG	C3-C4-C5	-2.05	106.51	110.23

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1	NAG	C1

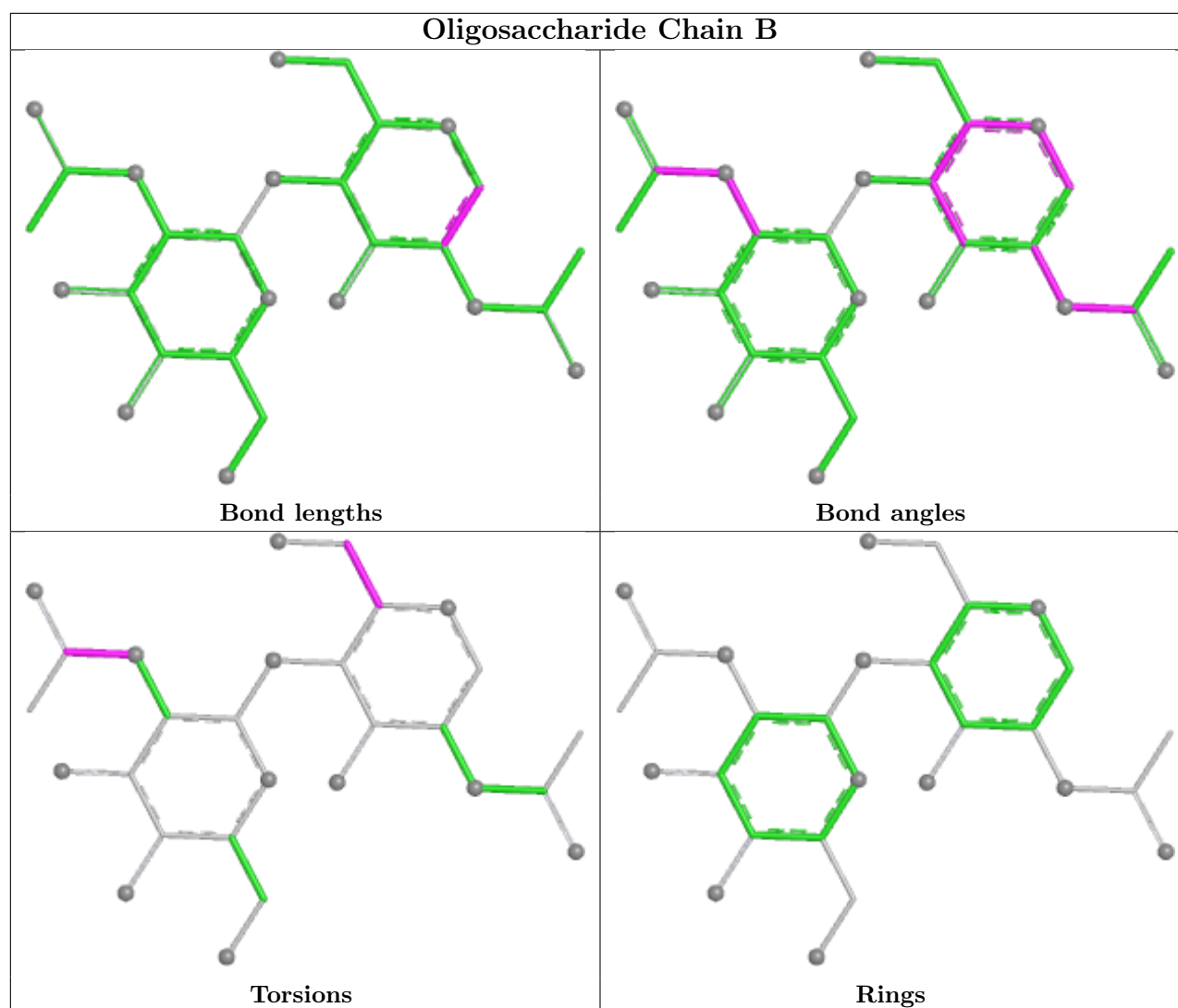
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	1	NAG	C4-C5-C6-O6
2	B	2	NAG	O7-C7-N2-C2
2	B	1	NAG	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, 2 are monoatomic - leaving 2 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	$\# Z > 2$
3	NAG	A	991	1	14,14,15	0.59	0	17,19,21	0.90	1 (5%)
5	IAN	A	560	1	9,13,14	2.34	5 (55%)	10,16,19	0.87	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	991	1	-	2/6/23/26	0/1/1/1
5	IAN	A	560	1	-	2/3/12/15	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	560	IAN	C6-C1	3.25	1.44	1.39
5	A	560	IAN	C1-C8	3.15	1.59	1.52
5	A	560	IAN	C2-C1	3.12	1.44	1.39
5	A	560	IAN	C5-C6	2.54	1.43	1.38
5	A	560	IAN	C3-C2	2.22	1.42	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	991	NAG	C2-N2-C7	-2.51	119.54	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	560	IAN	C2-C1-C8-O3
5	A	560	IAN	C6-C1-C8-O3
3	A	991	NAG	C4-C5-C6-O6
3	A	991	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	991	NAG	1	0

5.7 Other polymers ⓘ

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 [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	534/534 (100%)	-0.32	2 (0%) 88 87	12, 21, 37, 52	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	344	PHE	2.7
1	A	7	ALA	2.2

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

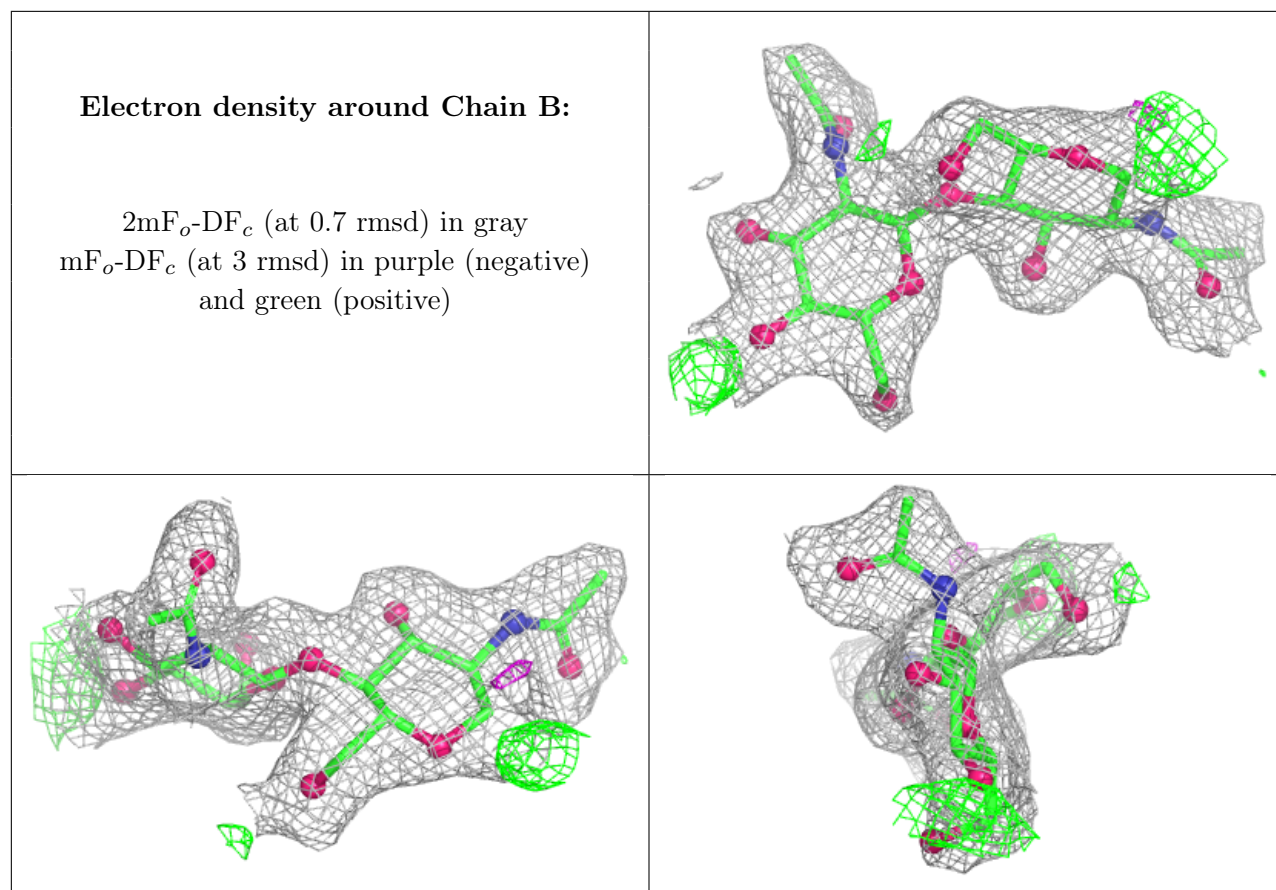
There are no non-standard protein/DNA/RNA residues in this entry.

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	NAG	B	2	14/15	0.89	0.10	37,37,40,43	0
2	NAG	B	1	14/15	0.90	0.09	29,32,34,35	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($\text{\AA}^2$)	Q<0.9
3	NAG	A	991	14/15	0.88	0.11	34,36,37,38	0
4	CA	A	589	1/1	0.89	0.09	44,44,44,44	0
5	IAN	A	560	13/14	0.94	0.10	23,28,31,32	0
4	CA	A	590	1/1	0.99	0.26	35,35,35,35	1

6.5 Other polymers [i](#)

There are no such residues in this entry.