



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:08 AM UTC

PDB ID : 2W6C / pdb_00002w6c
Title : ACHE IN COMPLEX WITH A BIS-(-)-NOR-MEPTAZINOL DERIVATIVE
Authors : Paz, A.; Xie, Q.; Greenblatt, H.M.; Fu, W.; Tang, Y.; Silman, I.; Qiu, Z.;
Sussman, J.L.
Deposited on : 2008-12-18
Resolution : 2.69 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

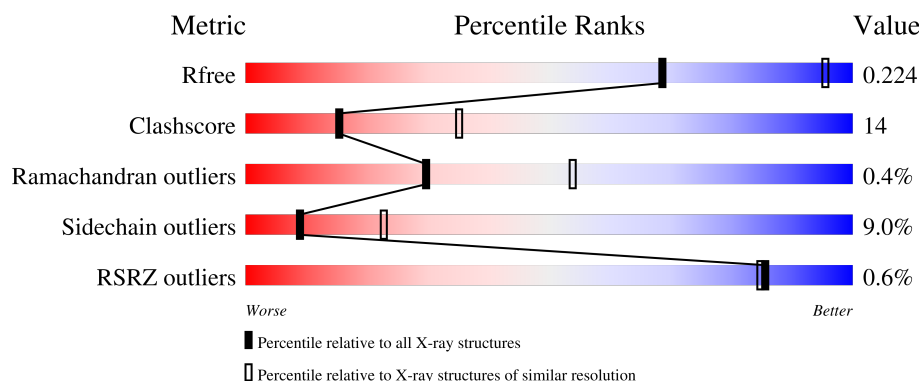
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	X	586	
2	A	2	

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
4	NAG	X	602	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4368 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 ACETYLCHOLINESTERASE.

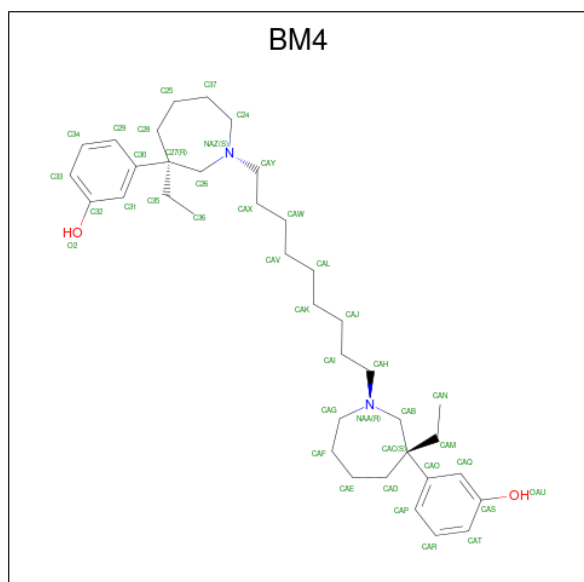
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	X	528	4171	2689	700	760	22	0	0	0

- 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
			Total	C	N	O			
2	A	2	28	16	2	10	0	0	0

- Molecule 3 is 3-[(3R)-3-ethyl-1-{9-[(3S)-3-ethyl-3-(3-hydroxyphenyl)azepan-1-yl]nonyl}azepan-3-yl]phenol (CCD ID: BM4) (formula: C₃₇H₅₈N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	X	1	Total	C	N	O	0	0
			26	23	2	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

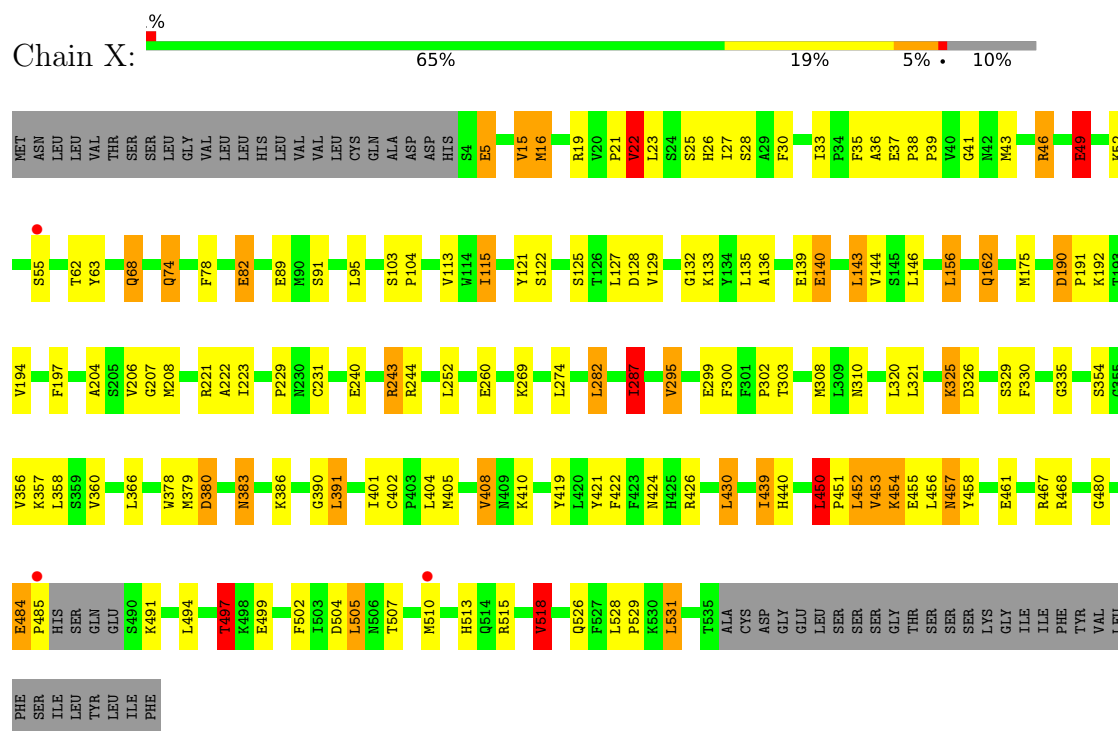
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	X	115	Total	O	0	0
			115	115		

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: ACETYLCHOLINESTERASE



• 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	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.17Å 112.17Å 137.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.68 – 2.69 39.68 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.68-2.69) 99.6 (39.68-2.69)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, R_{free}	0.185 , 0.235 (Not available) , 0.224	Depositor DCC
R_{free} test set	1452 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4368	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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: BM4, NAG

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	X	1.10	3/4292 (0.1%)	1.31	40/5829 (0.7%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	439	ILE	CA-CB	-5.73	1.47	1.54
1	X	497	THR	CA-CB	5.62	1.62	1.53
1	X	401	ILE	CA-CB	-5.11	1.48	1.54

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	518	VAL	CB-CA-C	-9.70	99.55	111.97
1	X	190	ASP	CA-C-N	-9.06	110.06	120.12
1	X	190	ASP	C-N-CA	-9.06	110.06	120.12
1	X	282	LEU	CA-C-N	-7.50	111.94	120.04
1	X	282	LEU	C-N-CA	-7.50	111.94	120.04
1	X	295	VAL	CB-CA-C	-7.45	99.35	110.82
1	X	287	ILE	CB-CA-C	7.03	121.65	110.82
1	X	329	SER	N-CA-C	6.97	119.77	111.33
1	X	401	ILE	N-CA-C	6.93	117.04	110.53
1	X	402	CYS	CA-C-N	-6.88	111.89	119.19
1	X	402	CYS	C-N-CA	-6.88	111.89	119.19
1	X	231	CYS	CA-C-N	-6.82	112.78	119.87
1	X	231	CYS	C-N-CA	-6.82	112.78	119.87
1	X	360	VAL	CA-C-N	6.71	126.66	119.28
1	X	360	VAL	C-N-CA	6.71	126.66	119.28
1	X	33	ILE	CB-CA-C	-6.52	104.88	110.94
1	X	63	TYR	CA-C-N	6.45	126.91	120.52
1	X	63	TYR	C-N-CA	6.45	126.91	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	378	TRP	CA-C-N	-6.11	113.42	122.83
1	X	378	TRP	C-N-CA	-6.11	113.42	122.83
1	X	287	ILE	CA-CB-CG2	5.94	120.60	110.50
1	X	439	ILE	CB-CA-C	-5.92	102.86	111.68
1	X	125	SER	N-CA-C	-5.88	106.11	113.28
1	X	49	GLU	CA-C-N	5.76	125.69	119.76
1	X	49	GLU	C-N-CA	5.76	125.69	119.76
1	X	22	VAL	CB-CA-C	-5.70	101.94	111.29
1	X	424	ASN	N-CA-C	5.62	117.64	110.61
1	X	491	LYS	N-CA-C	5.52	118.45	110.28
1	X	16	MET	N-CA-C	5.45	117.78	108.90
1	X	507	THR	N-CA-C	5.36	117.13	111.28
1	X	391	LEU	N-CA-C	-5.32	105.57	111.36
1	X	390	GLY	N-CA-C	-5.30	106.27	113.37
1	X	62	THR	N-CA-C	5.11	117.57	109.50
1	X	46	ARG	N-CA-C	5.10	118.03	110.48
1	X	450	LEU	CA-C-N	-5.10	114.46	120.12
1	X	450	LEU	C-N-CA	-5.10	114.46	120.12
1	X	156	LEU	N-CA-C	-5.08	102.33	109.96
1	X	191	PRO	CA-C-N	-5.06	114.58	122.73
1	X	191	PRO	C-N-CA	-5.06	114.58	122.73
1	X	162	GLN	N-CA-C	-5.02	106.58	113.30

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	X	4171	0	4007	109	0
2	A	28	0	25	0	0
3	X	26	0	38	1	0
4	X	28	0	26	3	0
5	X	115	0	0	17	0
All	All	4368	0	4096	113	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 14.

All (113) 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:X:526:GLN:HG3	5:X:774:HOH:O	1.39	1.19
1:X:497:THR:HB	5:X:702:HOH:O	0.98	1.15
1:X:74:GLN:HA	1:X:74:GLN:HE21	1.34	0.91
1:X:383:ASN:C	1:X:383:ASN:HD22	1.79	0.90
1:X:287:ILE:HD11	1:X:335:GLY:HA3	1.55	0.89
1:X:22:VAL:HG13	1:X:133:LYS:HG3	1.56	0.87
1:X:16:MET:SD	5:X:811:HOH:O	2.37	0.81
1:X:439:ILE:HG22	1:X:440:HIS:O	1.83	0.79
1:X:504:ASP:HB2	5:X:761:HOH:O	1.84	0.76
1:X:74:GLN:HE21	1:X:74:GLN:CA	2.01	0.72
1:X:23:LEU:HD11	1:X:452:LEU:HD12	1.71	0.72
1:X:49:GLU:HG2	5:X:813:HOH:O	1.92	0.69
1:X:484:GLU:OE2	1:X:484:GLU:HA	1.91	0.69
1:X:35:PHE:O	1:X:175:MET:HE3	1.92	0.68
1:X:450:LEU:CD2	1:X:450:LEU:N	2.57	0.68
1:X:5:GLU:OE2	1:X:104:PRO:HA	1.94	0.67
1:X:310:ASN:OD1	1:X:410:LYS:NZ	2.21	0.67
1:X:456:LEU:O	1:X:457:ASN:HB2	1.96	0.64
1:X:421:TYR:HB2	1:X:505:LEU:HD22	1.78	0.64
1:X:450:LEU:HD23	1:X:450:LEU:H	1.62	0.64
1:X:74:GLN:HA	1:X:74:GLN:NE2	2.11	0.63
1:X:497:THR:CB	5:X:702:HOH:O	1.79	0.62
1:X:484:GLU:OE2	1:X:485:PRO:HD2	2.01	0.61
1:X:531:LEU:HD12	1:X:531:LEU:C	2.26	0.60
1:X:321:LEU:HD23	1:X:321:LEU:N	2.18	0.58
1:X:287:ILE:HD11	1:X:335:GLY:CA	2.33	0.56
1:X:16:MET:CG	5:X:811:HOH:O	2.54	0.56
1:X:453:VAL:CG2	1:X:456:LEU:HG	2.36	0.55
1:X:330:PHE:HE2	1:X:439:ILE:HG21	1.72	0.55
1:X:43:MET:O	1:X:46:ARG:HB2	2.08	0.54
1:X:325:LYS:HB2	1:X:422:PHE:CZ	2.43	0.54
1:X:497:THR:C	5:X:702:HOH:O	2.49	0.54
1:X:190:ASP:OD1	1:X:192:LYS:HG2	2.07	0.54
4:X:605:NAG:H62	5:X:806:HOH:O	2.07	0.54
1:X:37:GLU:OE2	1:X:52:LYS:HG3	2.09	0.53
1:X:19:ARG:NH2	1:X:26:HIS:HB2	2.24	0.53
1:X:299:GLU:HB2	5:X:803:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:528:LEU:HB3	1:X:529:PRO:HD3	1.90	0.53
1:X:207:GLY:HA3	1:X:229:PRO:HD3	1.91	0.53
1:X:320:LEU:C	1:X:320:LEU:HD23	2.34	0.53
1:X:74:GLN:CA	1:X:74:GLN:NE2	2.70	0.52
1:X:16:MET:HG3	5:X:811:HOH:O	2.09	0.52
1:X:452:LEU:HD13	1:X:467:ARG:NH2	2.25	0.52
1:X:260:GLU:H	1:X:260:GLU:CD	2.18	0.52
1:X:468:ARG:HH21	1:X:510:MET:HE3	1.75	0.51
1:X:451:PRO:HA	1:X:458:TYR:CD1	2.45	0.51
4:X:602:NAG:H3	4:X:602:NAG:H83	1.93	0.51
1:X:450:LEU:CD2	1:X:450:LEU:H	2.22	0.50
1:X:405:MET:HA	1:X:408:VAL:HG12	1.92	0.50
1:X:419:TYR:CZ	1:X:494:LEU:HD13	2.46	0.50
1:X:484:GLU:OE2	1:X:485:PRO:CD	2.58	0.50
1:X:450:LEU:N	1:X:450:LEU:HD22	2.25	0.49
1:X:405:MET:HA	1:X:408:VAL:CG1	2.43	0.49
1:X:68:GLN:HE21	1:X:68:GLN:HA	1.77	0.48
1:X:269:LYS:HB2	1:X:274:LEU:HD11	1.95	0.48
1:X:162:GLN:HG3	5:X:815:HOH:O	2.14	0.48
1:X:25:SER:OG	1:X:26:HIS:N	2.45	0.47
1:X:404:LEU:C	1:X:404:LEU:HD23	2.38	0.47
1:X:515:ARG:O	1:X:518:VAL:HG22	2.13	0.47
1:X:36:ALA:HB2	1:X:175:MET:HE2	1.96	0.47
1:X:197:PHE:CB	1:X:223:ILE:HB	2.44	0.47
1:X:121:TYR:CD1	1:X:122:SER:HB3	2.50	0.47
1:X:321:LEU:N	1:X:321:LEU:CD2	2.78	0.47
1:X:468:ARG:HD3	5:X:701:HOH:O	2.14	0.47
1:X:282:LEU:HD23	1:X:282:LEU:HA	1.77	0.46
1:X:206:VAL:CG1	1:X:222:ALA:HB1	2.46	0.46
1:X:531:LEU:C	1:X:531:LEU:CD1	2.89	0.46
1:X:383:ASN:C	1:X:383:ASN:ND2	2.54	0.45
1:X:404:LEU:O	1:X:408:VAL:HG12	2.16	0.45
1:X:357:LYS:HD2	5:X:797:HOH:O	2.16	0.45
1:X:502:PHE:CZ	1:X:513:HIS:HB2	2.51	0.45
1:X:82:GLU:HG3	5:X:798:HOH:O	2.18	0.44
1:X:455:GLU:CD	1:X:455:GLU:H	2.25	0.44
1:X:452:LEU:HD23	1:X:452:LEU:N	2.32	0.44
1:X:468:ARG:HH21	1:X:510:MET:CE	2.31	0.43
1:X:15:VAL:CG1	1:X:30:PHE:HD2	2.32	0.43
1:X:103:SER:HA	1:X:104:PRO:C	2.44	0.43
1:X:379:MET:O	1:X:380:ASP:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:197:PHE:HB3	1:X:223:ILE:HB	2.01	0.43
1:X:35:PHE:O	1:X:175:MET:CE	2.64	0.42
1:X:303:THR:HB	5:X:734:HOH:O	2.17	0.42
1:X:325:LYS:NZ	1:X:326:ASP:OD1	2.52	0.42
1:X:454:LYS:HA	1:X:454:LYS:HD3	1.73	0.42
1:X:204:ALA:O	1:X:208:MET:HG3	2.19	0.42
1:X:78:PHE:O	1:X:82:GLU:HB2	2.19	0.42
1:X:113:VAL:HG22	1:X:144:VAL:HB	2.01	0.42
1:X:456:LEU:O	1:X:457:ASN:CB	2.67	0.42
1:X:223:ILE:HA	1:X:320:LEU:O	2.19	0.42
1:X:21:PRO:HA	1:X:25:SER:O	2.19	0.42
1:X:302:PRO:HD2	1:X:308:MET:SD	2.59	0.42
1:X:27:ILE:HD13	1:X:27:ILE:HG21	1.79	0.42
1:X:41:GLY:C	1:X:43:MET:H	2.28	0.42
1:X:366:LEU:HD23	1:X:531:LEU:CD1	2.50	0.42
3:X:601:BM4:HAF	3:X:601:BM4:HABA	1.84	0.42
1:X:240:GLU:OE1	1:X:243:ARG:HD3	2.20	0.41
1:X:115:ILE:HG23	1:X:146:LEU:HD11	2.01	0.41
1:X:39:PRO:HG3	1:X:95:LEU:HD11	2.03	0.41
1:X:252:LEU:HB3	1:X:269:LYS:NZ	2.35	0.41
1:X:330:PHE:CE2	1:X:439:ILE:HG21	2.54	0.41
1:X:426:ARG:CZ	1:X:430:LEU:HD12	2.50	0.41
1:X:240:GLU:O	1:X:244:ARG:HG3	2.20	0.41
1:X:383:ASN:ND2	1:X:386:LYS:H	2.18	0.41
1:X:127:LEU:O	1:X:128:ASP:C	2.63	0.41
1:X:135:LEU:O	1:X:136:ALA:C	2.64	0.41
1:X:299:GLU:HB3	1:X:300:PHE:H	1.78	0.41
1:X:450:LEU:N	1:X:450:LEU:HD23	2.23	0.41
1:X:274:LEU:N	1:X:274:LEU:HD12	2.36	0.40
4:X:602:NAG:H3	4:X:602:NAG:C8	2.51	0.40
1:X:221:ARG:HD3	1:X:480:GLY:HA2	2.04	0.40
1:X:46:ARG:CD	5:X:731:HOH:O	2.68	0.40
1:X:132:GLY:HA3	1:X:143:LEU:HD22	2.03	0.40
1:X:139:GLU:O	1:X:140:GLU:CB	2.68	0.40
1:X:515:ARG:HB3	1:X:518:VAL:HG22	2.02	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	X	524/586 (89%)	492 (94%)	30 (6%)	2 (0%)	30	54

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	380	ASP
1	X	457	ASN

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	X	446/513 (87%)	406 (91%)	40 (9%)	9	23

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	5	GLU
1	X	15	VAL
1	X	22	VAL
1	X	28	SER
1	X	38	PRO
1	X	49	GLU
1	X	55	SER
1	X	68	GLN
1	X	74	GLN

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Mol	Chain	Res	Type
1	X	82	GLU
1	X	89	GLU
1	X	91	SER
1	X	115	ILE
1	X	129	VAL
1	X	140	GLU
1	X	143	LEU
1	X	156	LEU
1	X	194	VAL
1	X	243	ARG
1	X	287	ILE
1	X	295	VAL
1	X	325	LYS
1	X	354	SER
1	X	356	VAL
1	X	358	LEU
1	X	383	ASN
1	X	391	LEU
1	X	408	VAL
1	X	430	LEU
1	X	450	LEU
1	X	452	LEU
1	X	453	VAL
1	X	454	LYS
1	X	461	GLU
1	X	484	GLU
1	X	497	THR
1	X	499	GLU
1	X	505	LEU
1	X	518	VAL
1	X	531	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	68	GLN
1	X	74	GLN
1	X	383	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	A	1	1,2	14,14,15	0.75	1 (7%)	17,19,21	1.67	5 (29%)
2	NAG	A	2	2	14,14,15	0.63	0	17,19,21	1.87	5 (29%)

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	A	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	A	2	2	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	NAG	O5-C1	-2.25	1.39	1.43

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2	NAG	C4-C3-C2	3.63	116.34	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2	NAG	C2-N2-C7	-3.55	118.14	122.90
2	A	2	NAG	O5-C1-C2	-3.04	106.59	111.29
2	A	1	NAG	O5-C1-C2	-3.03	106.61	111.29
2	A	1	NAG	C3-C4-C5	-3.01	104.78	110.23
2	A	1	NAG	C2-N2-C7	-2.83	119.11	122.90
2	A	2	NAG	O4-C4-C5	2.68	115.93	109.32
2	A	1	NAG	O5-C5-C4	-2.51	104.71	110.83
2	A	1	NAG	O4-C4-C5	2.39	115.20	109.32
2	A	2	NAG	O6-C6-C5	-2.13	104.07	111.33

There are no chirality outliers.

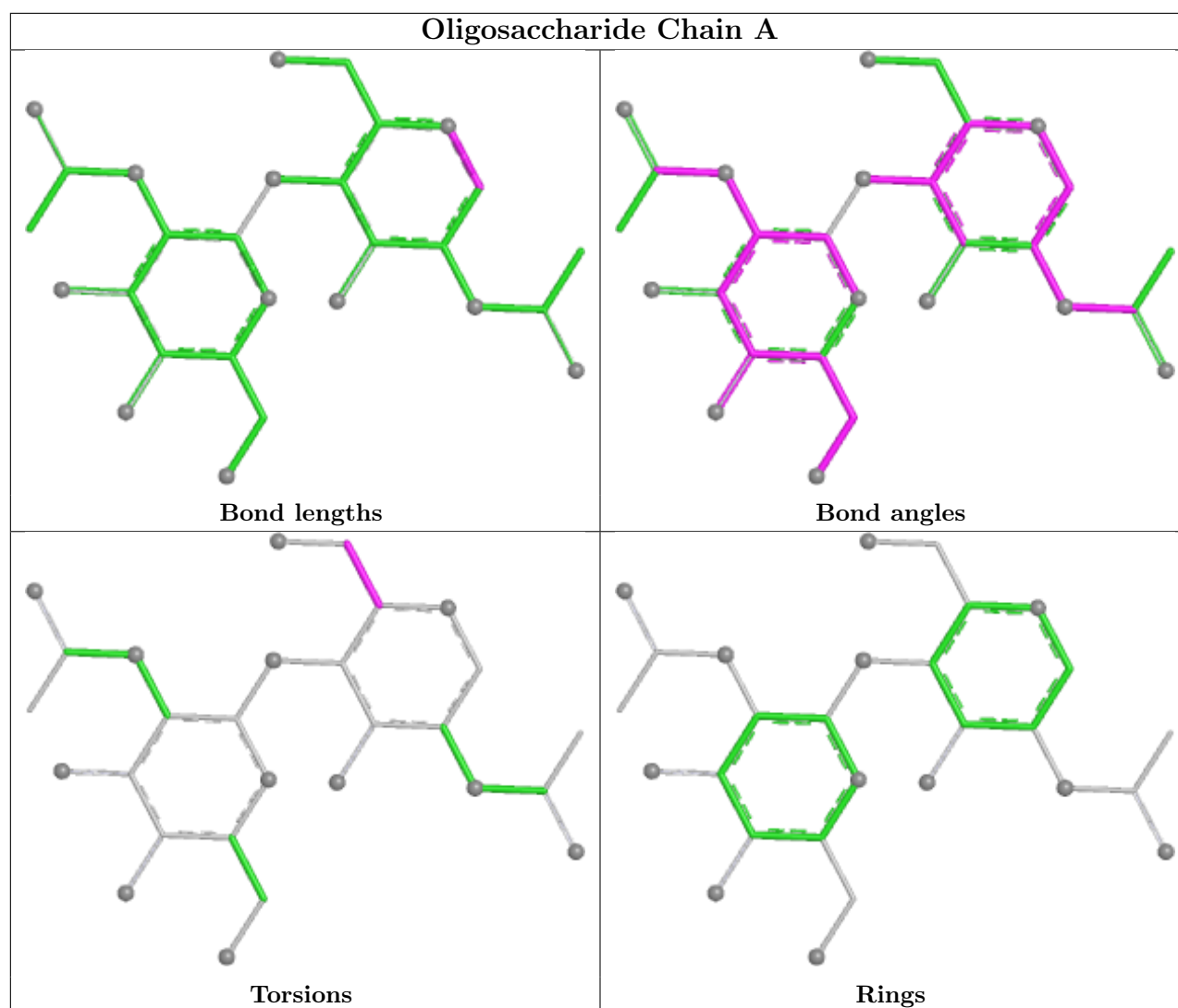
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	NAG	O5-C5-C6-O6
2	A	1	NAG	C4-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](#)

3 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	X	602	1	14,14,15	1.01	1 (7%)	17,19,21	1.81	4 (23%)
4	NAG	X	605	1	14,14,15	0.78	0	17,19,21	3.59	9 (52%)
3	BM4	X	601	-	26,27,44	0.90	1 (3%)	24,34,59	1.36	4 (16%)

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	X	602	1	1/1/5/7	3/6/23/26	0/1/1/1
4	NAG	X	605	1	-	2/6/23/26	0/1/1/1
3	BM4	X	601	-	-	13/19/32/56	0/2/2/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	X	601	BM4	CAB-NAA	3.11	1.48	1.46
4	X	602	NAG	C1-C2	2.53	1.55	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	X	605	NAG	C2-N2-C7	-9.06	110.75	122.90
4	X	605	NAG	C3-C4-C5	-7.67	96.33	110.23
4	X	605	NAG	C1-O5-C5	5.29	119.27	112.19
3	X	601	BM4	CAN-CAM-CAC	-4.42	110.81	115.83
4	X	602	NAG	C4-C3-C2	3.97	116.84	111.02
4	X	602	NAG	C2-N2-C7	3.25	127.25	122.90
4	X	605	NAG	O7-C7-N2	-3.14	116.43	121.98
4	X	602	NAG	C1-C2-N2	3.02	115.19	110.43
3	X	601	BM4	CAF-CAG-NAA	-3.00	109.68	115.35
4	X	605	NAG	O4-C4-C5	2.93	116.54	109.32
4	X	605	NAG	O5-C5-C6	2.87	113.25	107.66
4	X	602	NAG	O7-C7-C8	-2.75	117.16	122.05
4	X	605	NAG	O3-C3-C2	2.75	115.11	109.40
4	X	605	NAG	C4-C3-C2	-2.45	107.42	111.02
3	X	601	BM4	CAM-CAC-CAD	-2.42	105.81	108.66
4	X	605	NAG	C8-C7-N2	2.37	120.05	116.12
3	X	601	BM4	CAI-CAH-NAA	-2.02	108.25	113.93

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	X	602	NAG	C1

All (18) torsion outliers are listed below:

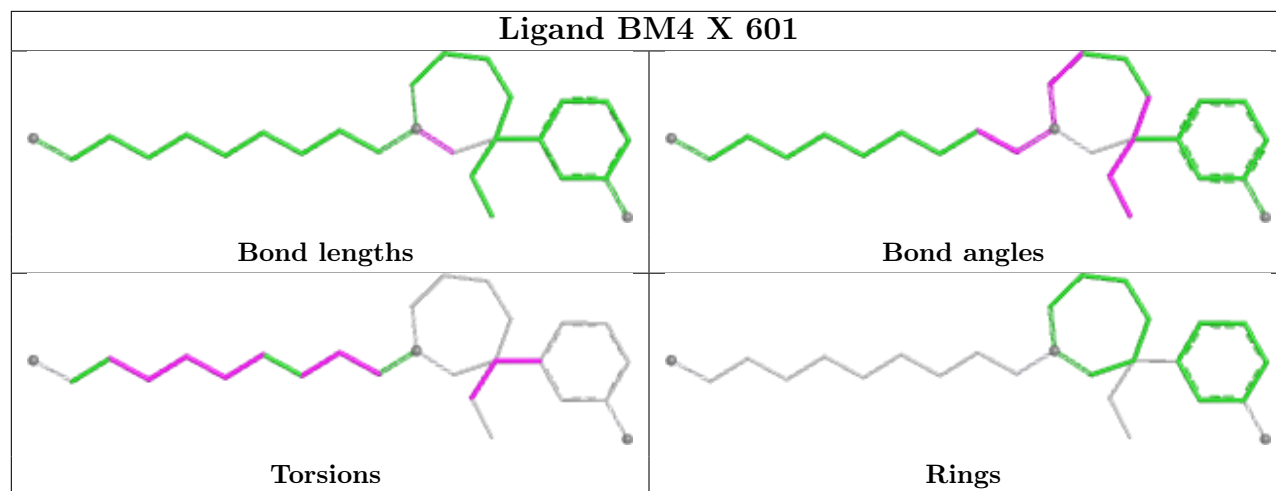
Mol	Chain	Res	Type	Atoms
3	X	601	BM4	CAB-CAC-CAM-CAN
3	X	601	BM4	CAD-CAC-CAM-CAN
4	X	602	NAG	C8-C7-N2-C2
4	X	602	NAG	O7-C7-N2-C2
4	X	605	NAG	C8-C7-N2-C2
4	X	605	NAG	O7-C7-N2-C2
3	X	601	BM4	NAA-CAH-CAI-CAJ
3	X	601	BM4	CAV-CAW-CAX-CAY
3	X	601	BM4	CAK-CAL-CAV-CAW
3	X	601	BM4	CAL-CAV-CAW-CAX
3	X	601	BM4	CAD-CAC-CAO-CAQ
3	X	601	BM4	CAD-CAC-CAO-CAP
3	X	601	BM4	CAO-CAC-CAM-CAN
3	X	601	BM4	CAH-CAI-CAJ-CAK
3	X	601	BM4	CAJ-CAK-CAL-CAV
4	X	602	NAG	C3-C2-N2-C7
3	X	601	BM4	CAM-CAC-CAO-CAQ
3	X	601	BM4	CAM-CAC-CAO-CAP

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	X	602	NAG	2	0
4	X	605	NAG	1	0
3	X	601	BM4	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	X	528/586 (90%)	-0.54	3 (0%) 85 85	19, 32, 49, 62	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	510	MET	2.6
1	X	55	SER	2.3
1	X	485	PRO	2.2

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

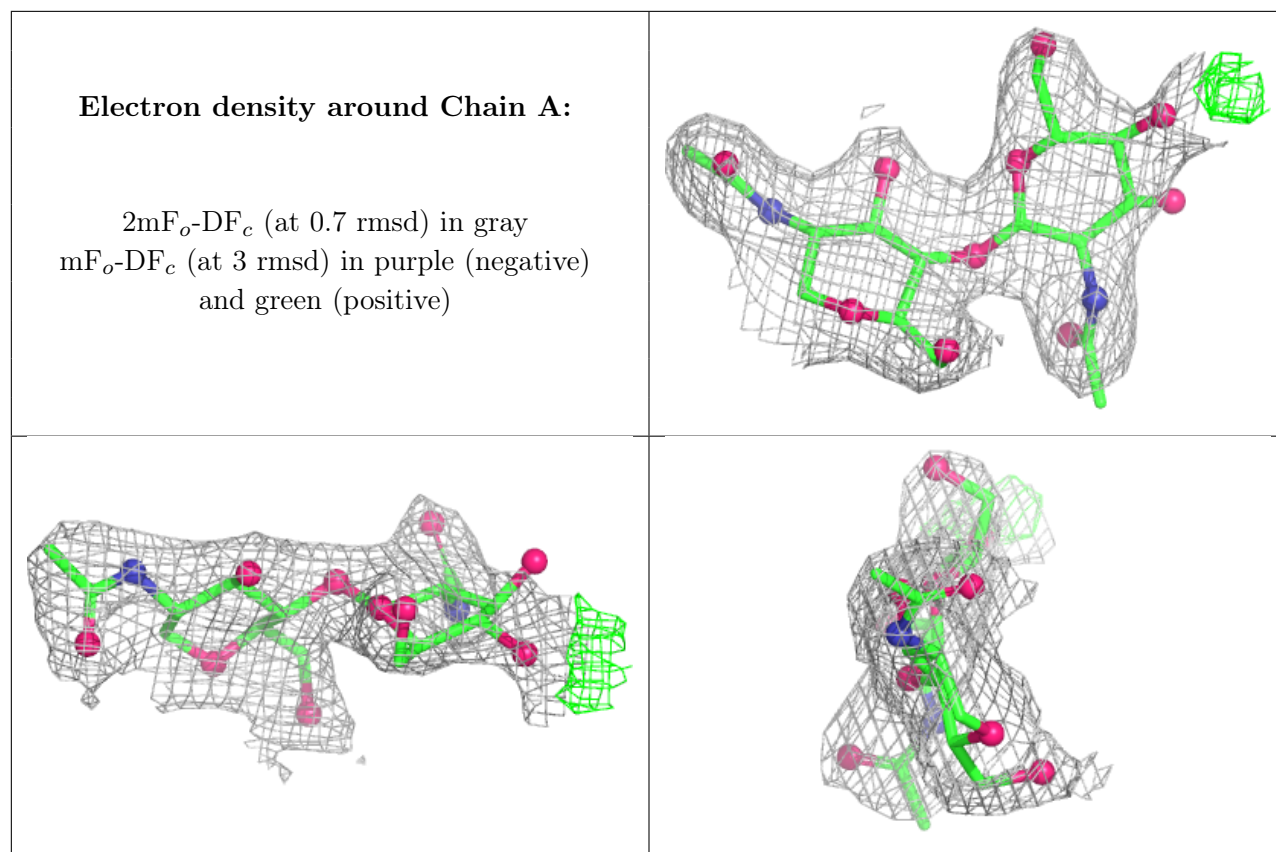
There are no non-standard protein/DNA/RNA residues in this entry.

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	A	1	14/15	-	-	22,33,38,41	14
2	NAG	A	2	14/15	-	-	41,44,49,50	14

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.

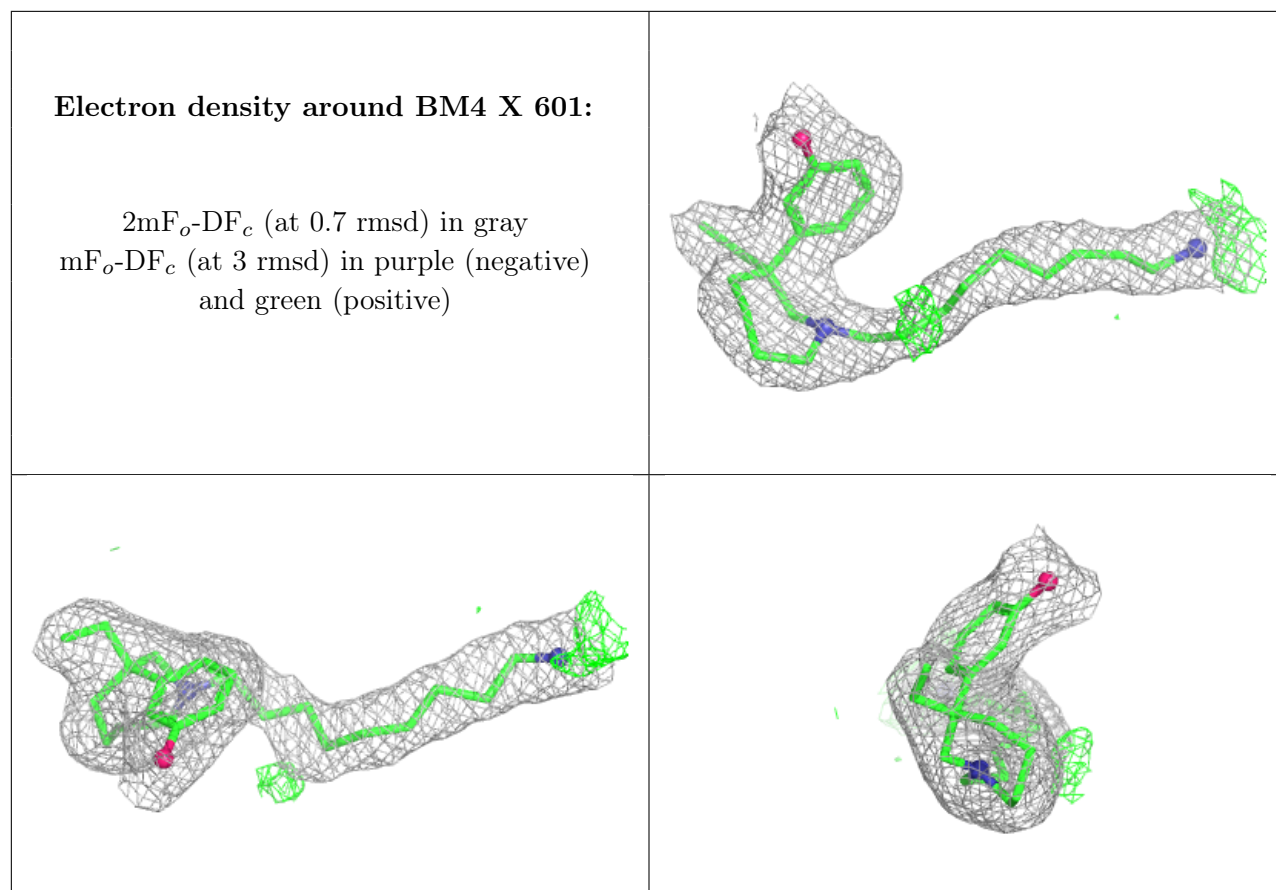


6.4 Ligands [i](#)

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	NAG	X	602	14/15	0.74	0.21	52,55,57,57	14
4	NAG	X	605	14/15	0.87	0.16	55,57,60,60	14
3	BM4	X	601	26/41	0.96	0.09	17,26,41,41	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.