



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:02 AM UTC

PDB ID : 3NKR / pdb_00003nkr
Title : Crystal structure of mouse autotaxin in complex with 22:6-LPA
Authors : Nishimasu, H.; Ishitani, R.; Mihara, E.; Takagi, J.; Aoki, J.; Nureki, O.
Deposited on : 2010-06-20
Resolution : 1.70 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

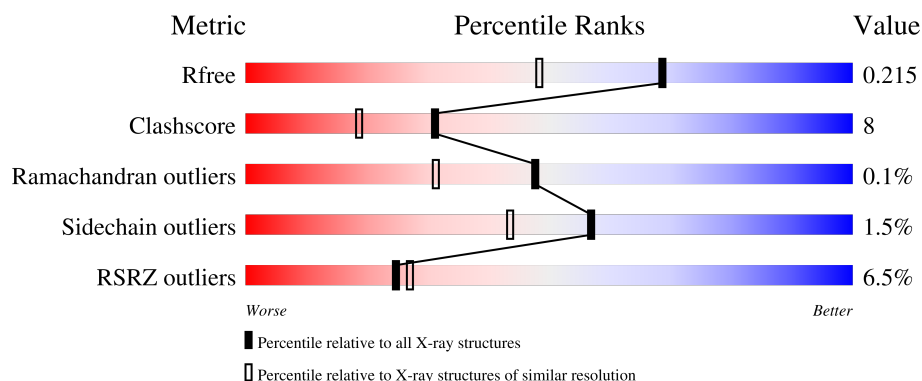
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	A	831	6% 80% 13% 6%
2	B	2	100%
2	D	2	50% 50%
3	C	6	50% 33% 17%

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
10	EDO	A	1024	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7130 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	779	Total	C	N	O	S	0	5	0
			6234	3964	1062	1158	50			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LYS	SEE REMARK 999	UNP Q9R1E6
A	?	-	VAL	SEE REMARK 999	UNP Q9R1E6
A	?	-	GLU	SEE REMARK 999	UNP Q9R1E6
A	?	-	PRO	SEE REMARK 999	UNP Q9R1E6
A	859	SER	-	expression tag	UNP Q9R1E6
A	860	ARG	-	expression tag	UNP Q9R1E6
A	861	GLU	-	expression tag	UNP Q9R1E6
A	862	ASN	-	expression tag	UNP Q9R1E6
A	863	LEU	-	expression tag	UNP Q9R1E6
A	864	TYR	-	expression tag	UNP Q9R1E6
A	865	PHE	-	expression tag	UNP Q9R1E6
A	866	GLN	-	expression tag	UNP Q9R1E6

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

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



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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

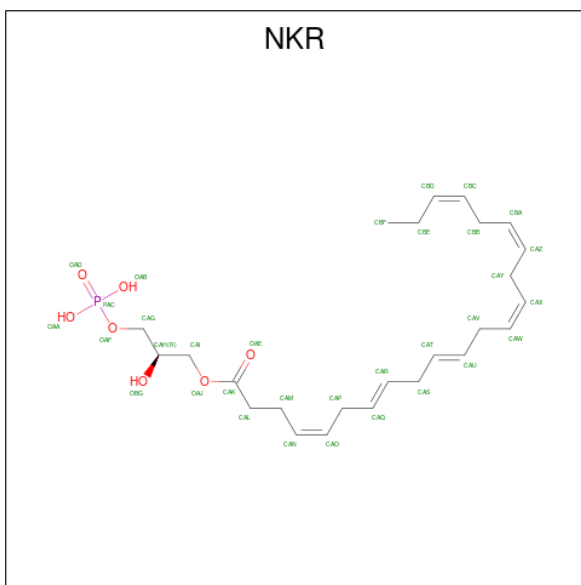
- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Na	0	0
			1	1		

- Molecule 7 is POTASSIUM ION (CCD ID: K) (formula: K).

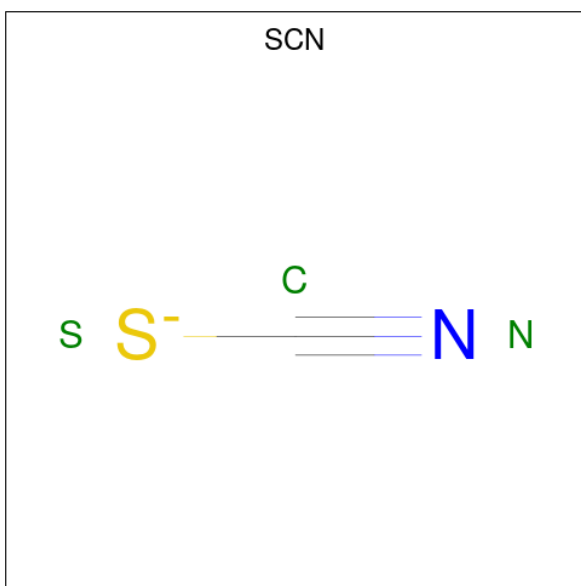
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	K	0	0
			1	1		

- Molecule 8 is (2R)-2-hydroxy-3-(phosphonoxy)propyl (4Z,7E,10E,13Z,16Z,19Z)-docosa-4,7,10,13,16,19-hexaenoate (CCD ID: NKR) (formula: C₂₅H₃₉O₇P).



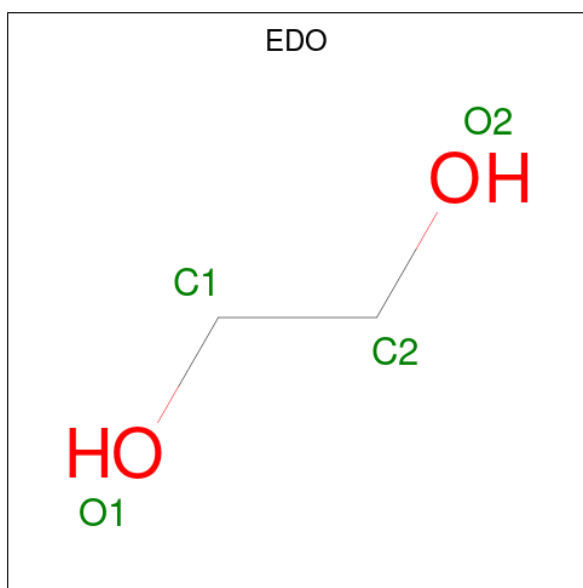
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
8	A	1	Total	C	O	P	0	0	
			33	25	7	1			
8	A	1	Total	C				0	0
			18	18					

- Molecule 9 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total 3	C 1	N 1	S 1	0	0
9	A	1	Total 3	C 1	N 1	S 1	0	0

- Molecule 10 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		

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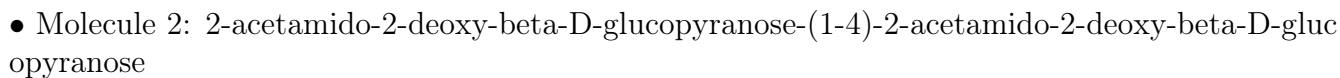
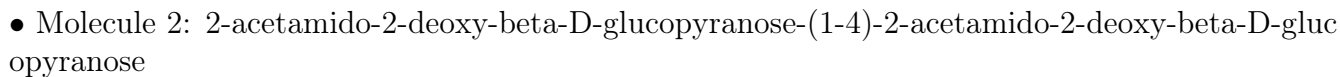
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 11 is water.

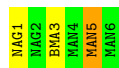
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	622	Total	O	0	0
			622	622		

- Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



- Molecule 3: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)- α -D-mannopyranose-(1-6)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain C: 50% 33% 17%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.54Å 94.11Å 75.31Å 90.00° 95.26° 90.00°	Depositor
Resolution (Å)	24.89 – 1.70 24.89 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.1 (24.89-1.70) 99.1 (24.89-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 1.71Å)	Xtriage
Refinement program	PHENIX 1.6_289	Depositor
R, R_{free}	0.192 , 0.220 0.188 , 0.215	Depositor DCC
R_{free} test set	4625 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 49.2	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	7130	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% 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: MAN, NKR, K, NA, ZN, CA, NAG, SCN, EDO, BMA

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	0.51	1/6430 (0.0%)	0.81	0/8746

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	645	THR	C-N	-5.91	1.26	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6234	0	5915	99	1
2	B	28	0	25	0	0
2	D	28	0	25	0	0
3	C	72	0	61	2	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
8	A	51	0	62	10	0
9	A	6	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	84	0	126	19	0
11	A	622	0	0	14	2
All	All	7130	0	6214	104	2

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 (104) 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)
8:A:1007:NKR:HAP	3:C:5:MAN:O4	1.49	1.10
1:A:208:LYS:HG3	9:A:1008:SCN:S	2.10	0.91
8:A:1007:NKR:CAP	3:C:5:MAN:O4	2.22	0.87
1:A:134:GLN:NE2	11:A:1484:HOH:O	2.06	0.86
1:A:835:ARG:HH21	10:A:1024:EDO:H11	1.42	0.84
1:A:254:TRP:O	8:A:1007:NKR:HASA	1.77	0.83
1:A:78:LEU:O	1:A:82:TYR:HD1	1.65	0.79
1:A:852:HIS:HD2	1:A:854:TYR:CZ	2.03	0.76
1:A:235:PRO:HG2	11:A:1226:HOH:O	1.88	0.73
1:A:251:HIS:O	8:A:1007:NKR:HAS	1.90	0.71
1:A:836:LYS:HE2	10:A:1024:EDO:H21	1.74	0.69
1:A:835:ARG:HE	10:A:1024:EDO:C2	2.07	0.68
1:A:389:LEU:CD1	11:A:1470:HOH:O	2.42	0.67
1:A:840:SER:OG	1:A:843:GLU:HG3	1.95	0.66
1:A:682:SER:OG	1:A:688:LYS:NZ	2.28	0.66
1:A:330:GLU:HG2	11:A:1483:HOH:O	1.96	0.65
1:A:178:MET:HE2	1:A:192:ARG:HD3	1.78	0.65
1:A:675:PHE:H	10:A:1012:EDO:H11	1.61	0.64
1:A:254:TRP:O	8:A:1007:NKR:CAS	2.47	0.63
8:A:1006:NKR:CAU	8:A:1006:NKR:HAZ	2.28	0.63
1:A:68:VAL:O	1:A:74:ARG:HD2	1.99	0.62
1:A:78:LEU:O	1:A:82:TYR:CD1	2.48	0.62
1:A:281:HIS:ND1	10:A:1023:EDO:H21	2.15	0.62
1:A:835:ARG:HE	10:A:1024:EDO:H22	1.64	0.62
1:A:98:ARG:HG3	1:A:115:ASN:OD1	2.00	0.61
1:A:555:ILE:HG12	1:A:652:VAL:HG23	1.83	0.60
1:A:519:LYS:HE3	11:A:1206:HOH:O	2.01	0.60
1:A:702:PRO:HB2	10:A:1025:EDO:H22	1.84	0.60
1:A:678:PRO:HB3	1:A:712:GLN:HB3	1.83	0.59
1:A:122:ASP:HA	11:A:1467:HOH:O	2.04	0.58
1:A:121:GLU:O	11:A:1467:HOH:O	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:558:LEU:N	1:A:561:ASP:OD2	2.28	0.57
1:A:61:ARG:HD2	1:A:64:GLU:OE1	2.04	0.56
8:A:1006:NKR:CAZ	8:A:1006:NKR:CAT	2.83	0.56
1:A:408:ILE:HD11	1:A:424:MET:SD	2.45	0.56
1:A:617:TYR:CE1	1:A:695:THR:HG22	2.41	0.56
1:A:254:TRP:O	8:A:1007:NKR:HAU	2.05	0.56
1:A:675:PHE:H	10:A:1012:EDO:C1	2.18	0.55
1:A:558:LEU:O	1:A:561:ASP:HB2	2.06	0.55
1:A:277:VAL:HG22	11:A:1404:HOH:O	2.06	0.55
1:A:685:PRO:O	1:A:689:TYR:HD2	1.90	0.54
1:A:222:PRO:HA	1:A:225:HIS:CE1	2.42	0.54
1:A:389:LEU:HD12	11:A:1470:HOH:O	2.03	0.54
1:A:587:THR:N	11:A:1368:HOH:O	2.40	0.53
1:A:835:ARG:NH2	10:A:1024:EDO:H11	2.19	0.53
8:A:1006:NKR:HAZ	8:A:1006:NKR:CAT	2.39	0.53
1:A:151:ILE:HD12	10:A:1011:EDO:H21	1.91	0.53
1:A:111:ARG:NH2	1:A:126:ARG:HD3	2.24	0.52
1:A:678:PRO:HG2	1:A:681:LEU:HD12	1.93	0.51
1:A:306:TYR:CD2	8:A:1006:NKR:HAPA	2.47	0.50
1:A:550:PRO:HB3	1:A:605:TYR:CE1	2.46	0.50
1:A:348:HIS:H	1:A:348:HIS:CD2	2.30	0.50
1:A:424:MET:HE1	1:A:442:ASP:HB3	1.92	0.50
1:A:687:ALA:O	1:A:690:ASP:HB2	2.12	0.50
1:A:343:LYS:HA	1:A:348:HIS:CD2	2.48	0.49
1:A:663:LEU:O	1:A:667:ASN:HB3	2.12	0.49
1:A:678:PRO:CG	1:A:681:LEU:HD12	2.42	0.49
1:A:817:MET:HA	1:A:817:MET:HE2	1.94	0.49
1:A:281:HIS:ND1	10:A:1023:EDO:C2	2.76	0.49
1:A:690:ASP:O	1:A:693:LEU:HB2	2.12	0.49
1:A:206:PRO:HB3	1:A:389:LEU:HD13	1.94	0.49
1:A:667:ASN:ND2	1:A:667:ASN:C	2.71	0.48
1:A:359:HIS:CE1	1:A:474:HIS:CE1	3.02	0.48
1:A:554:GLY:O	1:A:556:MET:SD	2.72	0.48
1:A:536:THR:O	1:A:537:ASN:HB2	2.14	0.47
1:A:64:GLU:OE2	11:A:1475:HOH:O	2.20	0.47
1:A:638:SER:OG	1:A:688:LYS:NZ	2.41	0.47
1:A:437:ASN:HD21	10:A:1030:EDO:C2	2.27	0.47
1:A:437:ASN:HD21	10:A:1030:EDO:H22	1.80	0.47
1:A:543:LEU:HD12	1:A:544:PRO:HD2	1.97	0.47
1:A:555:ILE:HG12	1:A:652:VAL:CG2	2.45	0.47
1:A:839:ARG:HE	10:A:1026:EDO:C2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:LYS:NZ	11:A:1171:HOH:O	2.47	0.46
1:A:835:ARG:HB3	10:A:1024:EDO:H22	1.98	0.46
1:A:415:LYS:HB3	1:A:415:LYS:HE2	1.60	0.46
1:A:470:PHE:CD1	1:A:470:PHE:C	2.94	0.45
1:A:380:ASP:HA	1:A:455:ARG:NH1	2.31	0.45
1:A:637:VAL:HG22	1:A:681:LEU:HD23	1.99	0.45
1:A:148[B]:CYS:SG	1:A:496:TYR:HE2	2.39	0.45
1:A:95:LYS:HG3	11:A:1053:HOH:O	2.17	0.44
1:A:637:VAL:HG22	1:A:681:LEU:CD2	2.47	0.44
1:A:201:MET:HE1	1:A:356:VAL:CG2	2.47	0.44
1:A:52:THR:OG1	1:A:70:PRO:HB3	2.18	0.44
1:A:761:THR:HA	10:A:1015:EDO:H12	2.00	0.44
1:A:617:TYR:HA	1:A:624:PRO:HA	2.00	0.44
1:A:667:ASN:ND2	1:A:668:ASP:N	2.66	0.43
1:A:670:GLN:NE2	11:A:1424:HOH:O	2.51	0.43
1:A:479:LYS:O	1:A:855:GLU:HG3	2.19	0.43
1:A:736:TYR:OH	1:A:750:GLN:HB3	2.18	0.43
1:A:852:HIS:HD2	1:A:854:TYR:CE1	2.36	0.43
1:A:54:THR:O	1:A:54:THR:OG1	2.34	0.43
1:A:703:ALA:N	10:A:1025:EDO:H21	2.34	0.42
1:A:783:PRO:HA	10:A:1026:EDO:H21	2.01	0.42
1:A:375:TYR:OH	1:A:415:LYS:HD3	2.19	0.42
1:A:58:CYS:SG	1:A:86:CYS:HB2	2.60	0.42
1:A:550:PRO:HB2	1:A:607:ILE:HG12	2.03	0.41
1:A:667:ASN:HD22	1:A:668:ASP:N	2.18	0.41
1:A:643:HIS:H	1:A:643:HIS:CD2	2.38	0.41
1:A:324:MET:C	1:A:327:PRO:HD2	2.46	0.41
1:A:812:GLU:O	1:A:816:LYS:HG3	2.21	0.41
1:A:835:ARG:NE	10:A:1024:EDO:H22	2.32	0.41
1:A:508:LEU:HD23	1:A:508:LEU:HA	1.93	0.40
1:A:389:LEU:N	1:A:389:LEU:HD23	2.37	0.40
1:A:541:PRO:HB2	1:A:841:TYR:CE2	2.57	0.40

All (2) 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)
11:A:927:HOH:O	11:A:1411:HOH:O[1_655]	2.01	0.19
1:A:400:LEU:O	11:A:1384:HOH:O[2_655]	2.19	0.01

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	778/831 (94%)	758 (97%)	19 (2%)	1 (0%)	48	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	386	PRO

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	693/756 (92%)	683 (99%)	10 (1%)	59	46

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

Mol	Chain	Res	Type
1	A	52	THR
1	A	54	THR
1	A	95	LYS
1	A	152	ARG
1	A	232	MET
1	A	608	LEU
1	A	667	ASN
1	A	686	GLU
1	A	693	LEU
1	A	695	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	134	GLN
1	A	337	GLN
1	A	348	HIS
1	A	374	ASN
1	A	471	GLN
1	A	484	GLN
1	A	643	HIS
1	A	646	ASN
1	A	660	GLN
1	A	661	ASN
1	A	667	ASN
1	A	797	ASN
1	A	802	ASN
1	A	827	HIS
1	A	852	HIS

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 ⓘ

10 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	0.69	0	17,19,21	1.24	1 (5%)
2	NAG	B	2	2	14,14,15	0.47	0	17,19,21	1.96	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	1	1,3	14,14,15	0.45	0	17,19,21	1.08	1 (5%)
3	NAG	C	2	3	14,14,15	0.53	0	17,19,21	0.95	0
3	BMA	C	3	3	11,11,12	0.78	0	15,15,17	1.07	1 (6%)
3	MAN	C	4	3	11,11,12	0.66	0	15,15,17	0.88	0
3	MAN	C	5	3	11,11,12	0.59	0	15,15,17	1.08	1 (6%)
3	MAN	C	6	3	11,11,12	0.69	0	15,15,17	0.84	0
2	NAG	D	1	1,2	14,14,15	0.65	0	17,19,21	1.00	0
2	NAG	D	2	2	14,14,15	0.64	0	17,19,21	1.20	2 (11%)

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	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	0/2/19/22	0/1/1/1
3	MAN	C	5	3	-	0/2/19/22	0/1/1/1
3	MAN	C	6	3	-	0/2/19/22	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C1-O5-C5	6.78	121.28	112.19
2	B	1	NAG	C1-O5-C5	3.90	117.42	112.19
3	C	5	MAN	C2-C3-C4	-2.94	105.69	110.86
2	D	2	NAG	C3-C4-C5	-2.47	105.75	110.23
2	D	2	NAG	C1-O5-C5	2.46	115.48	112.19
3	C	1	NAG	O5-C1-C2	-2.30	107.72	111.29
3	C	3	BMA	O5-C1-C2	-2.07	105.86	110.79

There are no chirality outliers.

All (6) torsion outliers are listed below:

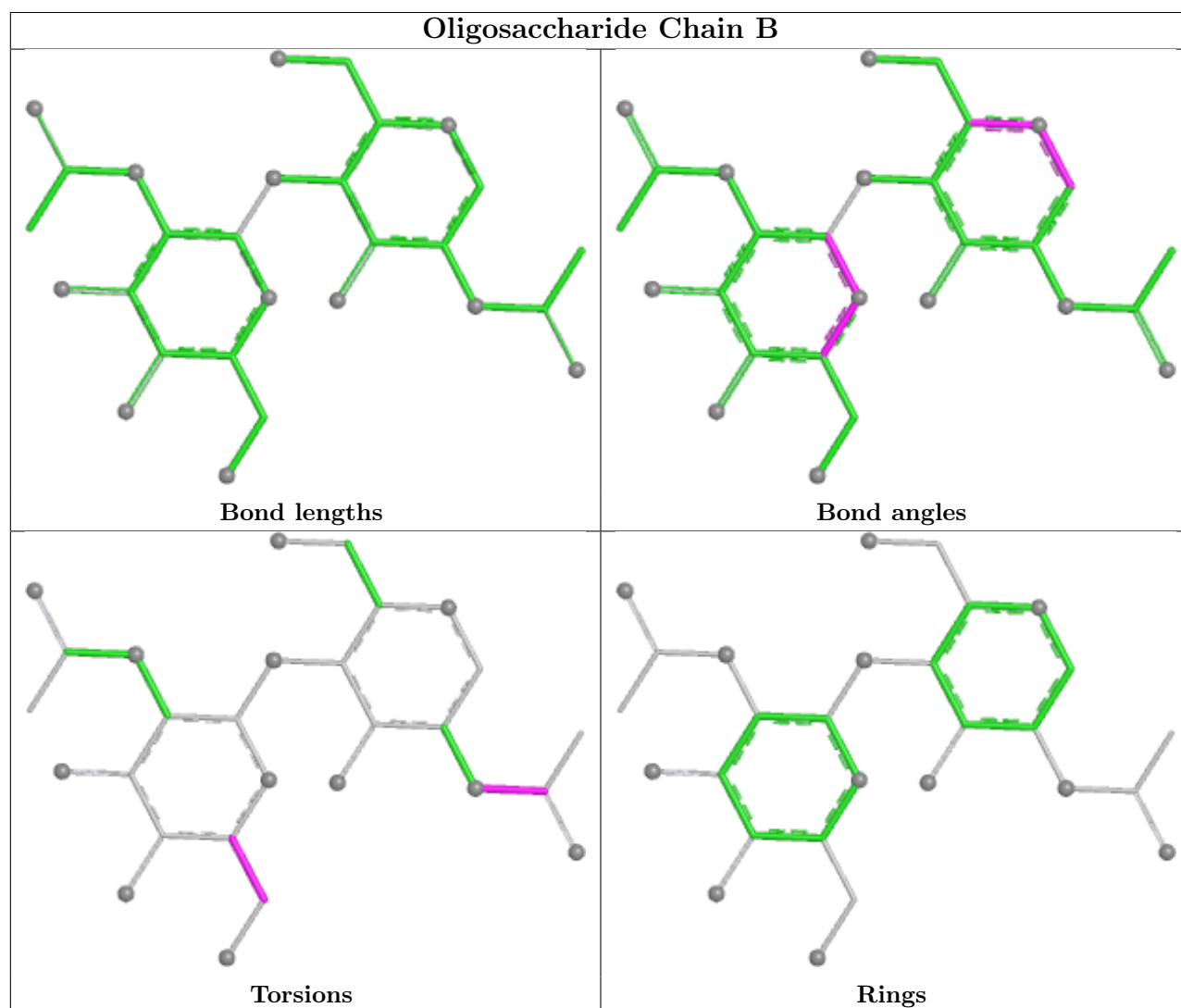
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
2	B	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O7-C7-N2-C2

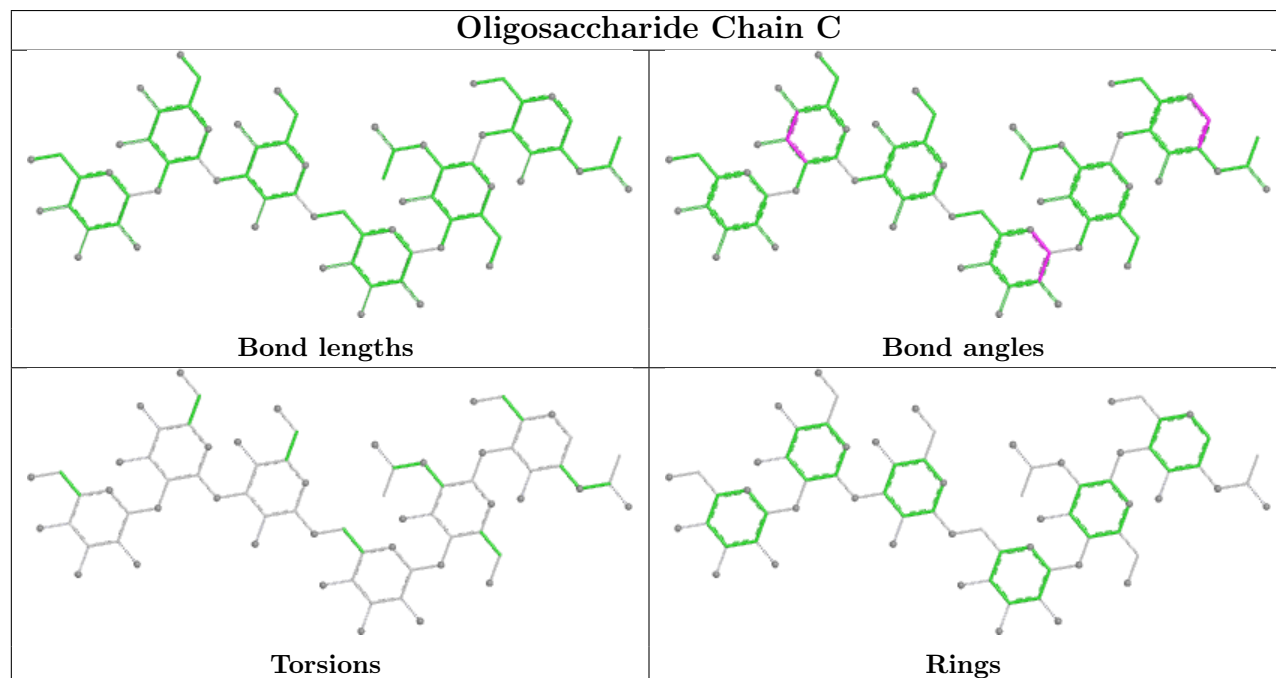
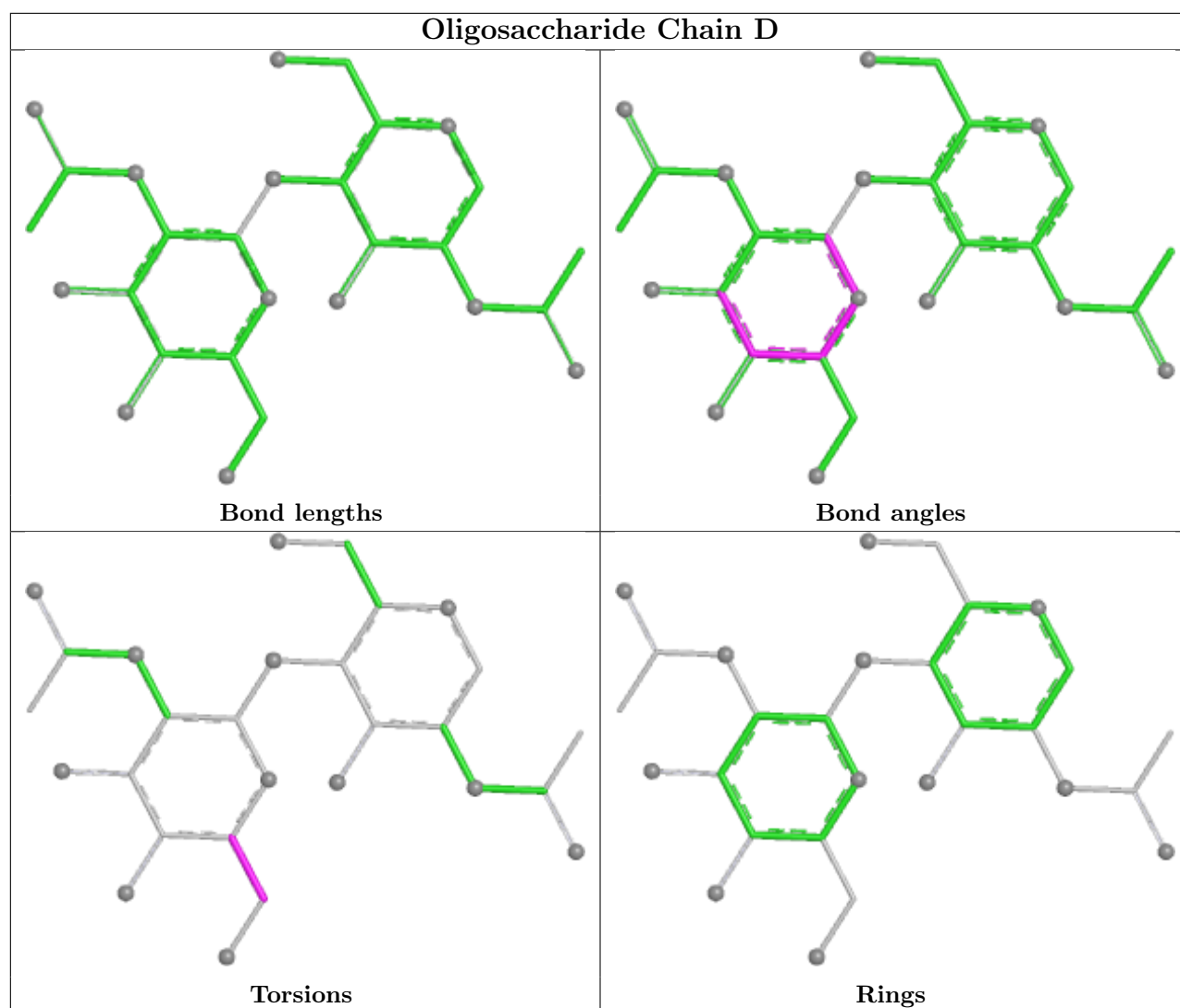
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	5	MAN	2	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

Of 30 ligands modelled in this entry, 5 are monoatomic - leaving 25 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
10	EDO	A	1021	-	3,3,3	0.42	0	2,2,2	0.49	0
10	EDO	A	1015	-	3,3,3	0.33	0	2,2,2	0.54	0
10	EDO	A	1026	-	3,3,3	0.30	0	2,2,2	0.44	0
10	EDO	A	1027	-	3,3,3	0.51	0	2,2,2	0.34	0
10	EDO	A	1029	-	3,3,3	0.50	0	2,2,2	0.34	0
10	EDO	A	1016	-	3,3,3	0.48	0	2,2,2	0.19	0
10	EDO	A	1019	-	3,3,3	0.40	0	2,2,2	0.37	0
10	EDO	A	1030	-	3,3,3	0.42	0	2,2,2	0.13	0
10	EDO	A	1020	-	3,3,3	0.42	0	2,2,2	0.38	0
10	EDO	A	1028	-	3,3,3	0.49	0	2,2,2	0.35	0
10	EDO	A	1011	-	3,3,3	0.63	0	2,2,2	0.09	0
10	EDO	A	1022	-	3,3,3	0.47	0	2,2,2	0.36	0
8	NKR	A	1007	-	17,17,32	1.74	3 (17%)	16,16,36	1.04	1 (6%)
10	EDO	A	1012	-	3,3,3	0.35	0	2,2,2	0.60	0
9	SCN	A	1008	-	1,2,2	0.42	0	0,1,1	-	-
10	EDO	A	1025	-	3,3,3	0.40	0	2,2,2	0.36	0
8	NKR	A	1006	4	32,32,32	1.36	2 (6%)	34,36,36	1.21	5 (14%)
10	EDO	A	1018	-	3,3,3	0.57	0	2,2,2	0.28	0
10	EDO	A	1023	-	3,3,3	0.40	0	2,2,2	0.67	0
9	SCN	A	1009	-	1,2,2	0.98	0	0,1,1	-	-
10	EDO	A	1010	-	3,3,3	0.44	0	2,2,2	0.52	0
10	EDO	A	1013	-	3,3,3	0.50	0	2,2,2	0.32	0
10	EDO	A	1024	-	3,3,3	0.47	0	2,2,2	0.27	0
10	EDO	A	1014	-	3,3,3	0.50	0	2,2,2	0.18	0
10	EDO	A	1017	-	3,3,3	0.45	0	2,2,2	0.45	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
10	EDO	A	1021	-	-	1/1/1/1	-
10	EDO	A	1015	-	-	0/1/1/1	-
10	EDO	A	1026	-	-	0/1/1/1	-
10	EDO	A	1027	-	-	0/1/1/1	-
10	EDO	A	1029	-	-	0/1/1/1	-
10	EDO	A	1016	-	-	0/1/1/1	-
10	EDO	A	1019	-	-	0/1/1/1	-
10	EDO	A	1030	-	-	0/1/1/1	-
10	EDO	A	1020	-	-	0/1/1/1	-
10	EDO	A	1028	-	-	0/1/1/1	-
10	EDO	A	1011	-	-	0/1/1/1	-
10	EDO	A	1022	-	-	0/1/1/1	-
8	NKR	A	1007	-	-	6/15/15/32	-
10	EDO	A	1012	-	-	0/1/1/1	-
10	EDO	A	1025	-	-	0/1/1/1	-
8	NKR	A	1006	4	-	10/32/32/32	-
10	EDO	A	1018	-	-	0/1/1/1	-
10	EDO	A	1023	-	-	1/1/1/1	-
10	EDO	A	1010	-	-	0/1/1/1	-
10	EDO	A	1013	-	-	0/1/1/1	-
10	EDO	A	1024	-	-	0/1/1/1	-
10	EDO	A	1014	-	-	0/1/1/1	-
10	EDO	A	1017	-	-	0/1/1/1	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1007	NKR	CBE-CBD	-2.77	1.37	1.50
8	A	1006	NKR	PAC-OAB	2.54	1.64	1.54
8	A	1006	NKR	CBE-CBD	-2.44	1.39	1.50
8	A	1007	NKR	CAP-CAQ	-2.40	1.39	1.50
8	A	1007	NKR	CAS-CAT	-2.38	1.34	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1006	NKR	CAL-CAM-CAN	-3.62	104.70	112.57
8	A	1007	NKR	CBC-CBB-CBA	-3.10	96.75	112.02
8	A	1006	NKR	OBG-CAH-CAG	-2.54	100.90	109.70
8	A	1006	NKR	OAA-PAC-OAF	2.46	113.08	106.67
8	A	1006	NKR	OBG-CAH-CAI	-2.16	102.22	109.70
8	A	1006	NKR	CAI-OAJ-CAK	-2.08	109.51	117.12

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1006	NKR	CAU-CAV-CAW-CAX
8	A	1006	NKR	CAX-CAY-CAZ-CBA
8	A	1007	NKR	CAW-CAX-CAY-CAZ
8	A	1006	NKR	CAN-CAO-CAP-CAQ
8	A	1006	NKR	CAQ-CAR-CAS-CAT
8	A	1006	NKR	CAR-CAS-CAT-CAU
8	A	1006	NKR	CAZ-CBA-CBB-CBC
8	A	1007	NKR	CAR-CAS-CAT-CAU
8	A	1007	NKR	CAX-CAY-CAZ-CBA
8	A	1007	NKR	CAZ-CBA-CBB-CBC
8	A	1007	NKR	CBA-CBB-CBC-CBD
8	A	1007	NKR	CAO-CAP-CAQ-CAR
8	A	1006	NKR	CAO-CAP-CAQ-CAR
8	A	1006	NKR	CAW-CAX-CAY-CAZ
8	A	1006	NKR	CBC-CBD-CBE-CBF
10	A	1023	EDO	O1-C1-C2-O2
8	A	1006	NKR	CAL-CAM-CAN-CAO
10	A	1021	EDO	O1-C1-C2-O2

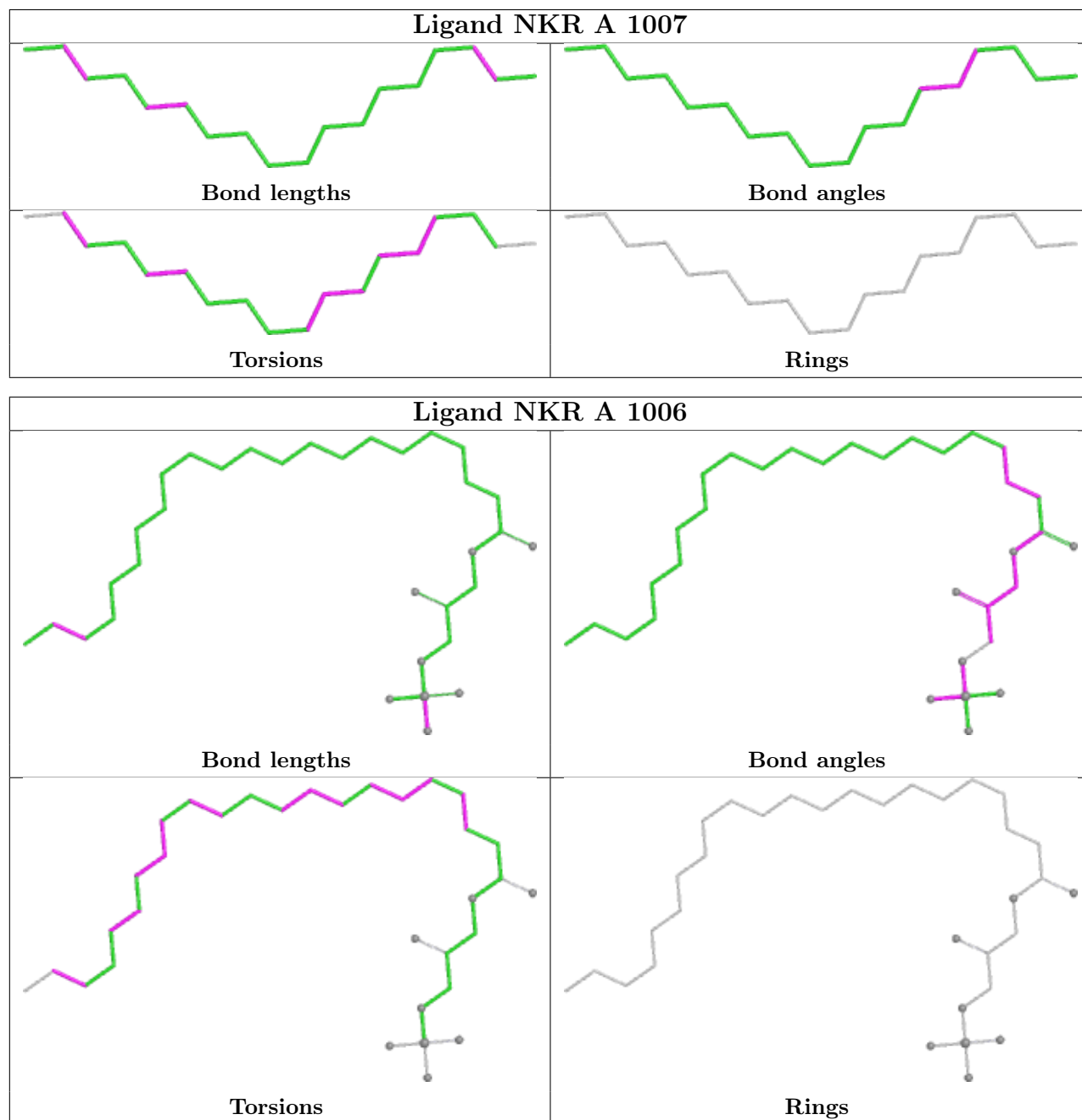
There are no ring outliers.

11 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	1015	EDO	1	0
10	A	1026	EDO	2	0
10	A	1030	EDO	2	0
10	A	1011	EDO	1	0
8	A	1007	NKR	6	0
10	A	1012	EDO	2	0
9	A	1008	SCN	1	0
10	A	1025	EDO	2	0
8	A	1006	NKR	4	0
10	A	1023	EDO	2	0
10	A	1024	EDO	7	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 ⓘ

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	779/831 (93%)	0.37	51 (6%)	25 27	12, 30, 54, 66	5 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	652	VAL	4.3
1	A	78	LEU	3.9
1	A	274	PHE	3.7
1	A	56	GLY	3.6
1	A	566	CYS	3.6
1	A	71	PRO	3.5
1	A	51	TRP	3.4
1	A	693	LEU	3.3
1	A	689	TYR	3.2
1	A	564	LEU	3.2
1	A	468	CYS	3.1
1	A	568	CYS	3.1
1	A	52	THR	3.1
1	A	685	PRO	3.0
1	A	637	VAL	3.0
1	A	562	PHE	2.9
1	A	73	CYS	2.9
1	A	565	GLY	2.9
1	A	70	PRO	2.9
1	A	555	ILE	2.9
1	A	644	LEU	2.8
1	A	55	SER	2.8
1	A	161	VAL	2.6
1	A	85	CYS	2.6
1	A	569	ASP	2.6
1	A	158	ALA	2.6
1	A	640	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	556	MET	2.5
1	A	557	TYR	2.5
1	A	273	PHE	2.4
1	A	687	ALA	2.4
1	A	554	GLY	2.4
1	A	69	GLY	2.3
1	A	683	SER	2.3
1	A	648	VAL	2.3
1	A	107	CYS	2.3
1	A	124	LEU	2.3
1	A	320	PHE	2.3
1	A	68	VAL	2.3
1	A	646	ASN	2.2
1	A	558	LEU	2.2
1	A	110	VAL	2.2
1	A	458	LEU	2.2
1	A	54	THR	2.2
1	A	684	SER	2.1
1	A	665	TYR	2.1
1	A	647	CYS	2.1
1	A	645	THR	2.1
1	A	82	TYR	2.1
1	A	53	ASN	2.0
1	A	667	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

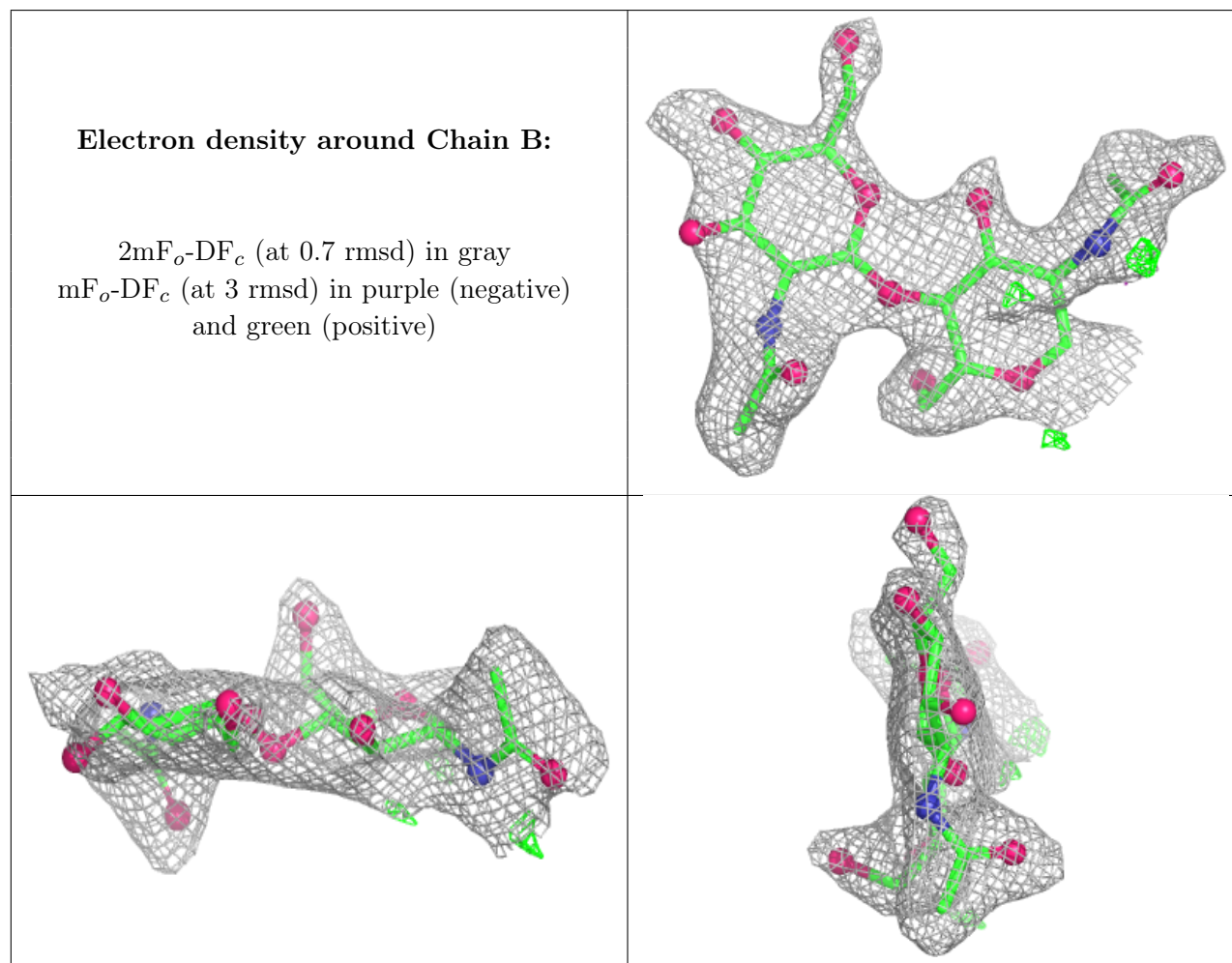
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	B	1	14/15	0.70	0.14	55,60,61,62	0
2	NAG	B	2	14/15	0.74	0.13	58,62,64,65	0
2	NAG	D	2	14/15	0.76	0.14	46,53,56,61	0
3	BMA	C	3	11/12	0.80	0.11	39,43,49,50	0

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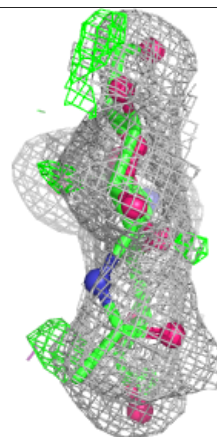
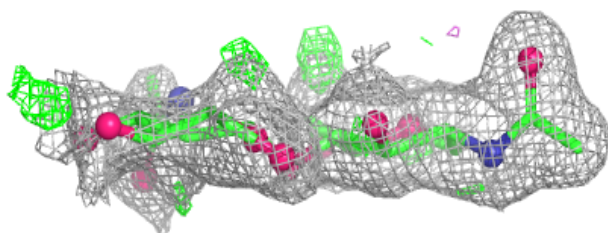
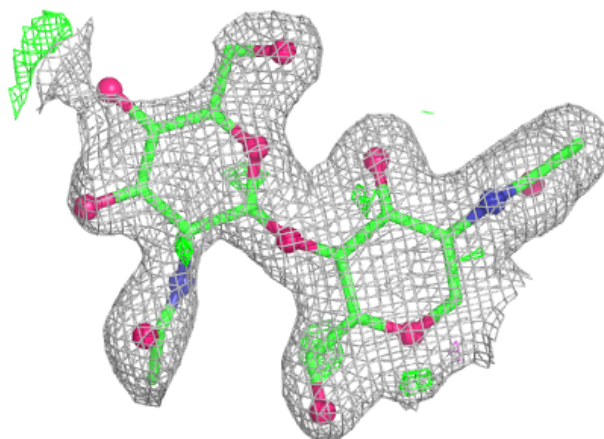
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	C	4	11/12	0.85	0.11	37,39,41,47	0
3	MAN	C	5	11/12	0.88	0.14	32,36,40,46	0
2	NAG	D	1	14/15	0.92	0.10	25,30,38,43	0
3	NAG	C	2	14/15	0.94	0.09	23,28,38,39	0
3	MAN	C	6	11/12	0.94	0.09	24,30,38,38	0
3	NAG	C	1	14/15	0.98	0.06	15,18,21,22	0

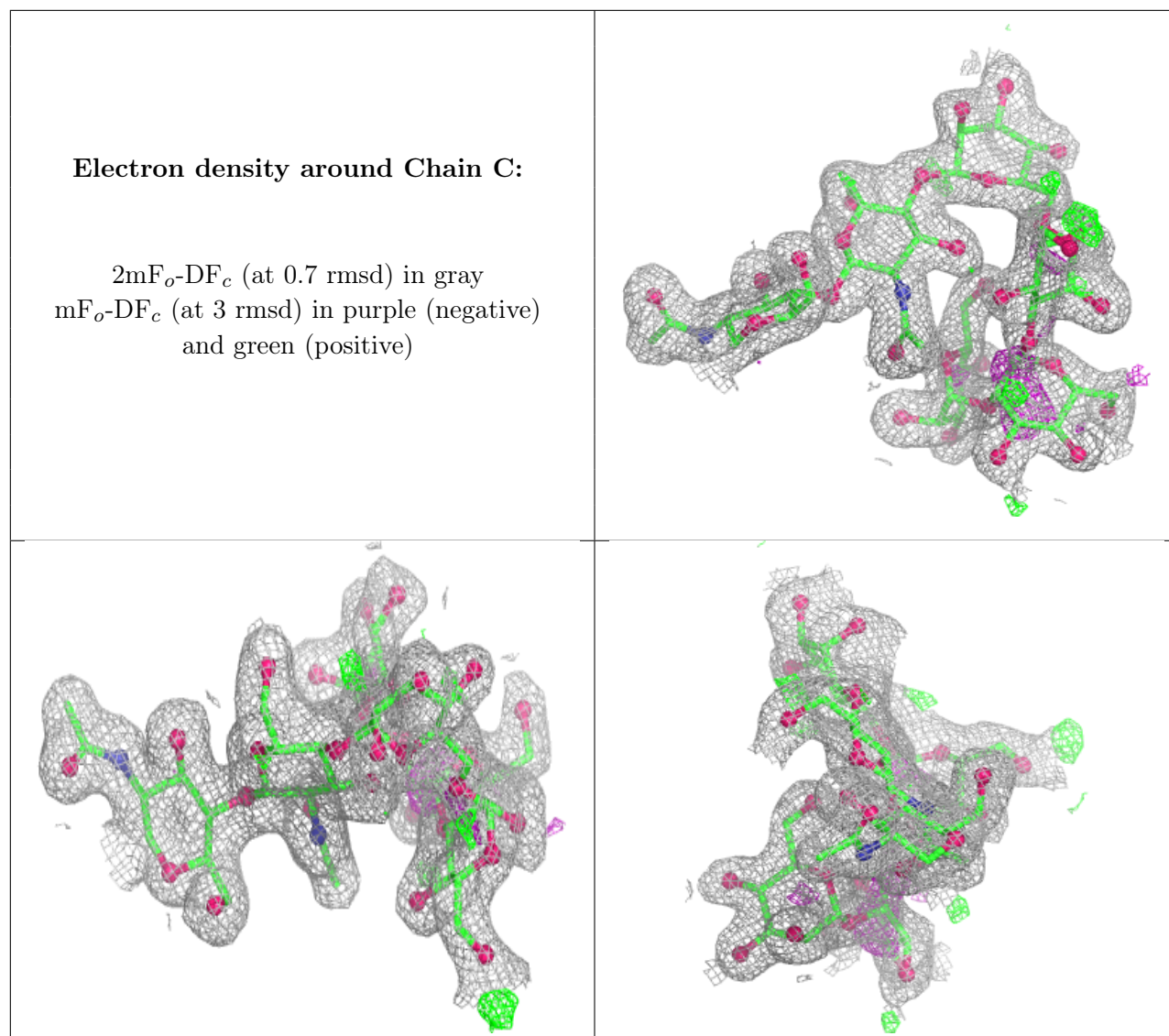
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain D:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





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
8	NKR	A	1007	18/33	0.72	0.14	31,38,43,43	0
9	SCN	A	1008	3/3	0.75	0.20	19,19,32,44	0
7	K	A	1005	1/1	0.82	0.16	44,44,44,44	0
10	EDO	A	1025	4/4	0.84	0.13	34,36,41,41	0
10	EDO	A	1022	4/4	0.87	0.10	37,38,40,45	0
10	EDO	A	1011	4/4	0.88	0.15	27,28,34,36	0
10	EDO	A	1024	4/4	0.88	0.11	39,40,43,47	0

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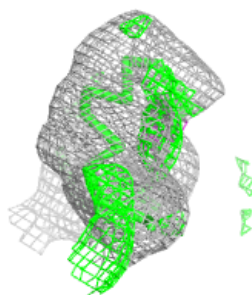
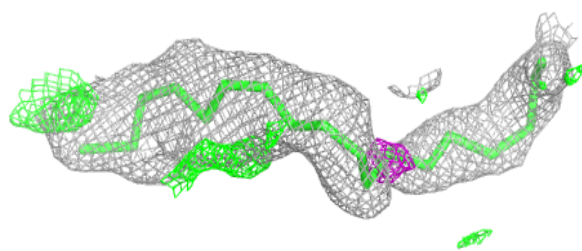
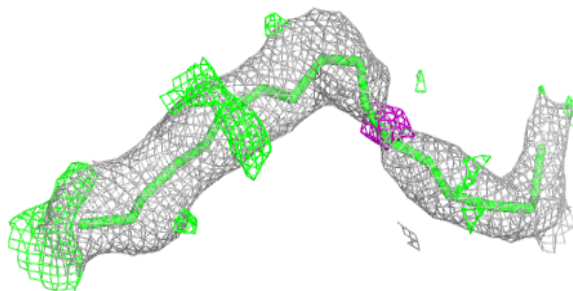
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	EDO	A	1012	4/4	0.88	0.14	33,36,38,41	0
10	EDO	A	1027	4/4	0.88	0.11	33,34,40,40	0
10	EDO	A	1015	4/4	0.90	0.12	27,28,33,36	0
10	EDO	A	1021	4/4	0.90	0.13	31,37,38,45	0
8	NKR	A	1006	33/33	0.90	0.11	19,36,41,46	0
10	EDO	A	1023	4/4	0.91	0.10	28,29,32,35	0
10	EDO	A	1017	4/4	0.91	0.12	31,32,36,38	0
10	EDO	A	1029	4/4	0.91	0.07	27,29,29,34	0
10	EDO	A	1030	4/4	0.92	0.11	19,30,33,37	0
10	EDO	A	1020	4/4	0.93	0.12	27,30,37,42	0
10	EDO	A	1010	4/4	0.93	0.12	31,33,33,35	0
10	EDO	A	1014	4/4	0.93	0.10	31,31,32,36	0
10	EDO	A	1019	4/4	0.94	0.07	35,36,37,42	0
10	EDO	A	1018	4/4	0.94	0.11	25,30,35,36	0
6	NA	A	1004	1/1	0.95	0.08	28,28,28,28	0
10	EDO	A	1013	4/4	0.95	0.10	30,31,33,34	0
10	EDO	A	1016	4/4	0.95	0.08	28,31,31,33	0
10	EDO	A	1026	4/4	0.96	0.08	26,32,36,38	0
9	SCN	A	1009	3/3	0.98	0.08	26,26,31,42	0
10	EDO	A	1028	4/4	0.98	0.04	22,23,23,24	0
5	CA	A	1003	1/1	0.99	0.02	21,21,21,21	0
4	ZN	A	1001	1/1	0.99	0.02	18,18,18,18	0
4	ZN	A	1002	1/1	1.00	0.01	16,16,16,16	0

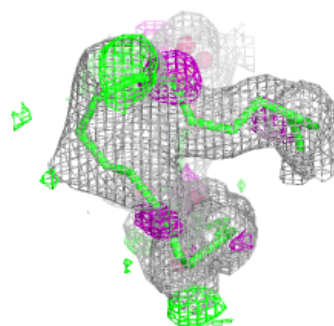
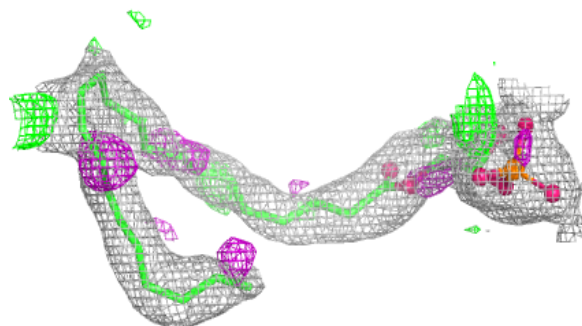
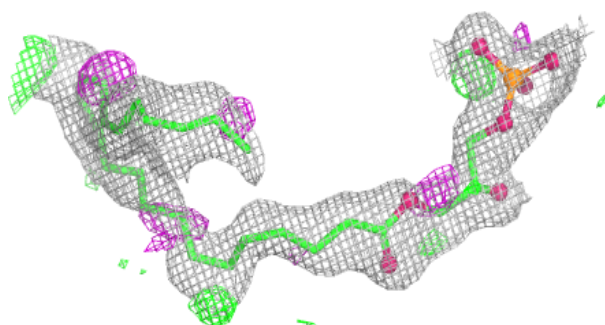
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NKR A 1007:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around NKR A 1006:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.