



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 09:52 PM BST

PDB ID : 4GTZ
Title : Crystal structure of mouse Enpp1 in complex with CMP
Authors : Kato, K.; Nishimasu, H.; Ishitani, R.; Nureki, O.
Deposited on : 2012-08-29
Resolution : 3.19 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
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) : 2.13.1

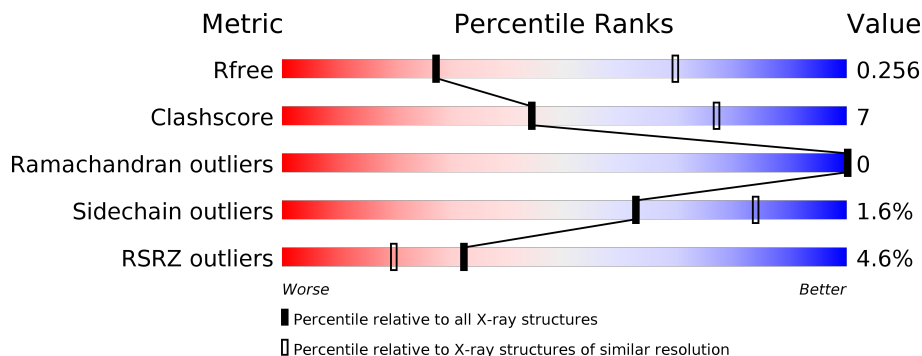
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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	823	 3% 72% 13% 14%
1	B	823	 5% 69% 15% 15%
2	C	6	 67% 33%
3	D	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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	B	1003	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 11156 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.

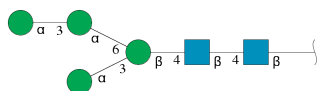
- Molecule 1 is a protein called Ectonucleotide pyrophosphatase/phosphodiesterase family member 2, Alkaline phosphodiesterase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	706	Total	C	N	O	S	0	0	0
			5502	3540	907	1026	29			
1	B	697	Total	C	N	O	S	0	0	0
			5450	3509	894	1018	29			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	ARG	LYS	engineered mutation	UNP Q9R1E6
B	59	ARG	LYS	engineered mutation	UNP Q9R1E6

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



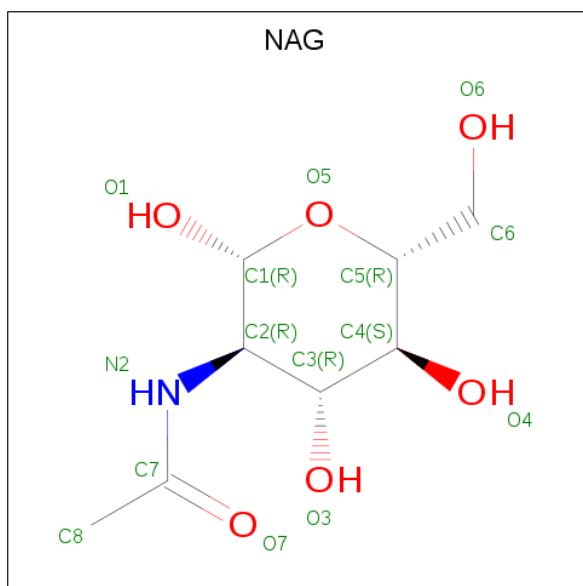
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	6	Total	C	N	O	0	0	0
			72	40	2	30			

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



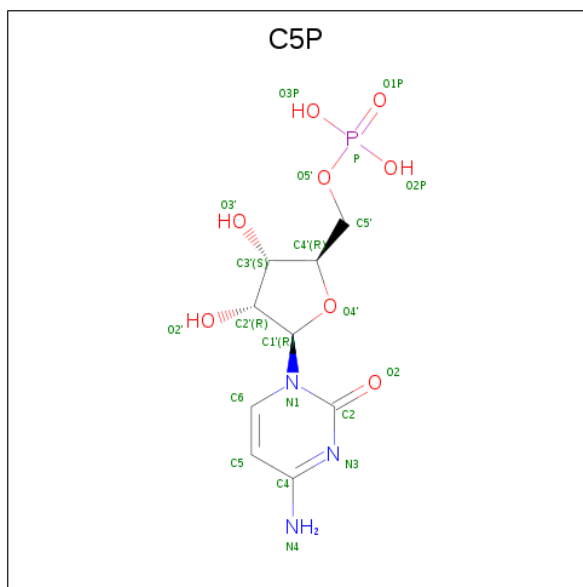
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	2	28	16	2	10	0	0	0

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



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

- Molecule 5 is CYTIDINE-5'-MONOPHOSPHATE (three-letter code: C5P) (formula: $C_9H_{14}N_3O_8P$).



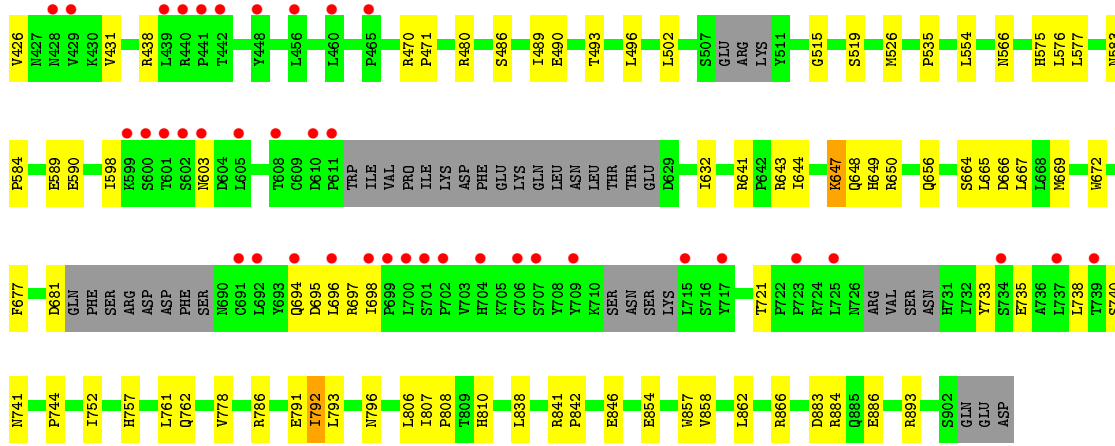
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	21	9	3	8	1	0	0
5	B	1	21	9	3	8	1	0	0

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
6	B	2	2	2	0	0
6	A	2	2	2	0	0

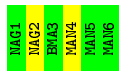
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
7	B	1	1	1	0	0
7	A	1	1	1	0	0



- Molecule 2: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 67% 33%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	105.21Å 105.21Å 174.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.06 – 3.19 49.06 – 3.19	Depositor EDS
% Data completeness (in resolution range)	97.1 (49.06-3.19) 97.1 (49.06-3.19)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.7.2_869	Depositor
R, R_{free}	0.233 , 0.263 0.224 , 0.256	Depositor DCC
R_{free} test set	1731 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	67.8	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.066 for -h,-k,l 0.076 for h,-h-k,-l 0.058 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	11156	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: ZN, BMA, NAG, C5P, CA, MAN

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	0.24	0/5666	0.42	0/7746
1	B	0.23	0/5611	0.42	0/7667
All	All	0.23	0/11277	0.42	0/15413

There are no bond length outliers.

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	5502	0	5138	66	0
1	B	5450	0	5099	77	0
2	C	72	0	61	1	0
3	D	28	0	25	1	0
4	A	28	0	26	0	0
4	B	28	0	26	0	0
5	A	21	0	12	1	0
5	B	21	0	12	5	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	1	0	0	0	0
All	All	11156	0	10399	142	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 7.

All (142) 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:B:301:THR:HG21	1:B:307:SER:HB2	1.66	0.77
1:A:225:THR:HG21	1:A:576:LEU:HG	1.69	0.75
1:B:470:ARG:NH1	1:B:846:GLU:O	2.20	0.74
1:B:225:THR:HG21	1:B:576:LEU:HG	1.74	0.70
1:B:603:ASN:H	1:B:694:GLN:HE22	1.43	0.66
1:A:752:ILE:HG23	1:A:858:VAL:HG13	1.80	0.64
1:A:316:PRO:HG2	1:A:319:TYR:HB3	1.80	0.64
1:A:760:LEU:HD21	1:A:859:GLU:HG2	1.80	0.63
1:A:438:ARG:HG2	1:A:493:THR:HG22	1.81	0.62
1:B:733:TYR:CZ	1:B:735:GLU:HB2	2.35	0.62
1:B:650:ARG:NH1	1:B:666:ASP:OD1	2.32	0.62
1:B:496:LEU:HD21	1:B:502:LEU:HB2	1.83	0.61
1:A:589:GLU:OE2	1:A:641:ARG:NH2	2.34	0.60
1:B:315:LEU:HD12	1:B:316:PRO:HD2	1.84	0.60
1:A:786:ARG:HH21	2:C:2:NAG:H62	1.66	0.59
1:B:589:GLU:OE2	1:B:641:ARG:NH2	2.35	0.59
1:B:590:GLU:HB3	1:B:647:LYS:HB3	1.85	0.59
1:B:744:PRO:HG2	1:B:808:PRO:HD3	1.84	0.59
1:A:486:SER:HB3	1:A:489:ILE:HG13	1.84	0.58
1:A:733:TYR:CZ	1:A:735:GLU:HB2	2.38	0.58
1:A:308:ASP:OD1	1:A:308:ASP:N	2.35	0.58
1:A:735:GLU:HA	1:A:738:LEU:HD13	1.86	0.57
1:A:259:ASN:ND2	5:A:1009:C5P:O3P	2.35	0.57
1:B:259:ASN:ND2	5:B:1005:C5P:O1P	2.38	0.57
1:B:793:LEU:HD22	1:B:806:LEU:HD21	1.86	0.57
1:A:649:HIS:NE2	1:A:664:SER:OG	2.32	0.56
1:A:643:ARG:NH2	1:A:883:ASP:OD2	2.38	0.56
1:B:197:PHE:HE1	1:B:354:LEU:HD13	1.70	0.56
1:B:649:HIS:NE2	1:B:664:SER:OG	2.29	0.56
1:A:721:THR:HB	1:A:741:ASN:HD21	1.70	0.56
1:A:778:VAL:HB	1:A:810:HIS:HB2	1.88	0.55
1:B:486:SER:HB3	1:B:489:ILE:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:PHE:HA	1:A:309:VAL:HG22	1.88	0.54
1:B:735:GLU:HA	1:B:738:LEU:HD13	1.90	0.54
1:B:643:ARG:NH2	1:B:883:ASP:OD2	2.40	0.53
1:B:575:HIS:CE1	1:B:893:ARG:HD3	2.44	0.53
1:B:667:LEU:HB3	1:B:669:MET:HG2	1.90	0.53
1:B:238:THR:OG1	5:B:1005:C5P:O2P	2.27	0.52
1:B:338:TRP:HA	1:B:341:LEU:HD13	1.92	0.52
1:B:366:PRO:HG3	1:B:408:MET:HG3	1.90	0.52
1:B:238:THR:OG1	5:B:1005:C5P:P	2.67	0.52
1:B:438:ARG:HG2	1:B:493:THR:HG22	1.92	0.52
1:B:786:ARG:HH21	3:D:2:NAG:H62	1.75	0.51
1:A:598:ILE:HG23	1:A:696:LEU:HB3	1.92	0.51
1:A:197:PHE:HE1	1:A:354:LEU:HD13	1.75	0.51
1:A:793:LEU:HD22	1:A:806:LEU:HD21	1.94	0.50
1:B:353:TYR:CE2	5:B:1005:C5P:H5	2.47	0.50
1:A:338:TRP:HA	1:A:341:LEU:HD13	1.94	0.50
1:B:677:PHE:HE2	1:B:762:GLN:HA	1.77	0.49
1:A:188:GLU:O	1:A:346:ARG:NH2	2.35	0.49
1:B:721:THR:HB	1:B:741:ASN:HD21	1.77	0.49
1:B:214:LEU:HD22	1:B:379:ASP:HB2	1.93	0.49
1:A:257:ILE:HG12	1:A:489:ILE:HG12	1.95	0.49
1:B:838:LEU:HD11	1:B:862:LEU:HD13	1.94	0.49
1:A:434:GLY:HA2	1:A:501:GLN:HE21	1.76	0.49
1:A:438:ARG:HB3	1:A:490:GLU:HB2	1.94	0.49
1:B:554:LEU:HD11	1:B:577:LEU:HD21	1.94	0.49
1:B:438:ARG:HB3	1:B:490:GLU:HB2	1.94	0.48
5:B:1005:C5P:H2'1	5:B:1005:C5P:H6	1.55	0.48
1:B:778:VAL:HB	1:B:810:HIS:HB2	1.94	0.48
1:A:656:GLN:OE1	1:A:697:ARG:NH2	2.46	0.48
1:A:302:TYR:CE2	1:A:320:LYS:HD2	2.47	0.48
1:A:698:ILE:HD13	1:A:740:SER:HB3	1.96	0.48
1:A:245:ILE:HD13	1:A:403:ILE:HD13	1.96	0.48
1:A:710:LYS:H	1:A:801:ARG:NH1	2.12	0.48
1:A:854:GLU:HA	1:A:857:TRP:NE1	2.28	0.48
1:A:649:HIS:HE1	1:A:667:LEU:HD13	1.78	0.48
1:A:884:ARG:HG3	1:A:886:GLU:HG2	1.95	0.47
1:B:752:ILE:HG23	1:B:858:VAL:HG13	1.96	0.47
1:A:419:LEU:HD12	1:A:431:VAL:HG21	1.96	0.47
1:B:647:LYS:HA	1:B:648:GLN:HA	1.51	0.47
1:B:278:PHE:HA	1:B:309:VAL:HG22	1.97	0.47
1:A:788:ASP:HB3	1:A:792:ILE:HG23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:689:SER:O	1:A:690:ASN:HB3	2.15	0.46
1:A:647:LYS:HA	1:A:648:GLN:HA	1.55	0.46
1:B:598:ILE:HG23	1:B:696:LEU:HB3	1.98	0.46
1:A:258:ASP:OD1	1:A:259:ASN:N	2.48	0.46
1:A:172:TRP:O	1:A:219:LYS:NZ	2.40	0.46
1:B:214:LEU:HD21	1:B:375:LEU:HB3	1.98	0.46
1:A:236:THR:OG1	1:A:519:SER:O	2.34	0.45
1:B:649:HIS:HE1	1:B:667:LEU:HD13	1.82	0.45
1:B:236:THR:OG1	1:B:519:SER:O	2.34	0.45
1:B:792:ILE:O	1:B:796:ASN:ND2	2.41	0.45
1:A:320:LYS:HE3	1:A:338:TRP:HZ2	1.81	0.45
1:A:659:PHE:HB3	1:A:675:TYR:HB3	1.99	0.45
1:B:236:THR:HG21	1:B:526:MET:HB3	1.99	0.45
1:B:698:ILE:HD13	1:B:740:SER:HB3	1.99	0.45
1:A:366:PRO:O	1:A:371:VAL:HG21	2.17	0.44
1:B:419:LEU:HD12	1:B:431:VAL:HG21	1.99	0.44
1:B:245:ILE:HD13	1:B:403:ILE:HD13	1.99	0.44
1:A:744:PRO:HG2	1:A:808:PRO:HD3	1.99	0.44
1:B:172:TRP:CZ3	1:B:219:LYS:HD3	2.52	0.44
1:A:283:TYR:CE1	1:A:309:VAL:HG21	2.53	0.44
1:A:715:LEU:O	1:A:801:ARG:NH2	2.51	0.44
1:A:172:TRP:CZ3	1:A:219:LYS:HD3	2.53	0.44
1:B:302:TYR:HD1	1:B:338:TRP:HH2	1.65	0.44
1:A:628:GLU:HG3	1:A:629:ASP:H	1.83	0.43
1:A:649:HIS:CE1	1:A:667:LEU:HD13	2.53	0.43
1:B:695:ASP:HB3	1:B:698:ILE:HG12	2.00	0.43
1:A:418:TYR:HA	1:A:503:ALA:O	2.19	0.43
1:A:395:ASP:N	1:A:395:ASP:OD1	2.50	0.43
1:A:664:SER:HB2	1:A:671:LEU:HG	2.01	0.43
1:B:480:ARG:HD3	1:B:866:ARG:O	2.19	0.43
1:A:474:LYS:HG2	1:A:484:ALA:HA	2.01	0.42
1:A:792:ILE:O	1:A:796:ASN:ND2	2.47	0.42
1:B:251:PRO:HA	1:B:254:HIS:NE2	2.35	0.42
1:B:681:ASP:N	1:B:681:ASP:OD1	2.51	0.42
1:B:884:ARG:HG3	1:B:886:GLU:OE1	2.18	0.42
1:A:203:ARG:NH2	1:A:205:GLU:OE1	2.52	0.42
1:B:248:GLY:O	1:B:566:ASN:HB2	2.20	0.42
1:B:644:ILE:HD11	1:B:672:TRP:HE1	1.85	0.42
1:B:884:ARG:HD2	1:B:884:ARG:HA	1.82	0.42
1:A:279:ASN:HA	1:A:280:PRO:HD3	1.83	0.42
1:B:854:GLU:HA	1:B:857:TRP:NE1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:LEU:HA	1:B:315:LEU:HD12	1.96	0.42
1:A:301:THR:HG21	1:A:307:SER:HB3	2.02	0.42
1:A:807:ILE:HA	1:A:808:PRO:HD3	1.84	0.41
1:B:356:GLU:OE2	1:B:357:PRO:HA	2.20	0.41
1:B:292:ALA:HB1	1:B:297:VAL:HB	2.02	0.41
1:B:242:HIS:CE1	1:B:405:ASP:HB3	2.56	0.41
1:B:757:HIS:HA	1:B:761:LEU:HB2	2.01	0.41
1:A:643:ARG:NH1	1:B:181:ASP:OD1	2.53	0.41
1:B:470:ARG:HA	1:B:471:PRO:HD3	1.90	0.41
1:B:362:HIS:ND1	1:B:515:GLY:O	2.50	0.41
1:B:270:PHE:CE1	1:B:277:LYS:HA	2.55	0.41
1:B:841:ARG:HA	1:B:842:PRO:HD3	1.86	0.41
1:A:346:ARG:HA	1:A:347:PRO:HD3	1.95	0.41
1:A:322:TYR:OH	1:A:355:GLU:OE2	2.30	0.41
1:B:438:ARG:NH1	1:B:490:GLU:OE1	2.51	0.41
1:B:656:GLN:OE1	1:B:697:ARG:NH2	2.47	0.41
1:A:199:LEU:HD11	1:A:402:LEU:HD11	2.03	0.41
1:B:365:GLY:HA2	1:B:366:PRO:HD3	1.92	0.41
1:A:658:GLN:NE2	1:A:726:ASN:HD22	2.19	0.41
1:B:632:ILE:HD12	1:B:632:ILE:HA	1.94	0.41
1:B:316:PRO:HG2	1:B:319:TYR:HB3	2.01	0.40
1:A:271:SER:HB2	1:A:274:SER:HB2	2.03	0.40
1:B:643:ARG:HA	1:B:643:ARG:HD3	1.97	0.40
1:A:641:ARG:NH1	1:B:179:SER:OG	2.54	0.40
1:B:807:ILE:HA	1:B:808:PRO:HD3	1.86	0.40
1:A:242:HIS:CE1	1:A:405:ASP:HB3	2.57	0.40
1:B:180:ILE:HB	1:B:535:PRO:HA	2.03	0.40
1:B:583:ASN:HA	1:B:584:PRO:HD2	1.99	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	698/823 (85%)	675 (97%)	23 (3%)	0	100	100
1	B	685/823 (83%)	660 (96%)	25 (4%)	0	100	100
All	All	1383/1646 (84%)	1335 (96%)	48 (4%)	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	592/755 (78%)	583 (98%)	9 (2%)	65	85
1	B	589/755 (78%)	579 (98%)	10 (2%)	60	83
All	All	1181/1510 (78%)	1162 (98%)	19 (2%)	62	84

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	PHE
1	A	236	THR
1	A	308	ASP
1	A	367	VAL
1	A	416	TYR
1	A	760	LEU
1	A	792	ILE
1	A	874	LEU
1	A	886	GLU
1	B	197	PHE
1	B	236	THR
1	B	308	ASP
1	B	317	ASP
1	B	416	TYR
1	B	426	VAL
1	B	647	LYS
1	B	665	LEU
1	B	791	GLU

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Mol	Chain	Res	Type
1	B	792	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	452	ASN
1	A	501	GLN
1	A	525	ASN
1	A	634	HIS
1	A	658	GLN
1	A	741	ASN
1	A	769	ASN
1	A	820	GLN
1	B	229	ASN
1	B	694	GLN
1	B	820	GLN

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](#)

8 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	C	1	1,2	14,14,15	0.56	0	17,19,21	0.98	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	2	2	14,14,15	0.55	0	17,19,21	0.59	0
2	BMA	C	3	2	11,11,12	0.62	0	15,15,17	0.70	0
2	MAN	C	4	2	11,11,12	0.61	0	15,15,17	1.41	3 (20%)
2	MAN	C	5	2	11,11,12	0.59	0	15,15,17	0.78	0
2	MAN	C	6	2	11,11,12	0.62	0	15,15,17	0.56	0
3	NAG	D	1	1,3	14,14,15	0.60	0	17,19,21	1.15	2 (11%)
3	NAG	D	2	3	14,14,15	0.54	0	17,19,21	0.62	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
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	2/2/19/22	0/1/1/1
2	MAN	C	5	2	-	1/2/19/22	0/1/1/1
2	MAN	C	6	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	MAN	C1-O5-C5	3.09	116.37	112.19
2	C	4	MAN	C1-C2-C3	2.64	112.92	109.67
2	C	4	MAN	O5-C5-C6	2.61	111.30	107.20
3	D	1	NAG	C3-C4-C5	2.39	114.51	110.24
3	D	1	NAG	C4-C3-C2	2.19	114.23	111.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	4	MAN	O5-C5-C6-O6
2	C	4	MAN	C4-C5-C6-O6
2	C	5	MAN	O5-C5-C6-O6

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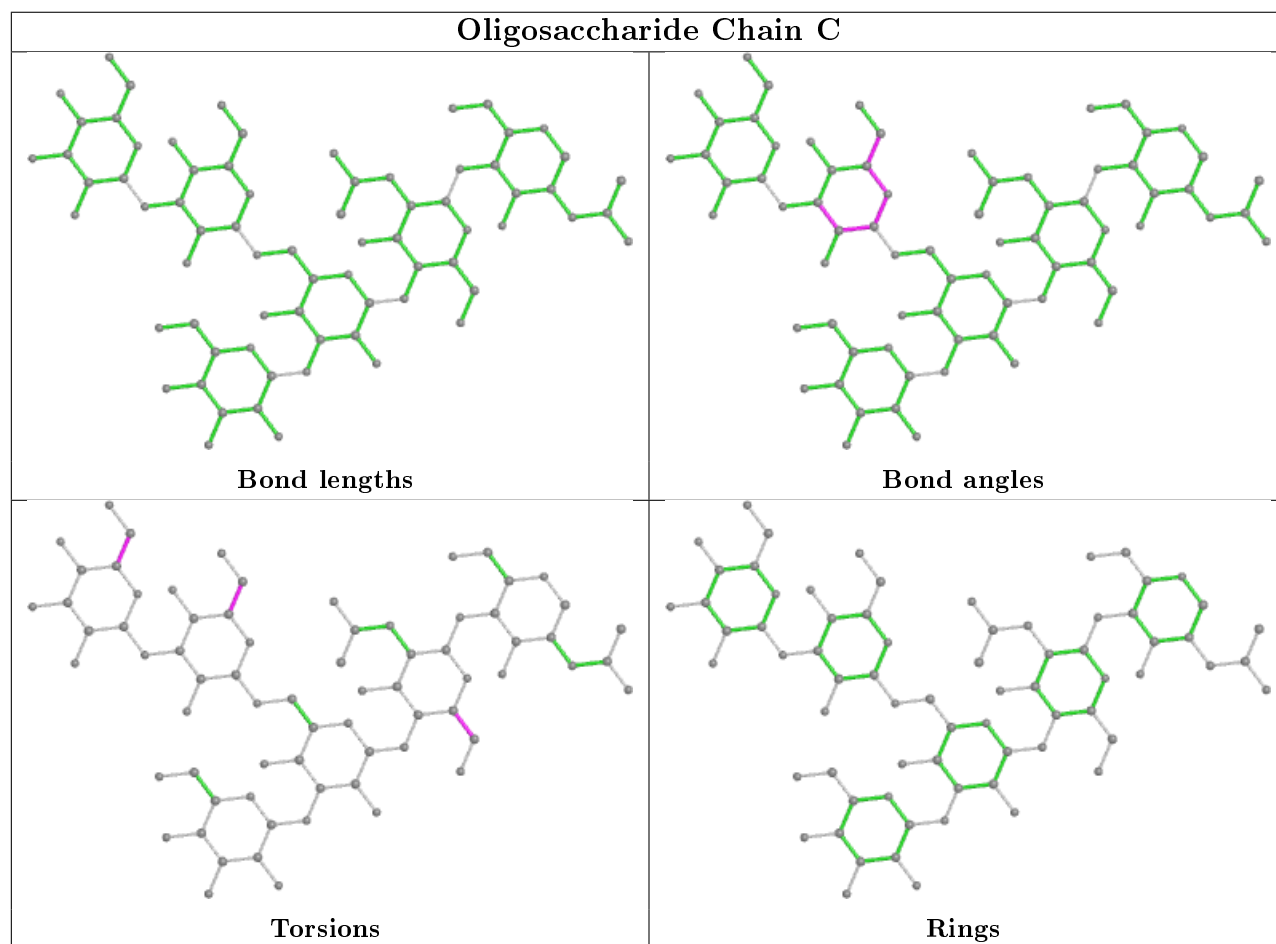
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6

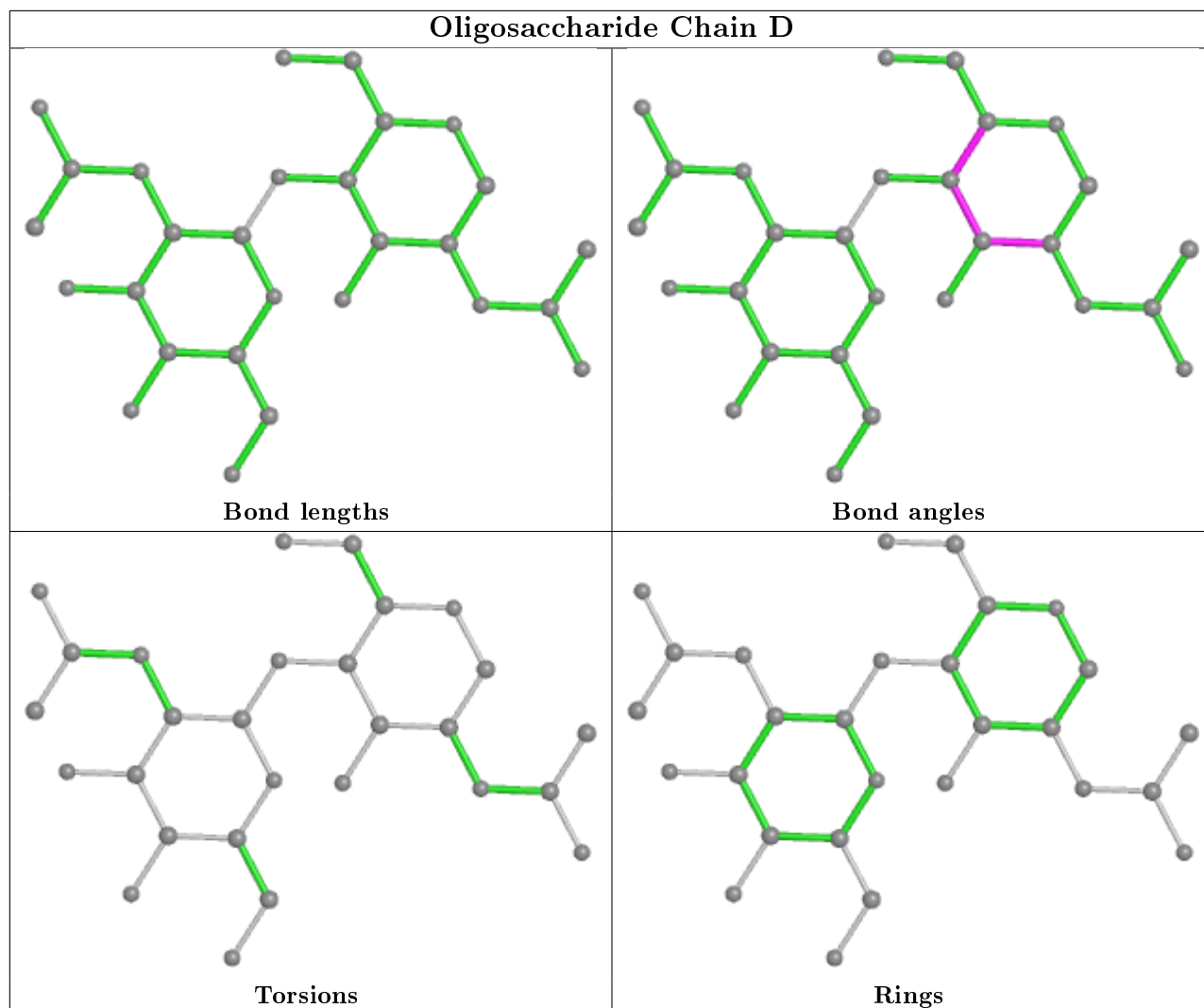
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
3	D	2	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 [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	$\# Z > 2$
4	NAG	B	1003	1	14,14,15	0.55	0	17,19,21	0.71	0
5	C5P	B	1005	6	19,22,22	2.26	5 (26%)	24,33,33	1.38	4 (16%)
4	NAG	B	1004	1	14,14,15	0.49	0	17,19,21	0.94	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	C5P	A	1009	6	19,22,22	2.31	5 (26%)	24,33,33	1.41	3 (12%)
4	NAG	A	1007	1	14,14,15	0.51	0	17,19,21	0.82	1 (5%)
4	NAG	A	1008	1	14,14,15	0.50	0	17,19,21	0.77	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
4	NAG	B	1003	1	-	2/6/23/26	0/1/1/1
5	C5P	B	1005	6	-	3/8/26/26	0/2/2/2
4	NAG	B	1004	1	-	2/6/23/26	0/1/1/1
5	C5P	A	1009	6	-	5/8/26/26	0/2/2/2
4	NAG	A	1007	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1008	1	-	0/6/23/26	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1009	C5P	C6-N1	5.83	1.43	1.35
5	B	1005	C5P	C6-N1	5.54	1.42	1.35
5	B	1005	C5P	C4-N3	4.79	1.43	1.35
5	A	1009	C5P	C4-N3	4.64	1.43	1.35
5	A	1009	C5P	C6-C5	4.19	1.47	1.38
5	B	1005	C5P	C6-C5	3.94	1.46	1.38
5	A	1009	C5P	C2-N3	3.82	1.45	1.38
5	B	1005	C5P	C2-N3	3.73	1.45	1.38
5	A	1009	C5P	C5-C4	2.76	1.47	1.41
5	B	1005	C5P	C5-C4	2.61	1.47	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1009	C5P	C2-N3-C4	4.27	120.66	116.34
5	B	1005	C5P	C2-N3-C4	3.38	119.77	116.34
4	B	1004	NAG	C1-O5-C5	2.82	116.01	112.19
5	A	1009	C5P	O2P-P-O1P	2.29	119.65	110.68
5	B	1005	C5P	N4-C4-N3	2.28	120.10	116.49
5	B	1005	C5P	O2P-P-O1P	2.25	119.47	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1005	C5P	C3'-C2'-C1'	2.20	104.30	100.98
4	A	1008	NAG	C1-O5-C5	2.13	115.08	112.19
5	A	1009	C5P	C3'-C2'-C1'	2.06	104.08	100.98
4	A	1007	NAG	O5-C5-C6	2.05	110.42	107.20

There are no chirality outliers.

All (12) torsion outliers are listed below:

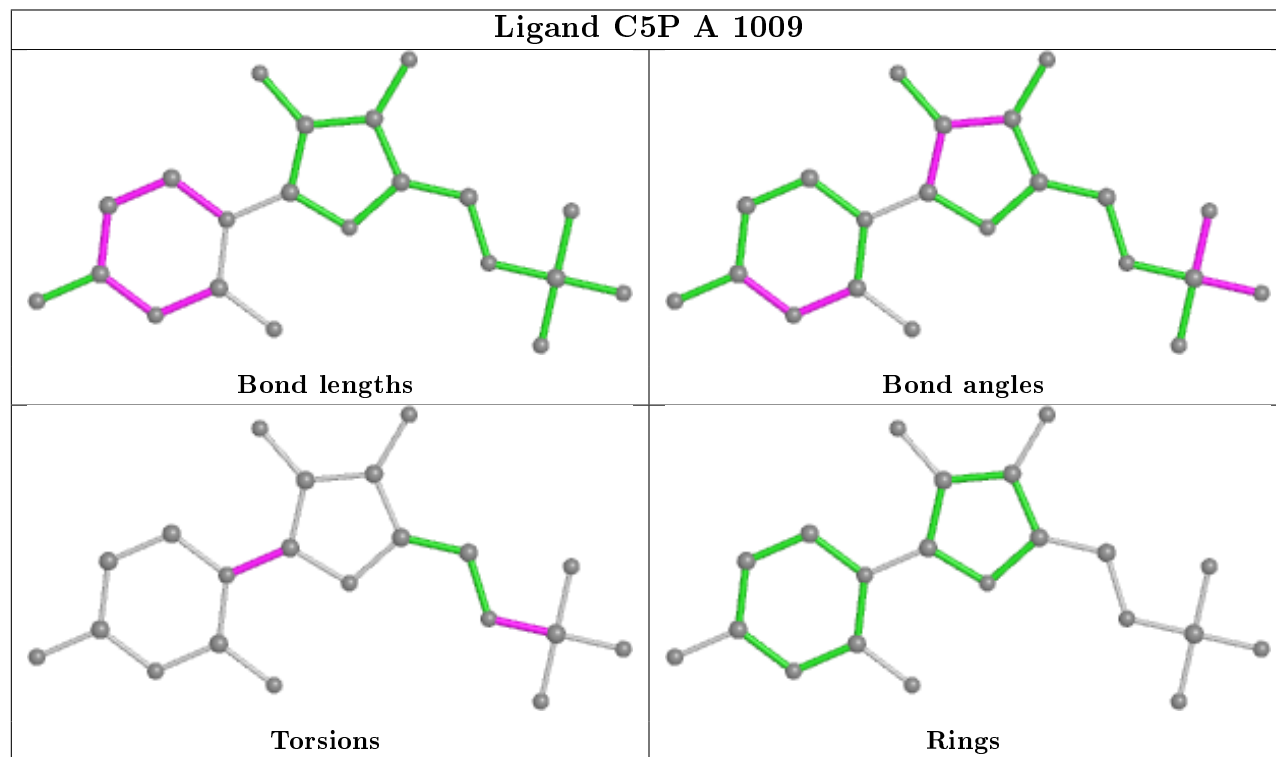
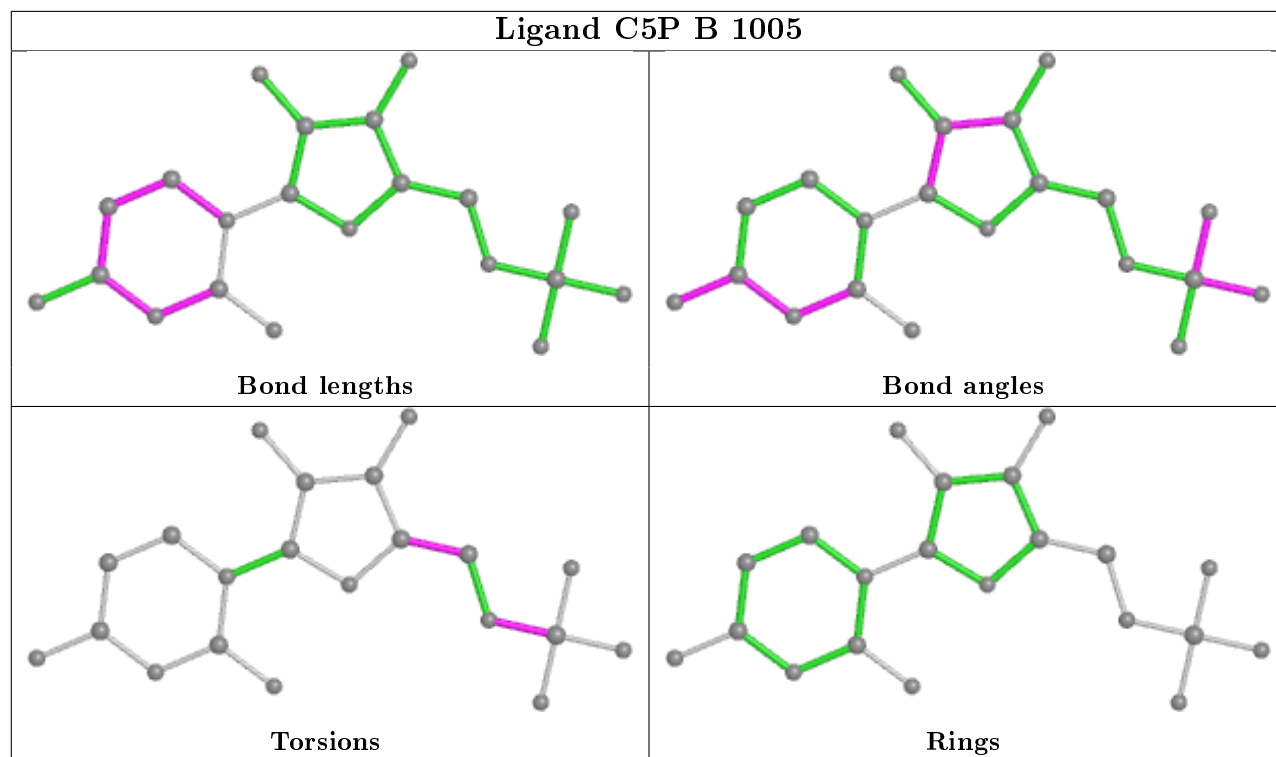
Mol	Chain	Res	Type	Atoms
5	B	1005	C5P	C5'-O5'-P-O3P
5	B	1005	C5P	C5'-O5'-P-O2P
5	A	1009	C5P	C5'-O5'-P-O3P
5	A	1009	C5P	C5'-O5'-P-O1P
5	A	1009	C5P	C5'-O5'-P-O2P
5	A	1009	C5P	O4'-C1'-N1-C6
5	A	1009	C5P	C2'-C1'-N1-C6
4	B	1004	NAG	C8-C7-N2-C2
4	B	1004	NAG	O7-C7-N2-C2
4	B	1003	NAG	C4-C5-C6-O6
4	B	1003	NAG	O5-C5-C6-O6
5	B	1005	C5P	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1005	C5P	5	0
5	A	1009	C5P	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

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	706/823 (85%)	0.10	21 (2%) 50 34	54, 94, 139, 188	0
1	B	697/823 (84%)	0.22	44 (6%) 20 11	54, 97, 145, 180	0
All	All	1403/1646 (85%)	0.16	65 (4%) 32 20	54, 96, 143, 188	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	698	ILE	5.9
1	B	441	PRO	5.7
1	B	700	LEU	4.3
1	A	600	SER	4.2
1	B	439	LEU	3.8
1	B	715	LEU	3.6
1	A	508	GLU	3.5
1	B	704	HIS	3.4
1	A	712	ASN	3.3
1	B	600	SER	3.3
1	B	611	PRO	3.2
1	A	602	SER	3.1
1	B	707	SER	3.1
1	A	598	ILE	3.1
1	A	601	THR	3.0
1	B	610	ASP	2.9
1	B	709	TYR	2.8
1	B	268	ALA	2.8
1	B	602	SER	2.8
1	B	702	PRO	2.7
1	A	439	LEU	2.7
1	B	442	THR	2.7
1	B	737	LEU	2.6
1	B	428	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	340	GLN	2.6
1	B	422	TYR	2.6
1	B	448	TYR	2.6
1	B	692	LEU	2.5
1	A	429	VAL	2.5
1	B	601	THR	2.5
1	A	339	LEU	2.5
1	A	512	CYS	2.5
1	B	608	THR	2.4
1	B	262	TYR	2.4
1	B	694	GLN	2.4
1	A	341	LEU	2.4
1	B	723	PRO	2.3
1	B	440	ARG	2.3
1	A	509	ARG	2.3
1	A	302	TYR	2.3
1	B	333	LEU	2.3
1	A	469	PHE	2.3
1	B	734	SER	2.3
1	B	187	ALA	2.2
1	B	429	VAL	2.2
1	B	696	LEU	2.2
1	A	507	SER	2.2
1	B	725	LEU	2.2
1	A	460	LEU	2.2
1	A	425	ASP	2.2
1	B	603	ASN	2.2
1	B	739	THR	2.2
1	B	599	LYS	2.2
1	B	465	PRO	2.1
1	B	699	PRO	2.1
1	B	717	TYR	2.1
1	B	605	LEU	2.1
1	A	343	SER	2.1
1	B	456	LEU	2.0
1	A	503	ALA	2.0
1	B	691	CYS	2.0
1	B	460	LEU	2.0
1	B	701	SER	2.0
1	A	320	LYS	2.0
1	B	706	CYS	2.0

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

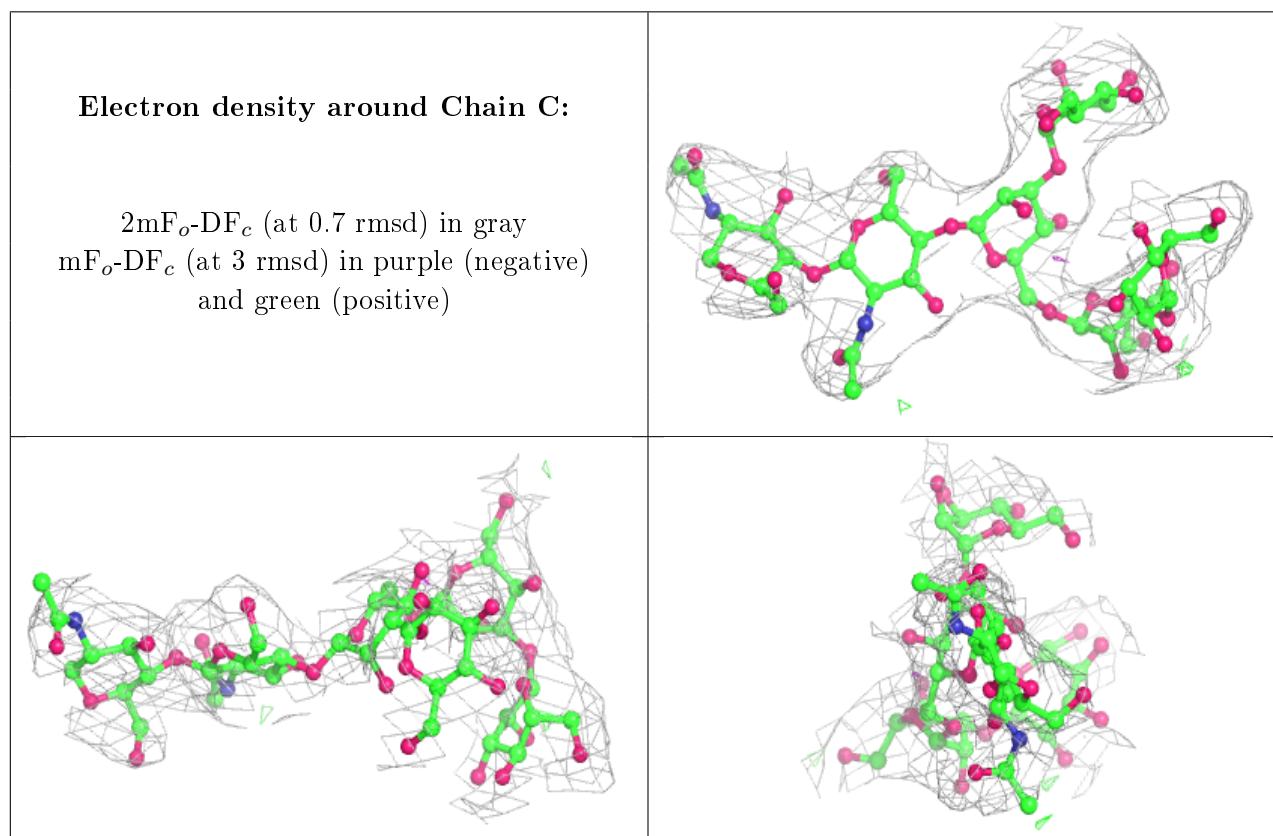
There are no non-standard protein/DNA/RNA residues in this entry.

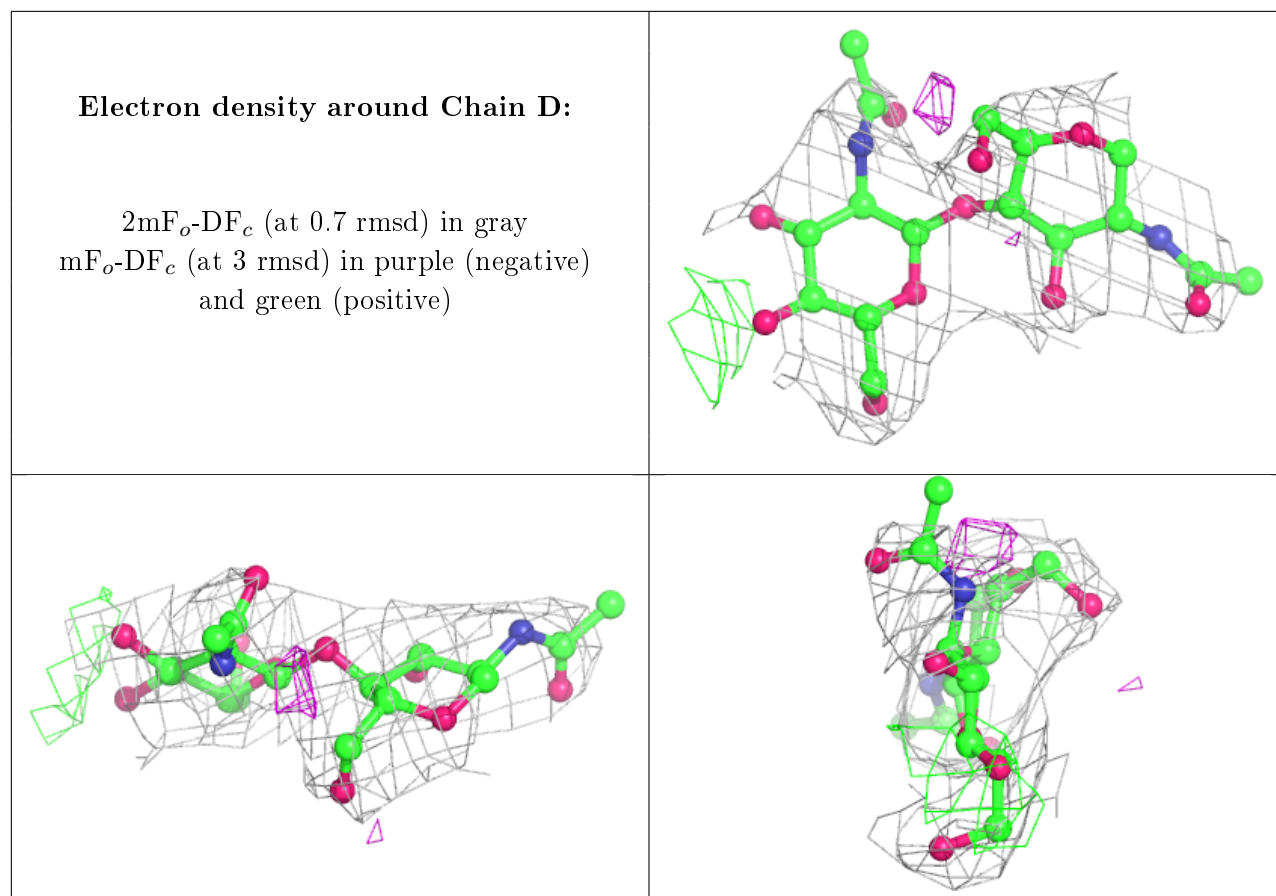
6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
2	BMA	C	3	11/12	0.72	0.16	114,117,126,131	0
2	MAN	C	4	11/12	0.75	0.21	131,133,135,136	0
2	MAN	C	5	11/12	0.77	0.16	132,136,138,139	0
3	NAG	D	2	14/15	0.77	0.32	112,117,121,122	0
2	MAN	C	6	11/12	0.89	0.13	106,111,115,116	0
2	NAG	C	2	14/15	0.91	0.20	78,98,105,111	0
3	NAG	D	1	14/15	0.93	0.23	80,84,93,104	0
2	NAG	C	1	14/15	0.94	0.18	64,69,74,84	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.



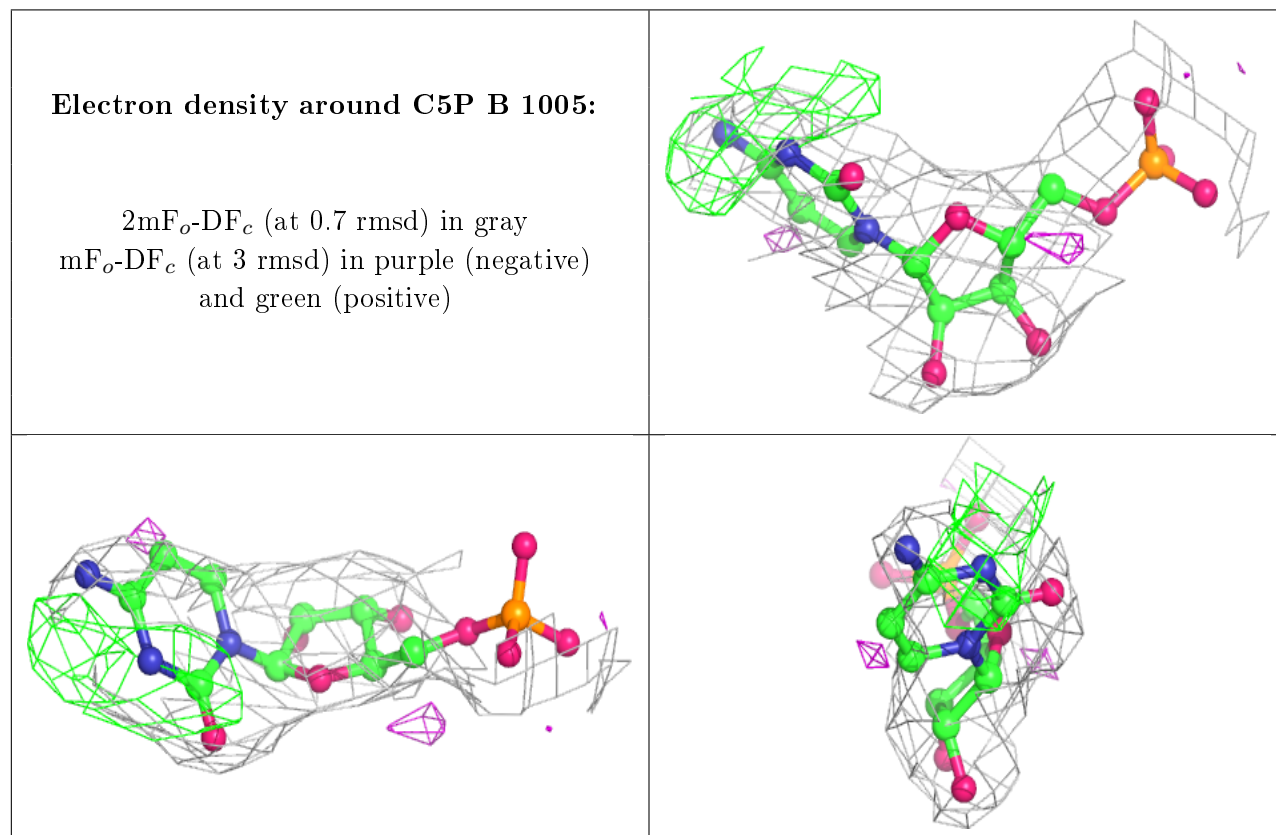


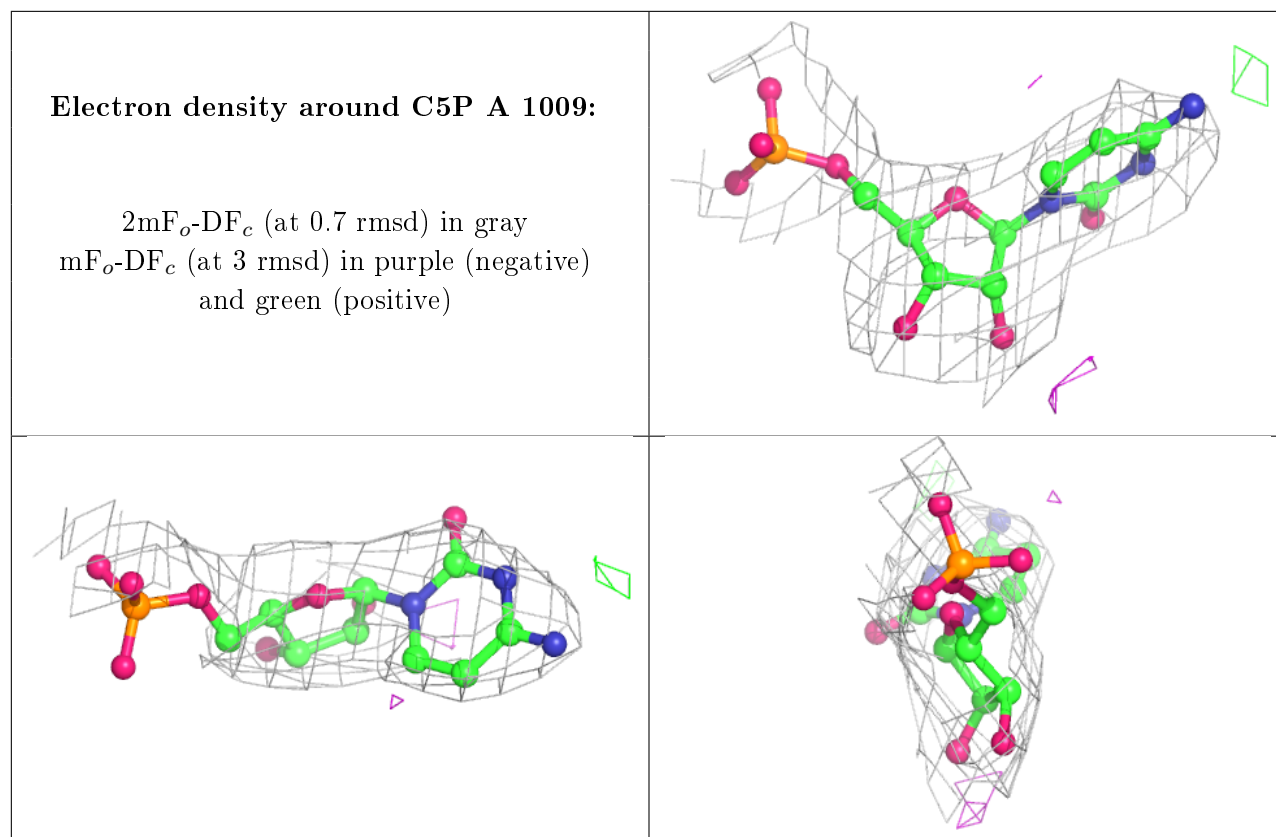
6.4 Ligands [i](#)

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	NAG	B	1003	14/15	0.70	0.43	112,116,118,119	0
4	NAG	B	1004	14/15	0.73	0.25	97,103,106,108	0
4	NAG	A	1007	14/15	0.79	0.40	109,115,116,116	0
4	NAG	A	1008	14/15	0.88	0.33	102,108,114,115	0
7	CA	B	1008	1/1	0.93	0.23	115,115,115,115	0
5	C5P	B	1005	21/21	0.94	0.20	104,108,112,114	0
5	C5P	A	1009	21/21	0.95	0.19	84,90,98,103	0
6	ZN	B	1006	1/1	0.96	0.19	98,98,98,98	0
6	ZN	A	1011	1/1	0.98	0.15	80,80,80,80	0
6	ZN	B	1007	1/1	0.98	0.15	84,84,84,84	0
7	CA	A	1012	1/1	0.99	0.12	96,96,96,96	0
6	ZN	A	1010	1/1	0.99	0.17	88,88,88,88	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 [i](#)

There are no such residues in this entry.