Full wwPDB X-ray Structure Validation Report (i)

Aug 5, 2026 – 06:22 PM JST

PDB ID	:	7D91 / pdb_00007d91
Title	:	Crystal Structure of the Na+,K+-ATPase in the E2P state with bound Mg2+ (P4(3)2(1)2 symmetry)
Authors	:	Kanai, R.; Cornelius, F.; Ogawa, H.; Motoyama, K.; Vilsen, B.; Toyoshima, C.
Deposited on	:	2020-10-12
Resolution	:	3.35 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 (i) 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 (1)) were used in the production of this report:

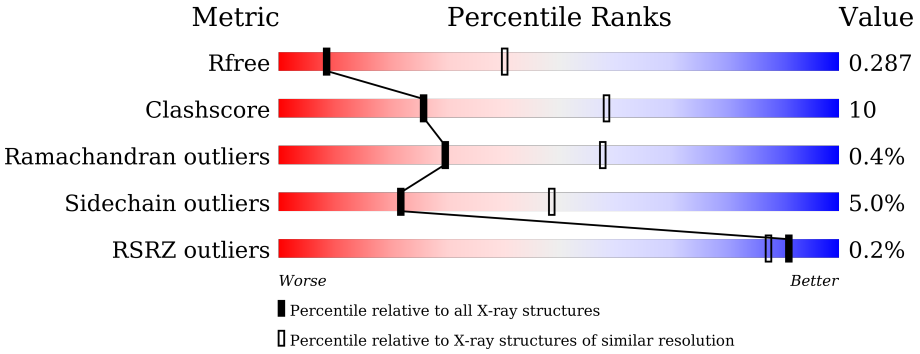
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)

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 <=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	1016	72% 25% • •
2	B	303	67% 26% • •
3	G	65	43% 6% 51%
4	C	2	100%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 10718 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 Sodium/potassium-transporting ATPase subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	996	7726	4922	1301	1456	47	0	0	0

- Molecule 2 is a protein called Sodium/potassium-transporting ATPase subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	291	2386	1546	390	437	13	0	0	0

- Molecule 3 is a protein called FXYD domain-containing ion transport regulator.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	32	255	174	37	44	0	0	0

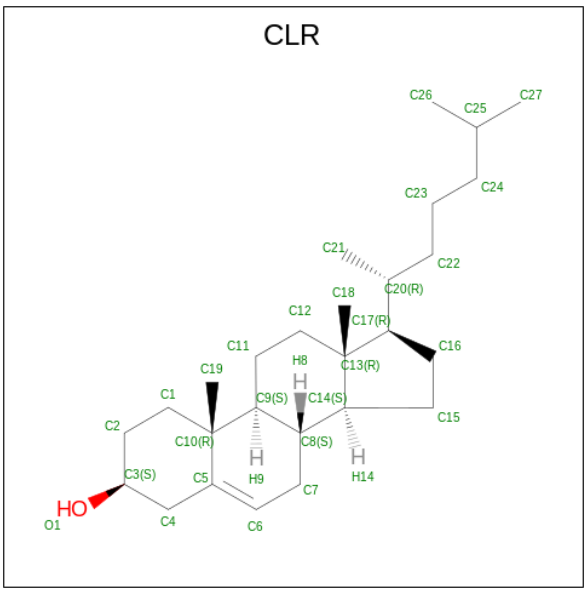
- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

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

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

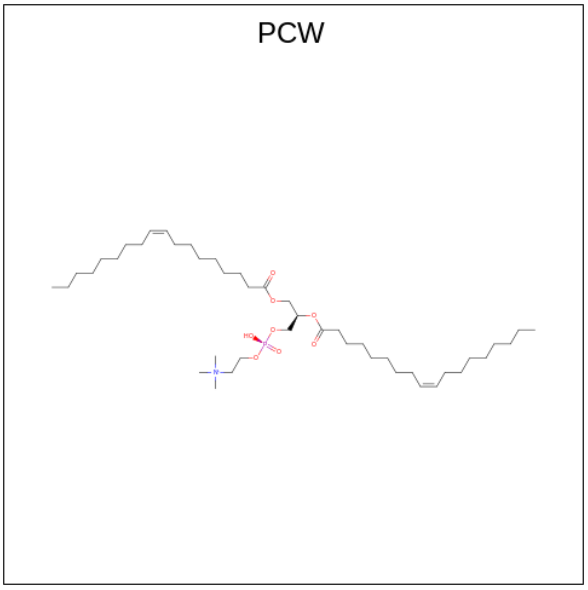
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
5	A	3	3	3	0	0

- Molecule 6 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



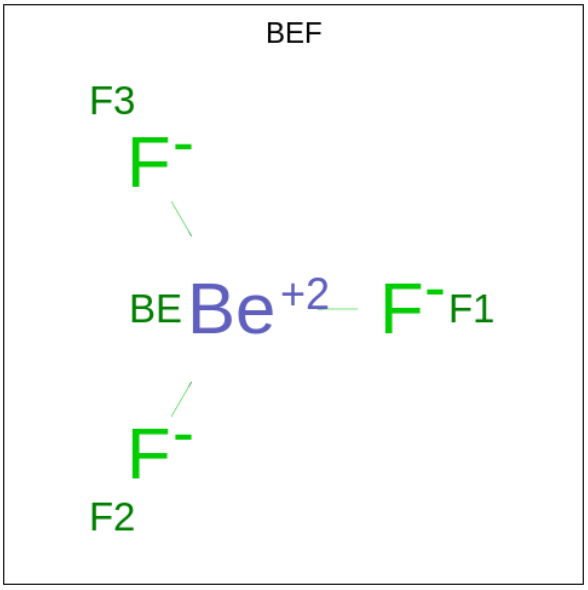
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	28	27	1	0	0
			Total	C	O		
6	G	1	28	27	1	0	0

- Molecule 7 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: $C_{44}H_{85}NO_8P$).



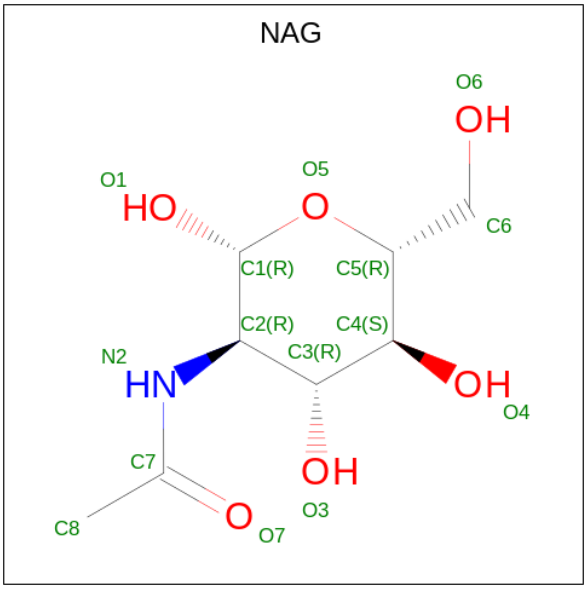
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0
7	A	1	22	12	1	8	1	0	0

- Molecule 8 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Be	F		
8	A	1	4	1	3	0	0

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 10 is water.

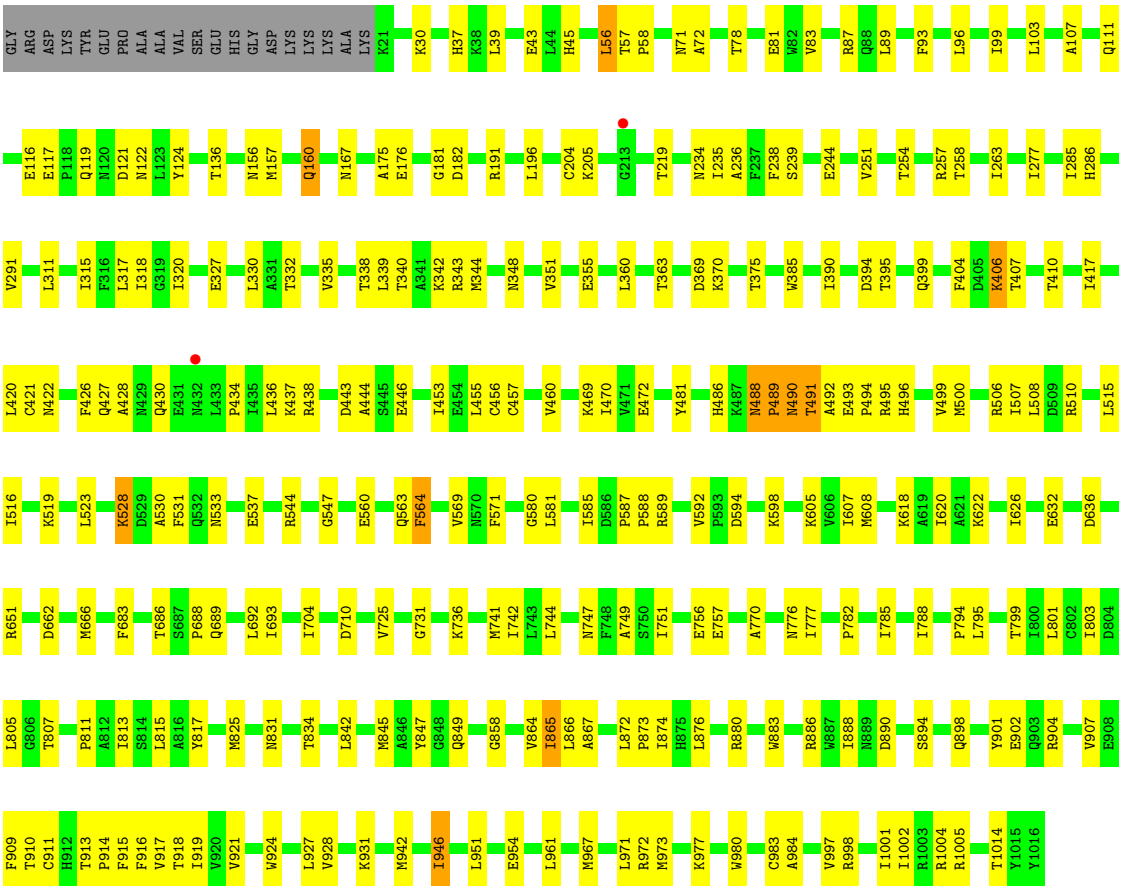
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	4	4	4	0	0

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.

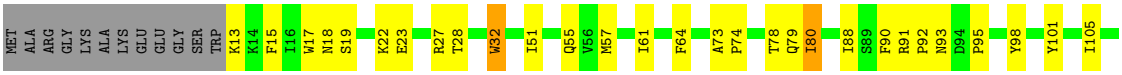
• Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

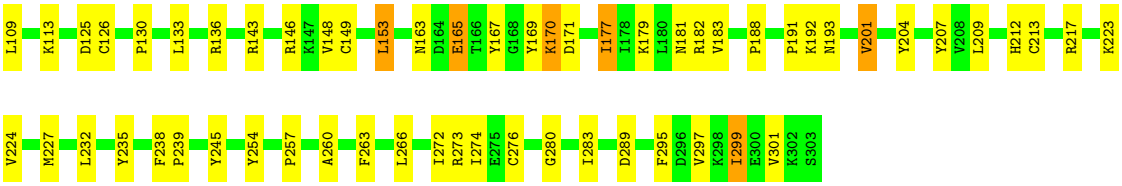
Chain A:



• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1

Chain B:



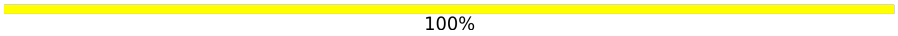


• Molecule 3: FXYD domain-containing ion transport regulator

Chain G:

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

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	84.33Å 84.33Å 646.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.95 – 3.35 14.95 – 3.35	Depositor EDS
% Data completeness (in resolution range)	53.5 (14.95-3.35) 57.5 (14.95-3.35)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 3.24Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.215 , 0.260 0.245 , 0.287	Depositor DCC
R_{free} test set	1082 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	85.2	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 37.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	10718	wwPDB-VP
Average B, all atoms (Å^2)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, PCW, BEF, CLR, MG

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	0.34	1/7876 (0.0%)	0.60	4/10688 (0.0%)
2	B	0.30	0/2449	0.65	3/3301 (0.1%)
3	G	0.30	0/261	0.44	0/354
All	All	0.33	1/10586 (0.0%)	0.61	7/14343 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	369	ASP	CG-OD2	10.66	1.45	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	492	ALA	N-CA-C	-7.38	106.20	114.62
1	A	428	ALA	N-CA-C	6.48	118.03	110.97
2	B	171	ASP	CA-C-N	6.32	136.76	122.29
2	B	171	ASP	C-N-CA	6.32	136.76	122.29
2	B	171	ASP	N-CA-C	-5.84	103.49	111.56
1	A	492	ALA	CA-C-N	5.83	136.02	121.80
1	A	492	ALA	C-N-CA	5.83	136.02	121.80

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	7726	0	7778	150	0
2	B	2386	0	2362	54	0
3	G	255	0	259	3	0
4	C	28	0	25	0	0
5	A	3	0	0	0	0
6	A	28	0	46	1	0
6	G	28	0	46	2	0
7	A	242	0	198	7	0
8	A	4	0	0	0	0
9	B	14	0	13	0	0
10	A	4	0	0	0	0
All	All	10718	0	10727	204	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (204) 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)
2:B:80:ILE:HG12	2:B:177:ILE:HG12	1.56	0.88
1:A:399:GLN:HE21	1:A:436:LEU:HD11	1.43	0.84
1:A:348:ASN:HB3	1:A:744:LEU:HB2	1.62	0.79
1:A:864:VAL:HG22	2:B:57:MET:HG3	1.64	0.77
1:A:998:ARG:HE	1:A:1014:THR:HB	1.50	0.75
1:A:254:THR:HG23	1:A:257:ARG:HH21	1.56	0.70
1:A:375:THR:HA	1:A:588:PRO:HA	1.74	0.69
1:A:430:GLN:HG3	1:A:438:ARG:HB2	1.75	0.69
1:A:807:THR:HB	1:A:954:GLU:HG3	1.74	0.69
1:A:931:LYS:HE3	1:A:942:MET:HA	1.77	0.67
1:A:238:PHE:HD2	1:A:258:THR:HG21	1.58	0.67
1:A:469:LYS:HD3	1:A:472:GLU:HB3	1.78	0.66
2:B:80:ILE:HB	2:B:105:ILE:HD12	1.78	0.65
1:A:420:LEU:HB3	1:A:486:HIS:CE1	2.33	0.63
1:A:370:LYS:HZ3	1:A:620:ILE:HG13	1.64	0.63
1:A:332:THR:HA	1:A:813:ILE:HD11	1.80	0.63
1:A:865:ILE:HD12	1:A:914:PRO:HG3	1.82	0.62
1:A:858:GLY:HA2	1:A:918:THR:HG21	1.83	0.60
1:A:972:ARG:HH12	7:A:1111:PCW:H62	1.66	0.60
2:B:79:GLN:HB3	2:B:295:PHE:CZ	2.36	0.60
1:A:72:ALA:HB2	1:A:176:GLU:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:811:PRO:HB3	1:A:927:LEU:HD22	1.82	0.59
1:A:888:ILE:O	1:A:904:ARG:NH2	2.36	0.59
1:A:725:VAL:HG11	1:A:751:ILE:HD11	1.83	0.59
1:A:286:HIS:HB3	7:A:1112:PCW:O2P	2.02	0.59
1:A:918:THR:HG23	1:A:984:ALA:HB2	1.85	0.59
2:B:209:LEU:HD21	2:B:283:ILE:HD11	1.83	0.59
2:B:113:LYS:HA	2:B:153:LEU:HD11	1.85	0.58
1:A:191:ARG:HE	1:A:239:SER:HA	1.69	0.58
2:B:148:VAL:HG11	2:B:254:TYR:HA	1.86	0.58
1:A:907:VAL:HA	1:A:910:THR:HG22	1.84	0.58
1:A:404:PHE:CZ	1:A:456:CYS:HB3	2.40	0.57
2:B:27:ARG:HG3	2:B:32:TRP:CD1	2.40	0.57
1:A:421:CYS:O	1:A:422:ASN:ND2	2.38	0.57
1:A:96:LEU:HD22	1:A:285:ILE:HG23	1.87	0.56
1:A:420:LEU:HB3	1:A:486:HIS:HE1	1.70	0.56
2:B:188:PRO:HB3	2:B:209:LEU:HD22	1.85	0.56
1:A:873:PRO:HA	1:A:876:LEU:HD12	1.88	0.56
2:B:136:ARG:O	2:B:146:ARG:NH1	2.39	0.56
2:B:280:GLY:HA3	2:B:283:ILE:HD13	1.88	0.56
2:B:80:ILE:HD11	2:B:177:ILE:H	1.71	0.55
2:B:204:TYR:HE1	2:B:207:TYR:HB2	1.71	0.55
1:A:37:HIS:HB2	1:A:234:ASN:HD21	1.72	0.55
1:A:385:TRP:O	1:A:580:GLY:HA3	2.07	0.55
1:A:913:THR:HG23	1:A:973:MET:HE2	1.88	0.55
1:A:103:LEU:HB3	1:A:318:ILE:HG23	1.89	0.54
1:A:946:ILE:HD13	3:G:45:ILE:HD11	1.88	0.54
1:A:443:ASP:OD1	1:A:444:ALA:N	2.41	0.54
1:A:608:MET:HE3	1:A:626:ILE:HD12	1.89	0.54
1:A:1004:ARG:NH1	7:A:1114:PCW:O1P	2.41	0.54
1:A:39:LEU:HD22	1:A:43:GLU:HG2	1.90	0.54
1:A:335:VAL:O	1:A:339:LEU:HG	2.08	0.54
2:B:224:VAL:HG21	2:B:274:ILE:HD11	1.90	0.53
1:A:845:MET:SD	1:A:849:GLN:NE2	2.81	0.53
2:B:191:PRO:HD3	2:B:280:GLY:HA2	1.89	0.53
1:A:491:THR:HA	1:A:493:GLU:OE2	2.09	0.53
1:A:446:GLU:N	1:A:446:GLU:OE1	2.41	0.53
2:B:143:ARG:HD2	2:B:146:ARG:NH1	2.24	0.52
2:B:88:ILE:HB	2:B:299:ILE:HG22	1.90	0.52
1:A:983:CYS:SG	6:A:1104:CLR:H21	2.49	0.52
1:A:136:THR:HG21	1:A:330:LEU:HG	1.92	0.52
1:A:495:ARG:O	1:A:496:HIS:ND1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:ASP:HB3	1:A:446:GLU:OE1	2.10	0.51
2:B:22:LYS:O	2:B:28:THR:HA	2.11	0.51
2:B:177:ILE:HA	2:B:260:ALA:HA	1.92	0.51
1:A:37:HIS:HB3	1:A:235:ILE:HD11	1.92	0.51
1:A:589:ARG:HB2	1:A:592:VAL:HG23	1.93	0.51
2:B:101:TYR:O	2:B:105:ILE:HG12	2.11	0.51
2:B:27:ARG:HG3	2:B:32:TRP:HD1	1.76	0.50
2:B:213:CYS:HA	2:B:276:CYS:HA	1.93	0.50
2:B:73:ALA:HB3	2:B:74:PRO:HD3	1.94	0.50
2:B:92:PRO:HG3	2:B:301:VAL:HG12	1.92	0.50
1:A:531:PHE:HE1	1:A:581:LEU:HD21	1.75	0.50
1:A:915:PHE:O	1:A:919:ILE:HG12	2.12	0.50
1:A:508:LEU:HD11	1:A:528:LYS:HE2	1.93	0.49
1:A:776:ASN:HB2	1:A:847:TYR:HE1	1.77	0.49
3:G:33:PHE:CZ	6:G:101:CLR:H151	2.48	0.49
1:A:238:PHE:HD1	1:A:239:SER:N	2.11	0.48
1:A:434:PRO:HG2	1:A:437:LYS:HB2	1.94	0.48
1:A:618:LYS:HG2	1:A:622:LYS:HE3	1.94	0.48
1:A:777:ILE:HG12	1:A:847:TYR:HD1	1.79	0.48
1:A:902:GLU:HB2	2:B:289:ASP:OD2	2.13	0.48
1:A:799:THR:HG22	1:A:973:MET:HE3	1.95	0.48
7:A:1105:PCW:H11	7:A:1105:PCW:O31	2.14	0.48
1:A:196:LEU:HB2	1:A:236:ALA:HB3	1.95	0.48
1:A:111:GLN:HG3	1:A:315:ILE:HG13	1.95	0.47
1:A:410:THR:HG23	1:A:515:LEU:HD23	1.96	0.47
1:A:815:LEU:HD11	1:A:931:LYS:HA	1.96	0.47
1:A:417:ILE:HG12	1:A:499:VAL:HG12	1.97	0.47
1:A:191:ARG:NE	1:A:239:SER:HA	2.28	0.47
1:A:205:LYS:HA	1:A:219:THR:HA	1.96	0.47
1:A:831:ASN:HB3	1:A:834:THR:HB	1.95	0.47
2:B:153:LEU:H	2:B:153:LEU:HD12	1.79	0.47
1:A:317:LEU:HA	1:A:320:ILE:HD12	1.97	0.46
1:A:385:TRP:HD1	1:A:390:ILE:HD13	1.80	0.46
2:B:263:PHE:HB3	2:B:266:LEU:HD21	1.97	0.46
1:A:924:TRP:CD1	1:A:951:LEU:HD22	2.51	0.46
1:A:58:PRO:HD3	1:A:167:ASN:HB2	1.97	0.46
1:A:500:MET:HE3	1:A:507:ILE:HD12	1.96	0.46
1:A:404:PHE:CE2	1:A:406:LYS:HB3	2.50	0.46
1:A:469:LYS:HE2	1:A:486:HIS:NE2	2.30	0.46
1:A:488:ASN:ND2	1:A:489:PRO:HD2	2.31	0.46
1:A:1005:ARG:NE	7:A:1109:PCW:H51	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:VAL:O	1:A:87:ARG:HG2	2.15	0.46
1:A:395:THR:HB	1:A:587:PRO:CB	2.46	0.46
1:A:683:PHE:HB3	1:A:686:THR:HG21	1.98	0.45
1:A:71:ASN:HB3	1:A:175:ALA:O	2.16	0.45
1:A:736:LYS:HG3	1:A:742:ILE:HD12	1.97	0.45
1:A:909:PHE:CE2	1:A:972:ARG:HD2	2.52	0.45
1:A:928:VAL:HG22	1:A:942:MET:HE1	1.97	0.45
2:B:133:LEU:HD12	2:B:133:LEU:H	1.81	0.45
1:A:263:ILE:HD13	1:A:688:PRO:HG2	1.98	0.45
2:B:238:PHE:HD1	2:B:257:PRO:HB2	1.82	0.45
1:A:1005:ARG:CZ	7:A:1115:PCW:H12	2.47	0.45
2:B:165:GLU:C	2:B:167:TYR:H	2.25	0.45
2:B:217:ARG:HH12	2:B:273:ARG:HD2	1.80	0.45
1:A:181:GLY:H	1:A:251:VAL:HB	1.82	0.45
1:A:470:ILE:HG21	1:A:564:PHE:CZ	2.52	0.45
2:B:204:TYR:CE1	2:B:207:TYR:HB2	2.51	0.45
1:A:204:CYS:HA	1:A:244:GLU:O	2.17	0.45
1:A:547:GLY:HA2	1:A:581:LEU:HD23	1.99	0.45
1:A:335:VAL:HG21	7:A:1113:PCW:C31	2.47	0.45
1:A:453:ILE:HG23	1:A:457:CYS:HB3	1.98	0.45
1:A:867:ALA:HB2	1:A:873:PRO:HD3	1.99	0.44
2:B:204:TYR:HB2	2:B:235:TYR:CE1	2.52	0.44
1:A:795:LEU:HD13	1:A:915:PHE:HB3	1.98	0.44
1:A:395:THR:HB	1:A:587:PRO:HB3	2.00	0.44
2:B:98:TYR:HA	2:B:101:TYR:HD2	1.82	0.44
2:B:227:MET:HG2	2:B:263:PHE:CD2	2.52	0.44
1:A:605:LYS:HE2	1:A:607:ILE:HD11	1.98	0.44
1:A:107:ALA:HB2	1:A:318:ILE:HG21	1.98	0.44
1:A:662:ASP:O	1:A:666:MET:HG3	2.18	0.44
1:A:880:ARG:HA	1:A:883:TRP:HB3	1.99	0.44
2:B:91:ARG:HG2	2:B:93:ASN:H	1.83	0.44
2:B:95:PRO:HA	2:B:98:TYR:CZ	2.52	0.44
1:A:339:LEU:HD13	1:A:817:TYR:CZ	2.53	0.44
1:A:747:ASN:HD21	1:A:749:ALA:HB3	1.83	0.44
1:A:340:THR:O	1:A:344:MET:HG2	2.17	0.43
1:A:363:THR:HA	1:A:704:ILE:HB	1.99	0.43
1:A:883:TRP:O	1:A:904:ARG:NH1	2.51	0.43
1:A:651:ARG:HD3	1:A:651:ARG:HA	1.79	0.43
1:A:801:LEU:HD22	1:A:805:LEU:HD12	2.00	0.43
1:A:917:VAL:O	1:A:921:VAL:HG23	2.19	0.43
2:B:239:PRO:HD2	2:B:257:PRO:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:770:ALA:HA	1:A:842:LEU:HD21	2.00	0.43
1:A:370:LYS:NZ	1:A:620:ILE:HG13	2.32	0.43
1:A:515:LEU:HD12	1:A:519:LYS:O	2.19	0.43
2:B:90:PHE:CZ	2:B:170:LYS:HG2	2.53	0.43
1:A:495:ARG:CZ	1:A:560:GLU:HG3	2.49	0.43
1:A:872:LEU:HD23	1:A:894:SER:HB2	2.00	0.43
1:A:530:ALA:HA	1:A:533:ASN:OD1	2.19	0.42
1:A:874:ILE:H	1:A:874:ILE:HD12	1.84	0.42
2:B:109:LEU:HD23	2:B:153:LEU:HD23	2.01	0.42
1:A:825:MET:HA	1:A:825:MET:HE2	2.00	0.42
1:A:488:ASN:ND2	1:A:494:PRO:HD2	2.33	0.42
2:B:182:ARG:HD2	2:B:245:TYR:CZ	2.54	0.42
1:A:506:ARG:HB3	1:A:510:ARG:HH22	1.85	0.42
1:A:632:GLU:HB3	1:A:636:ASP:HB2	2.02	0.42
1:A:801:LEU:HD23	1:A:801:LEU:HA	1.85	0.42
1:A:946:ILE:H	1:A:946:ILE:HG12	1.64	0.42
1:A:890:ASP:HB3	2:B:78:THR:HG21	2.02	0.42
2:B:51:ILE:O	2:B:55:GLN:HG2	2.20	0.42
1:A:585:ILE:HD12	1:A:585:ILE:HA	1.92	0.42
1:A:785:ILE:HA	1:A:788:ILE:HB	2.00	0.42
1:A:594:ASP:O	1:A:598:LYS:HG2	2.20	0.42
2:B:15:PHE:C	2:B:17:TRP:H	2.28	0.42
1:A:56:LEU:HD21	1:A:182:ASP:HB3	2.01	0.42
1:A:469:LYS:HE2	1:A:486:HIS:HE2	1.84	0.42
1:A:160:GLN:HE22	1:A:191:ARG:HD3	1.85	0.42
1:A:710:ASP:HB2	1:A:731:GLY:HA2	2.03	0.41
1:A:898:GLN:HE22	2:B:179:LYS:HE3	1.85	0.41
2:B:19:SER:HB3	2:B:23:GLU:HB2	2.01	0.41
1:A:997:VAL:O	1:A:1001:ILE:HG12	2.20	0.41
1:A:96:LEU:O	1:A:99:ILE:HG12	2.20	0.41
1:A:564:PHE:HB3	1:A:571:PHE:CZ	2.55	0.41
1:A:689:GLN:O	1:A:693:ILE:HG12	2.19	0.41
1:A:725:VAL:HG22	1:A:741:MET:HE2	2.03	0.41
2:B:130:PRO:HG2	2:B:204:TYR:CZ	2.56	0.41
2:B:192:LYS:HB3	2:B:193:ASN:H	1.69	0.41
6:G:101:CLR:H162	6:G:101:CLR:H222	1.71	0.41
1:A:427:GLN:HB2	1:A:430:GLN:OE1	2.21	0.41
1:A:782:PRO:HB3	1:A:794:PRO:HB2	2.03	0.41
1:A:803:ILE:HD13	1:A:803:ILE:HA	1.91	0.41
1:A:866:LEU:HD23	1:A:866:LEU:HA	1.86	0.41
2:B:18:ASN:HA	2:B:23:GLU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:201:VAL:HG11	2:B:212:HIS:CD2	2.55	0.41
3:G:42:LEU:HA	3:G:45:ILE:HG22	2.02	0.41
1:A:338:THR:O	1:A:342:LYS:HG3	2.20	0.41
1:A:343:ARG:NH2	1:A:757:GLU:OE1	2.53	0.41
1:A:927:LEU:HD23	1:A:951:LEU:HD21	2.01	0.41
1:A:564:PHE:HB3	1:A:571:PHE:HZ	1.85	0.41
1:A:756:GLU:HA	1:A:825:MET:HE3	2.02	0.41
1:A:977:LYS:HD2	1:A:980:TRP:CZ2	2.56	0.41
2:B:80:ILE:H	2:B:80:ILE:HG13	1.54	0.41
2:B:223:LYS:HB3	2:B:272:ILE:HG21	2.03	0.41
1:A:277:ILE:HG21	1:A:355:GLU:HB2	2.03	0.40
1:A:30:LYS:HE2	1:A:692:LEU:HD21	2.03	0.40
1:A:961:LEU:HA	1:A:967:MET:HE2	2.02	0.40
1:A:907:VAL:O	1:A:911:CYS:HB2	2.21	0.40
2:B:167:TYR:C	2:B:169:TYR:H	2.28	0.40
1:A:998:ARG:O	1:A:1002:ILE:HG13	2.22	0.40
2:B:181:ASN:O	2:B:183:VAL:HG23	2.20	0.40
1:A:93:PHE:HA	1:A:285:ILE:HD11	2.04	0.40
1:A:886:ARG:HA	1:A:901:TYR:CD1	2.57	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	994/1016 (98%)	923 (93%)	66 (7%)	5 (0%)	24 52
2	B	289/303 (95%)	258 (89%)	31 (11%)	0	100 100
3	G	30/65 (46%)	29 (97%)	1 (3%)	0	100 100
All	All	1313/1384 (95%)	1210 (92%)	98 (8%)	5 (0%)	30 58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	426	PHE
1	A	490	ASN
1	A	491	THR
1	A	489	PRO
1	A	569	VAL

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	847/862 (98%)	808 (95%)	39 (5%)	24	50
2	B	261/269 (97%)	244 (94%)	17 (6%)	15	42
3	G	26/52 (50%)	25 (96%)	1 (4%)	29	55
All	All	1134/1183 (96%)	1077 (95%)	57 (5%)	22	49

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	HIS
1	A	56	LEU
1	A	57	THR
1	A	78	THR
1	A	81	GLU
1	A	89	LEU
1	A	116	GLU
1	A	117	GLU
1	A	119	GLN
1	A	121	ASP
1	A	122	ASN
1	A	124	TYR
1	A	156	ASN
1	A	157	MET
1	A	160	GLN
1	A	291	VAL
1	A	311	LEU
1	A	327	GLU

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Mol	Chain	Res	Type
1	A	351	VAL
1	A	360	LEU
1	A	394	ASP
1	A	406	LYS
1	A	407	THR
1	A	455	LEU
1	A	460	VAL
1	A	481	TYR
1	A	488	ASN
1	A	490	ASN
1	A	516	ILE
1	A	523	LEU
1	A	528	LYS
1	A	537	GLU
1	A	544	ARG
1	A	563	GLN
1	A	564	PHE
1	A	865	ILE
1	A	916	PHE
1	A	946	ILE
1	A	971	LEU
2	B	13	LYS
2	B	32	TRP
2	B	61	ILE
2	B	64	PHE
2	B	80	ILE
2	B	125	ASP
2	B	126	CYS
2	B	149	CYS
2	B	153	LEU
2	B	163	ASN
2	B	165	GLU
2	B	170	LYS
2	B	177	ILE
2	B	201	VAL
2	B	232	LEU
2	B	297	VAL
2	B	299	ILE
3	G	46	LEU

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

Mol	Chain	Res	Type
1	A	119	GLN
1	A	160	GLN
1	A	161	GLN
1	A	399	GLN
1	A	427	GLN
1	A	488	ASN
1	A	690	GLN
1	A	747	ASN
1	A	849	GLN
1	A	854	GLN
1	A	898	GLN
2	B	82	GLN
2	B	193	ASN
2	B	212	HIS
2	B	256	GLN
2	B	262	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)

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	$\#\|Z\| > 2$
4	NAG	C	1	2,4	14,14,15	0.45	0	17,19,21	1.49	4 (23%)
4	NAG	C	2	4	14,14,15	0.97	2 (14%)	17,19,21	0.59	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
4	NAG	C	1	2,4	-	3/6/23/26	0/1/1/1
4	NAG	C	2	4	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	2	NAG	O5-C1	2.52	1.47	1.43
4	C	2	NAG	C1-C2	2.38	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	1	NAG	C1-O5-C5	3.13	116.43	112.19
4	C	1	NAG	O3-C3-C2	-3.05	103.16	109.47
4	C	1	NAG	O3-C3-C4	2.19	115.42	110.35
4	C	1	NAG	O4-C4-C3	2.03	115.04	110.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

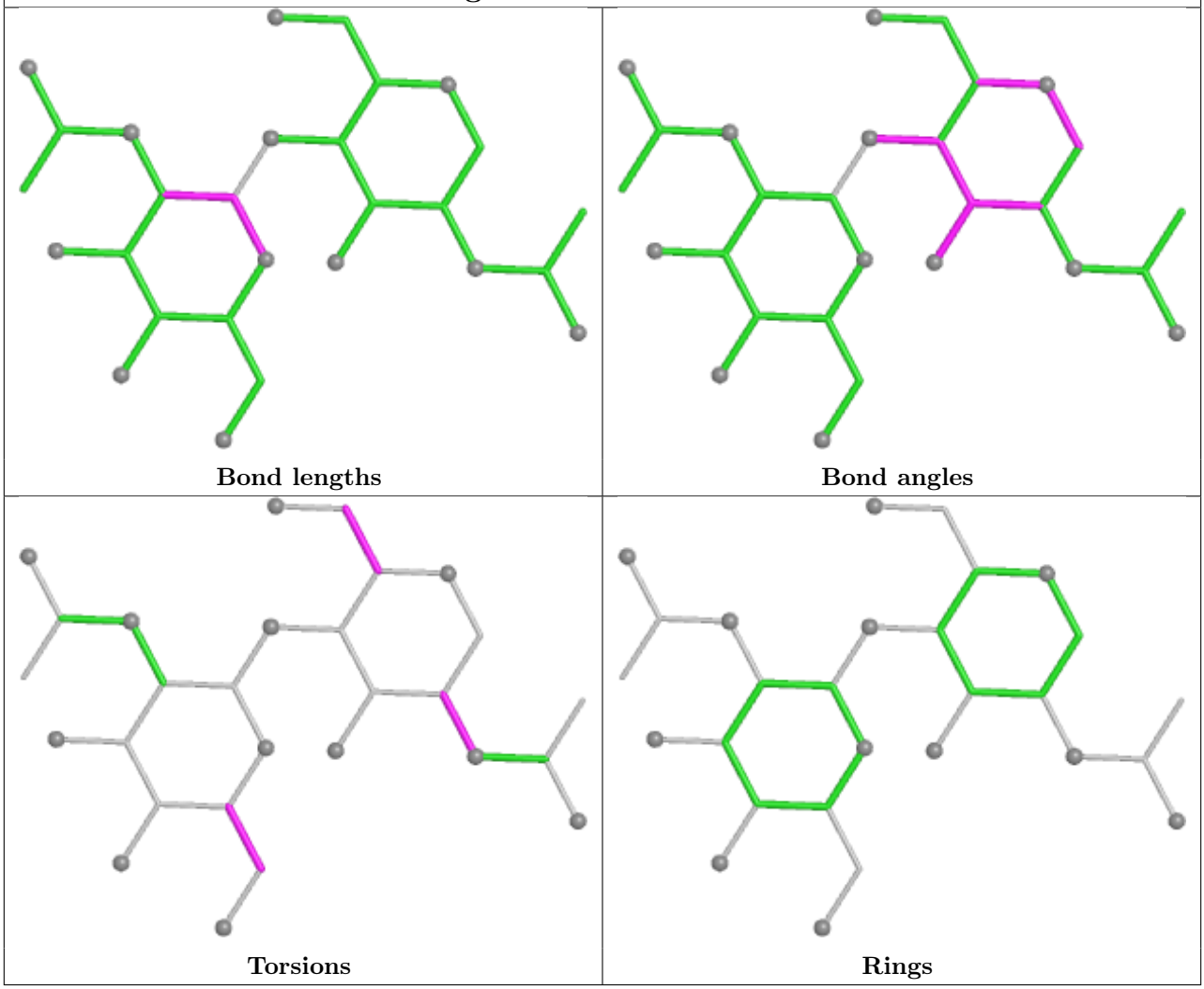
Mol	Chain	Res	Type	Atoms
4	C	1	NAG	C4-C5-C6-O6
4	C	1	NAG	O5-C5-C6-O6
4	C	1	NAG	C3-C2-N2-C7
4	C	2	NAG	C4-C5-C6-O6
4	C	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain C



5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 3 are monoatomic - leaving 15 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	$\#\|Z\| > 2$
8	BEF	A	1116	1	0,3,3	-	-	-		
9	NAG	B	421	2	14,14,15	0.78	1 (7%)	17,19,21	0.95	1 (5%)
7	PCW	A	1107	-	21,21,53	0.86	0	27,29,61	1.39	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
7	PCW	A	1110	-	21,21,53	0.85	0	27,29,61	1.18	3 (11%)
7	PCW	A	1109	-	21,21,53	0.88	0	27,29,61	1.29	3 (11%)
7	PCW	A	1113	-	21,21,53	0.87	0	27,29,61	1.06	3 (11%)
6	CLR	G	101	-	31,31,31	1.58	8 (25%)	48,48,48	1.48	7 (14%)
7	PCW	A	1114	-	21,21,53	0.87	0	27,29,61	1.25	4 (14%)
7	PCW	A	1108	-	21,21,53	0.84	0	27,29,61	1.13	3 (11%)
6	CLR	A	1104	-	31,31,31	1.70	7 (22%)	48,48,48	1.59	9 (18%)
7	PCW	A	1106	-	21,21,53	0.83	0	27,29,61	1.15	3 (11%)
7	PCW	A	1115	-	21,21,53	0.86	0	27,29,61	0.92	2 (7%)
7	PCW	A	1111	-	21,21,53	0.84	0	27,29,61	0.85	1 (3%)
7	PCW	A	1105	-	21,21,53	0.85	0	27,29,61	0.90	1 (3%)
7	PCW	A	1112	-	21,21,53	0.87	0	27,29,61	1.13	2 (7%)

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
9	NAG	B	421	2	-	1/6/23/26	0/1/1/1
7	PCW	A	1107	-	-	8/23/23/57	-
7	PCW	A	1110	-	-	8/23/23/57	-
7	PCW	A	1109	-	-	11/23/23/57	-
7	PCW	A	1113	-	-	5/23/23/57	-
6	CLR	G	101	-	-	5/10/68/68	0/4/4/4
7	PCW	A	1114	-	-	9/23/23/57	-
7	PCW	A	1108	-	-	9/23/23/57	-
6	CLR	A	1104	-	-	4/10/68/68	0/4/4/4
7	PCW	A	1106	-	-	13/23/23/57	-
7	PCW	A	1115	-	-	9/23/23/57	-
7	PCW	A	1111	-	-	12/23/23/57	-
7	PCW	A	1105	-	-	9/23/23/57	-
7	PCW	A	1112	-	-	10/23/23/57	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1104	CLR	C12-C13	3.98	1.61	1.54
6	A	1104	CLR	C12-C11	2.99	1.59	1.53
6	G	101	CLR	C12-C13	2.96	1.59	1.54
6	A	1104	CLR	C13-C17	2.83	1.60	1.55
6	G	101	CLR	C13-C17	2.83	1.60	1.55
6	G	101	CLR	C16-C17	2.57	1.59	1.54
9	B	421	NAG	C1-C2	2.57	1.56	1.52
6	A	1104	CLR	C10-C5	2.56	1.57	1.52
6	A	1104	CLR	C16-C17	2.53	1.59	1.54
6	G	101	CLR	C15-C14	2.52	1.59	1.54
6	G	101	CLR	C10-C5	2.43	1.57	1.52
6	G	101	CLR	C16-C15	2.31	1.60	1.54
6	G	101	CLR	C1-C10	2.17	1.58	1.54
6	A	1104	CLR	C2-C3	2.15	1.56	1.51
6	G	101	CLR	C2-C3	2.15	1.56	1.51
6	A	1104	CLR	C1-C2	2.11	1.57	1.53

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	1114	PCW	C3-O3-C11	-4.07	106.87	117.10
7	A	1107	PCW	C3-O3-C11	-4.05	106.91	117.10
7	A	1109	PCW	C2-O2-C31	-3.81	110.80	117.90
7	A	1109	PCW	C3-O3-C11	-3.62	108.01	117.10
7	A	1106	PCW	C2-O2-C31	-3.61	111.17	117.90
7	A	1112	PCW	C3-O3-C11	-3.51	108.29	117.10
7	A	1113	PCW	C2-O2-C31	-3.41	111.53	117.90
7	A	1107	PCW	O2-C31-C32	3.38	117.30	111.09
6	A	1104	CLR	C1-C2-C3	3.34	114.76	110.47
7	A	1110	PCW	C3-O3-C11	-3.23	108.99	117.10
9	B	421	NAG	C1-O5-C5	3.18	116.51	112.19
6	A	1104	CLR	C22-C20-C17	-3.08	103.92	110.28
7	A	1110	PCW	O2-C31-C32	3.07	116.74	111.09
7	A	1107	PCW	C2-O2-C31	-3.07	112.18	117.90
6	G	101	CLR	C1-C2-C3	3.02	114.34	110.47
7	A	1108	PCW	C3-O3-C11	-2.96	109.66	117.10
7	A	1108	PCW	C2-O2-C31	-2.96	112.39	117.90
6	A	1104	CLR	C11-C9-C10	2.91	116.92	113.08
6	G	101	CLR	C7-C8-C14	-2.89	106.72	110.91
6	G	101	CLR	C22-C20-C17	-2.84	104.42	110.28
7	A	1110	PCW	O2-C2-C3	2.81	118.57	108.40
7	A	1115	PCW	C3-O3-C11	-2.64	110.46	117.10
7	A	1106	PCW	C3-O3-C11	-2.63	110.50	117.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	G	101	CLR	C11-C9-C10	2.60	116.50	113.08
7	A	1111	PCW	O2-C31-C32	2.59	115.86	111.09
6	A	1104	CLR	C15-C14-C13	2.56	106.93	103.84
6	G	101	CLR	C19-C10-C9	-2.49	108.72	111.68
7	A	1112	PCW	O2-C2-C1	2.48	117.40	108.40
6	G	101	CLR	C18-C13-C12	2.48	114.51	110.59
6	A	1104	CLR	C18-C13-C12	2.47	114.49	110.59
7	A	1109	PCW	O2-C31-C32	2.45	115.59	111.09
6	A	1104	CLR	C19-C10-C9	-2.43	108.78	111.68
7	A	1114	PCW	O3-C3-C2	2.42	115.49	108.43
7	A	1106	PCW	O2-C31-C32	2.33	115.38	111.09
7	A	1113	PCW	O2-C31-C32	2.30	115.32	111.09
7	A	1108	PCW	O2-C31-C32	2.29	115.30	111.09
7	A	1114	PCW	O2-C31-C32	2.27	115.26	111.09
6	A	1104	CLR	C16-C17-C20	-2.24	108.68	112.15
7	A	1113	PCW	C3-O3-C11	-2.13	111.74	117.10
7	A	1105	PCW	C3-O3-C11	-2.13	111.75	117.10
6	G	101	CLR	C10-C5-C6	2.08	126.08	122.90
7	A	1114	PCW	C3-C2-C1	2.06	116.67	111.79
7	A	1115	PCW	O2-C2-C1	2.04	115.78	108.40
6	A	1104	CLR	C24-C23-C22	-2.03	103.92	113.24
6	A	1104	CLR	C19-C10-C5	2.00	111.58	108.34

There are no chirality outliers.

All (113) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1105	PCW	C1-O3P-P-O1P
7	A	1105	PCW	C1-O3P-P-O2P
7	A	1105	PCW	C1-O3P-P-O4P
7	A	1105	PCW	C4-O4P-P-O1P
7	A	1105	PCW	C4-O4P-P-O2P
7	A	1105	PCW	C4-O4P-P-O3P
7	A	1106	PCW	C32-C31-O2-C2
7	A	1106	PCW	O31-C31-O2-C2
7	A	1106	PCW	C1-O3P-P-O2P
7	A	1106	PCW	C4-O4P-P-O1P
7	A	1106	PCW	C4-O4P-P-O3P
7	A	1107	PCW	C32-C31-O2-C2
7	A	1107	PCW	O31-C31-O2-C2
7	A	1107	PCW	C1-O3P-P-O2P
7	A	1107	PCW	C1-O3P-P-O4P

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Mol	Chain	Res	Type	Atoms
7	A	1107	PCW	C4-O4P-P-O3P
7	A	1108	PCW	C32-C31-O2-C2
7	A	1108	PCW	C1-O3P-P-O1P
7	A	1108	PCW	C1-O3P-P-O2P
7	A	1108	PCW	C4-O4P-P-O1P
7	A	1108	PCW	C4-O4P-P-O2P
7	A	1109	PCW	C32-C31-O2-C2
7	A	1109	PCW	O31-C31-O2-C2
7	A	1109	PCW	C1-O3P-P-O1P
7	A	1109	PCW	C1-O3P-P-O2P
7	A	1109	PCW	C4-O4P-P-O2P
7	A	1110	PCW	C32-C31-O2-C2
7	A	1110	PCW	C1-O3P-P-O2P
7	A	1110	PCW	C1-O3P-P-O4P
7	A	1110	PCW	C4-O4P-P-O1P
7	A	1110	PCW	C4-O4P-P-O2P
7	A	1111	PCW	C1-O3P-P-O2P
7	A	1111	PCW	C4-O4P-P-O1P
7	A	1111	PCW	C4-O4P-P-O2P
7	A	1111	PCW	C4-O4P-P-O3P
7	A	1112	PCW	C1-O3P-P-O1P
7	A	1112	PCW	C1-O3P-P-O2P
7	A	1113	PCW	C32-C31-O2-C2
7	A	1113	PCW	O31-C31-O2-C2
7	A	1114	PCW	C4-O4P-P-O1P
7	A	1114	PCW	C4-O4P-P-O2P
7	A	1115	PCW	C1-O3P-P-O1P
7	A	1115	PCW	C1-O3P-P-O2P
7	A	1115	PCW	C4-O4P-P-O1P
7	A	1115	PCW	C4-O4P-P-O2P
7	A	1111	PCW	C32-C31-O2-C2
7	A	1111	PCW	O31-C31-O2-C2
7	A	1114	PCW	C32-C31-O2-C2
7	A	1110	PCW	O31-C31-O2-C2
7	A	1114	PCW	O31-C31-O2-C2
7	A	1108	PCW	O31-C31-O2-C2
7	A	1107	PCW	O11-C11-O3-C3
7	A	1111	PCW	O11-C11-O3-C3
7	A	1112	PCW	O11-C11-O3-C3
7	A	1111	PCW	C12-C11-O3-C3
7	A	1114	PCW	C12-C11-O3-C3
7	A	1106	PCW	O11-C11-O3-C3

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Mol	Chain	Res	Type	Atoms
7	A	1114	PCW	O11-C11-O3-C3
7	A	1106	PCW	C12-C11-O3-C3
7	A	1112	PCW	C12-C11-O3-C3
7	A	1107	PCW	C12-C11-O3-C3
6	G	101	CLR	C13-C17-C20-C21
6	A	1104	CLR	C20-C22-C23-C24
7	A	1108	PCW	C1-O3P-P-O4P
7	A	1108	PCW	C4-O4P-P-O3P
7	A	1109	PCW	C1-O3P-P-O4P
7	A	1109	PCW	C4-O4P-P-O3P
7	A	1110	PCW	C4-O4P-P-O3P
7	A	1111	PCW	C1-O3P-P-O4P
7	A	1112	PCW	C1-O3P-P-O4P
7	A	1112	PCW	C4-O4P-P-O3P
7	A	1114	PCW	C4-O4P-P-O3P
7	A	1115	PCW	C1-O3P-P-O4P
7	A	1115	PCW	C4-O4P-P-O3P
6	A	1104	CLR	C23-C24-C25-C26
6	G	101	CLR	C16-C17-C20-C21
6	G	101	CLR	C13-C17-C20-C22
7	A	1105	PCW	O31-C31-O2-C2
6	G	101	CLR	C20-C22-C23-C24
6	A	1104	CLR	C23-C24-C25-C27
7	A	1106	PCW	C1-O3P-P-O4P
9	B	421	NAG	O5-C5-C6-O6
7	A	1115	PCW	O31-C31-O2-C2
6	G	101	CLR	C16-C17-C20-C22
7	A	1109	PCW	O11-C11-O3-C3
7	A	1109	PCW	C12-C11-O3-C3
7	A	1106	PCW	C1-O3P-P-O1P
7	A	1106	PCW	C4-O4P-P-O2P
7	A	1111	PCW	C1-O3P-P-O1P
7	A	1112	PCW	C4-O4P-P-O2P
7	A	1113	PCW	C4-O4P-P-O2P
7	A	1105	PCW	O4P-C4-C5-N
7	A	1106	PCW	O4P-C4-C5-N
7	A	1107	PCW	O4P-C4-C5-N
7	A	1108	PCW	O4P-C4-C5-N
7	A	1109	PCW	O4P-C4-C5-N
7	A	1111	PCW	O4P-C4-C5-N
7	A	1112	PCW	O4P-C4-C5-N
7	A	1113	PCW	O4P-C4-C5-N

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Mol	Chain	Res	Type	Atoms
7	A	1114	PCW	O4P-C4-C5-N
7	A	1115	PCW	O4P-C4-C5-N
7	A	1106	PCW	C1-C2-O2-C31
7	A	1114	PCW	C3-C2-O2-C31
7	A	1112	PCW	O31-C31-O2-C2
7	A	1105	PCW	C3-C2-O2-C31
7	A	1106	PCW	C3-C2-O2-C31
7	A	1109	PCW	C3-C2-O2-C31
7	A	1110	PCW	C3-C2-O2-C31
7	A	1112	PCW	C3-C2-O2-C31
7	A	1115	PCW	C3-C2-O2-C31
7	A	1113	PCW	C4-O4P-P-O3P
6	A	1104	CLR	C13-C17-C20-C21
7	A	1111	PCW	C3-C2-O2-C31

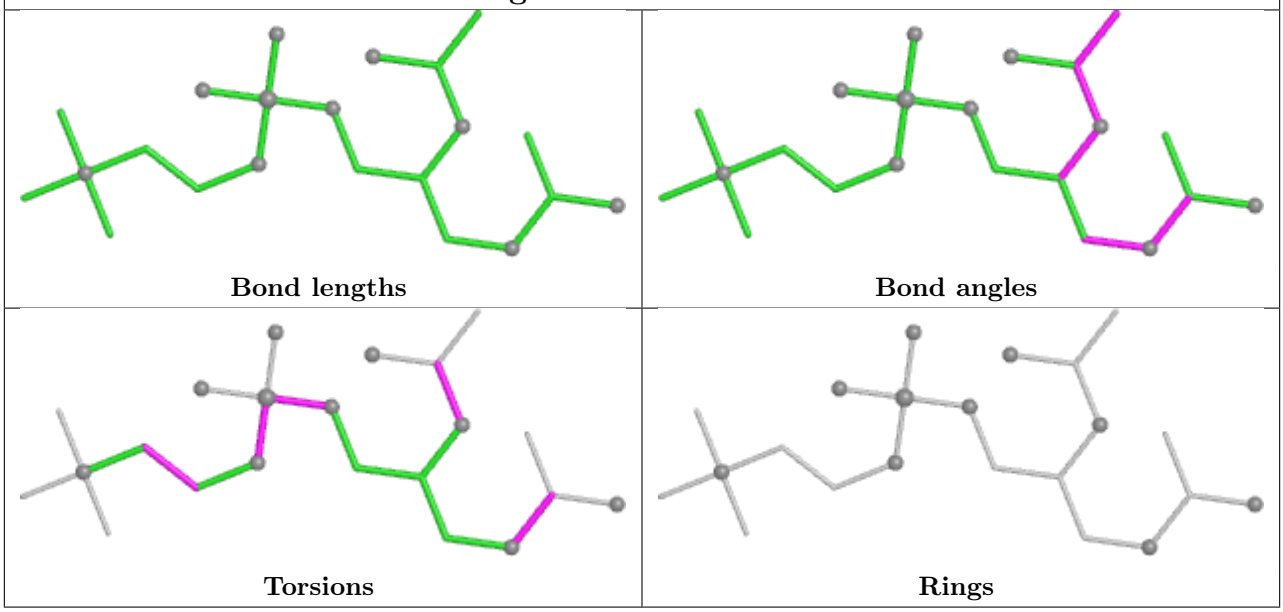
There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1109	PCW	1	0
7	A	1113	PCW	1	0
6	G	101	CLR	2	0
7	A	1114	PCW	1	0
6	A	1104	CLR	1	0
7	A	1115	PCW	1	0
7	A	1111	PCW	1	0
7	A	1105	PCW	1	0
7	A	1112	PCW	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 then 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.

Ligand PCW A 1107



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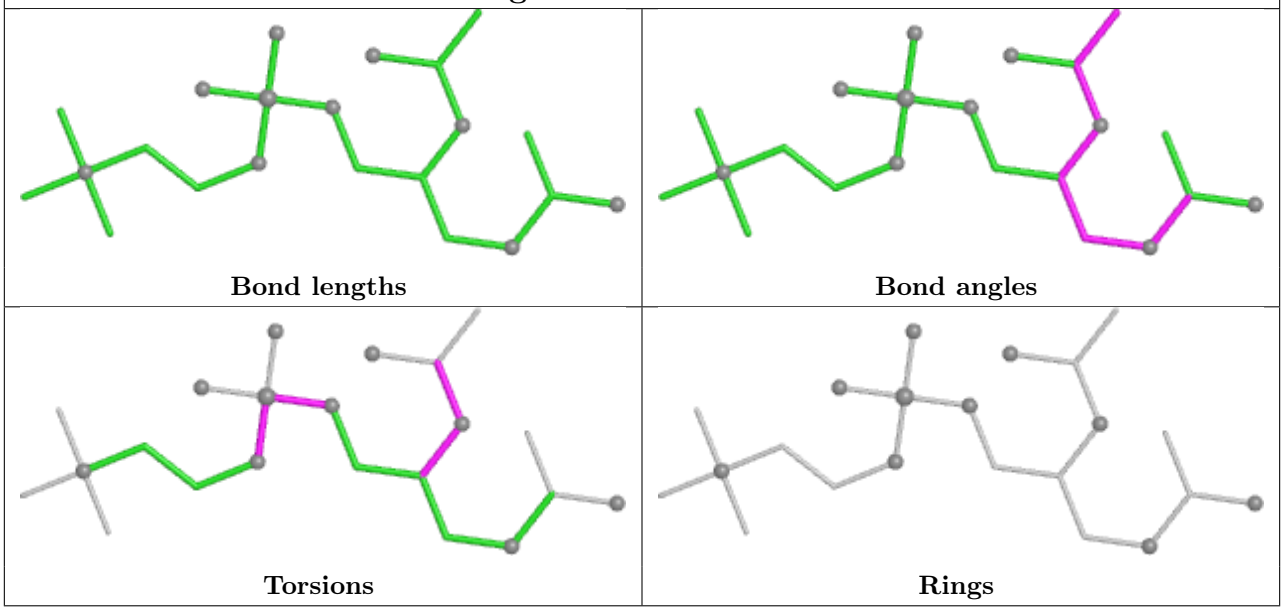

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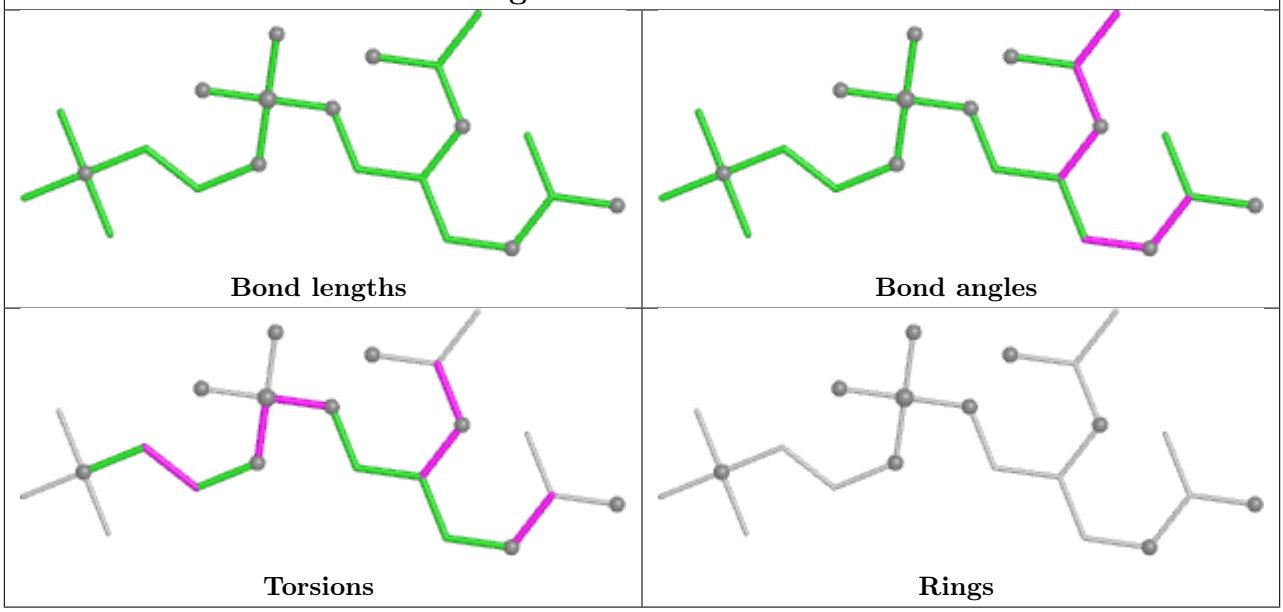

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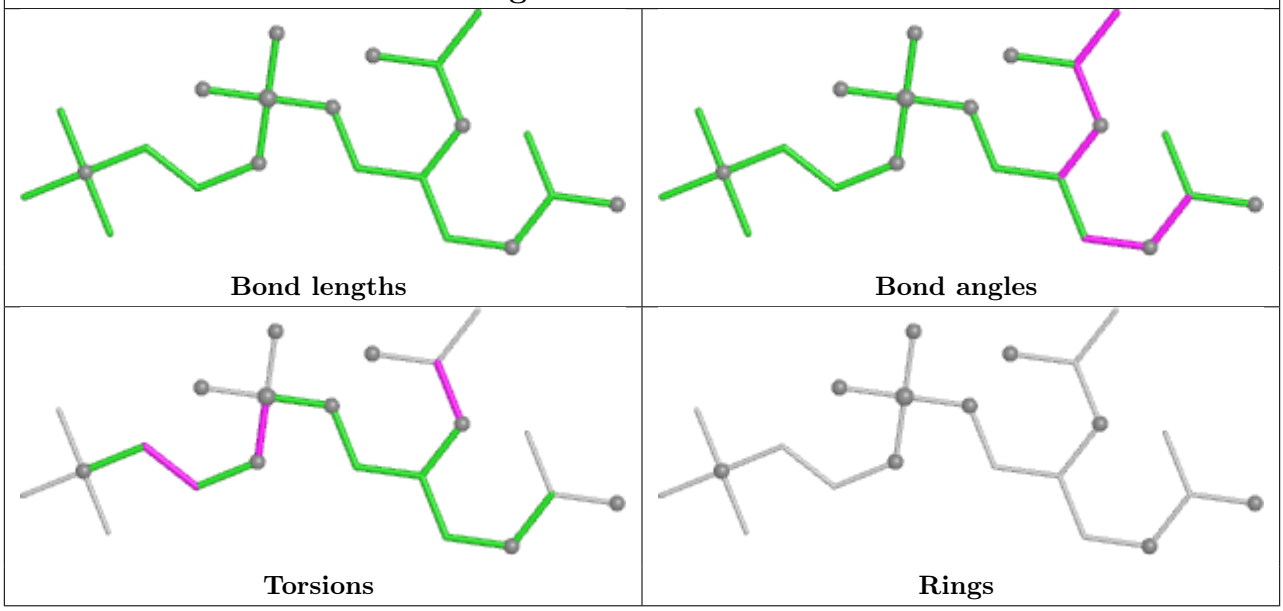

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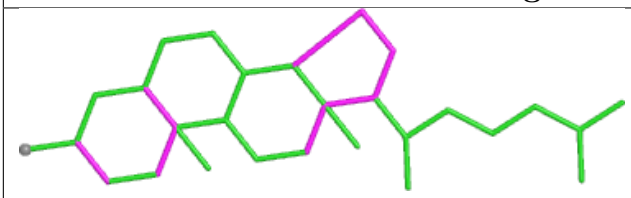
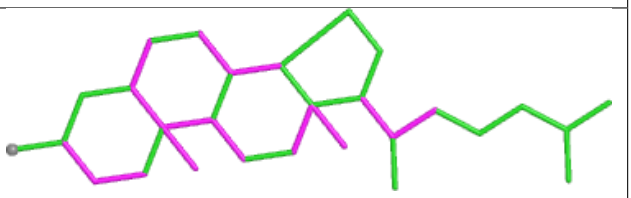
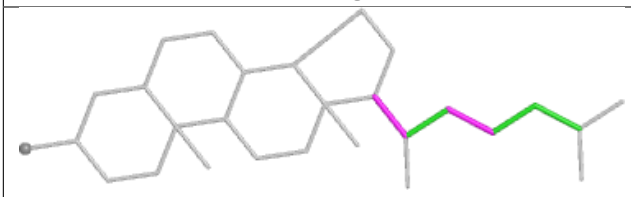
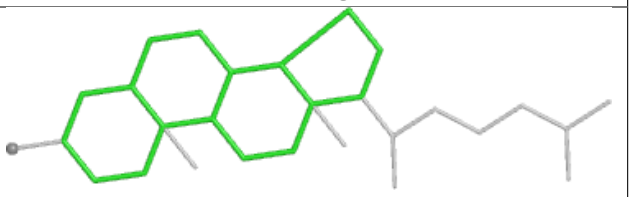
 Bond lengths	 Bond angles
 Torsions	 Rings

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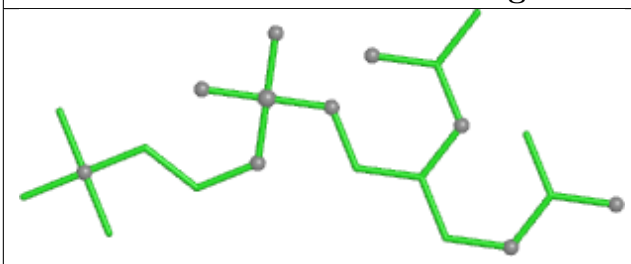
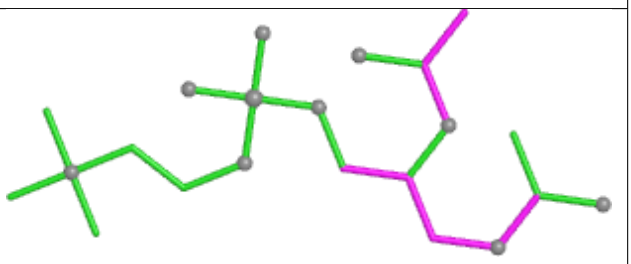
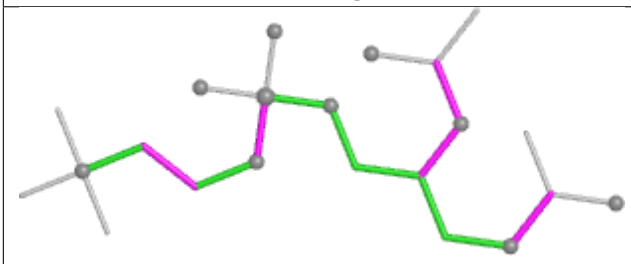
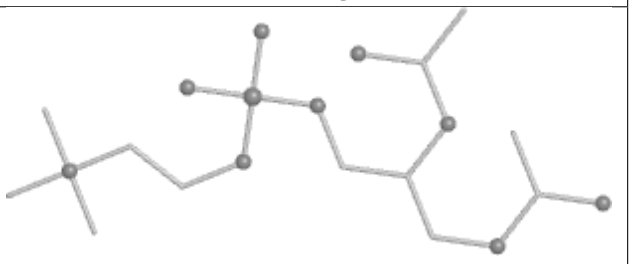
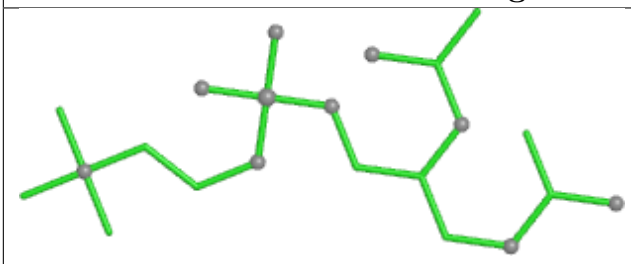
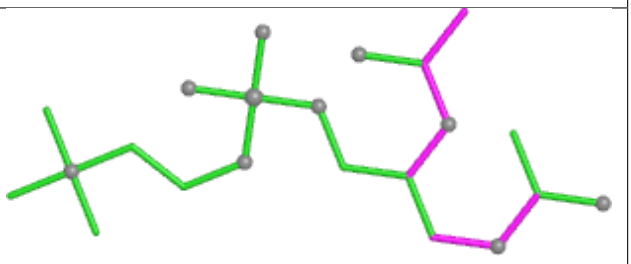
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand PCW A 1108



Bond lengths



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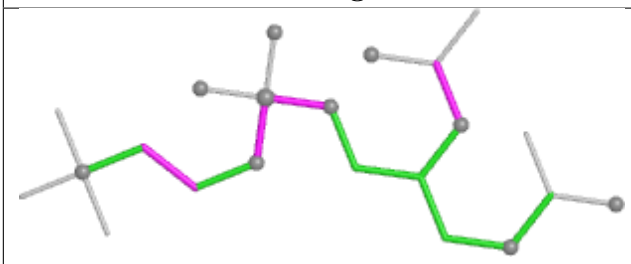

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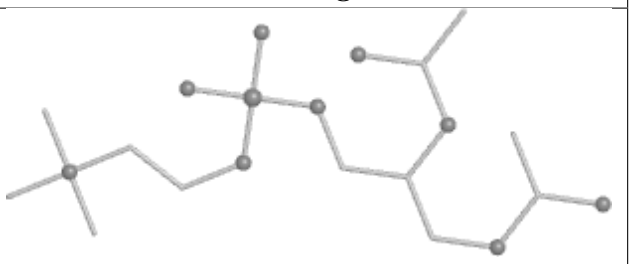
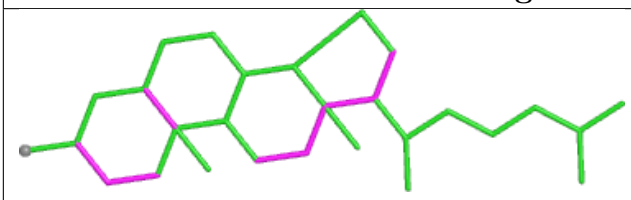


Rings

Ligand CLR A 1104



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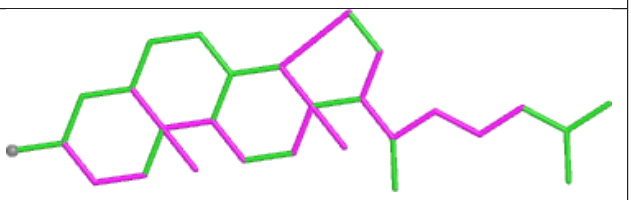
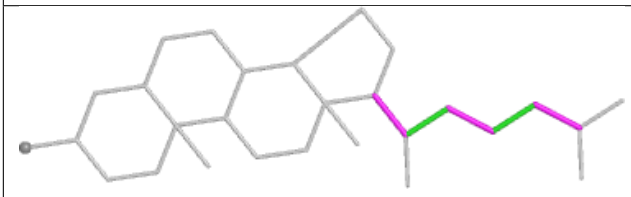


Bond angles



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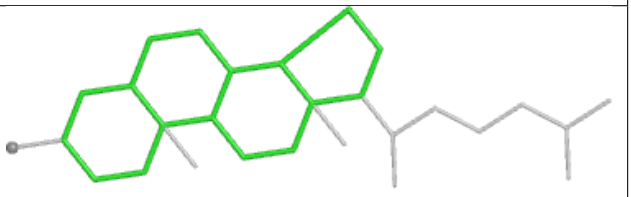
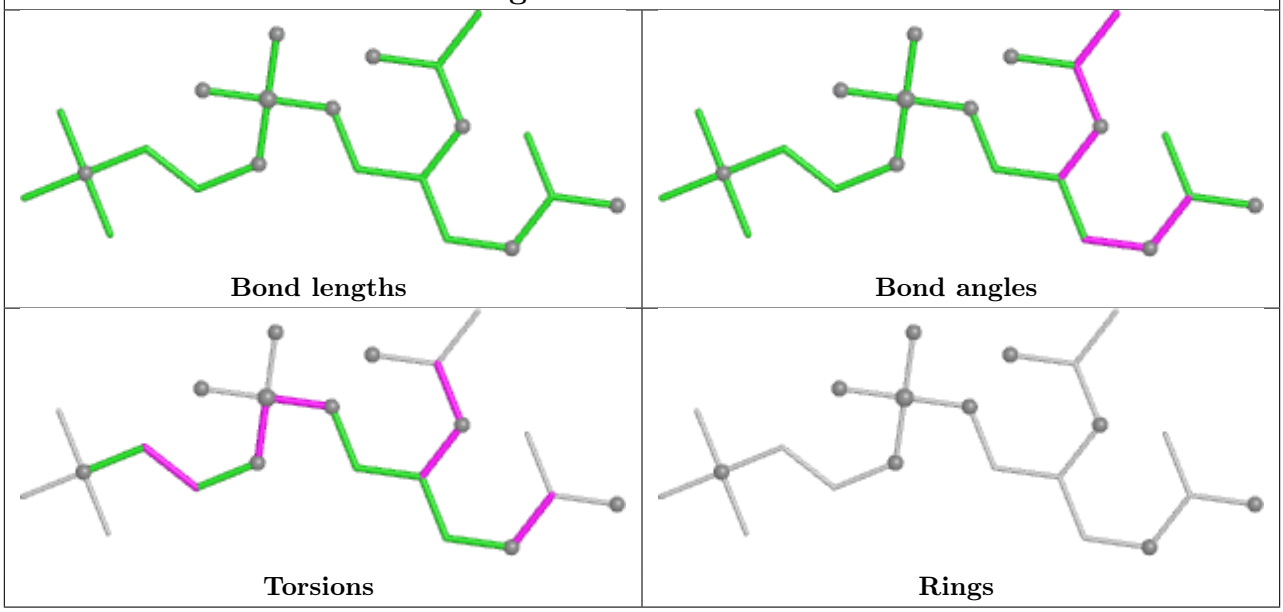


Rings

Ligand PCW A 1106



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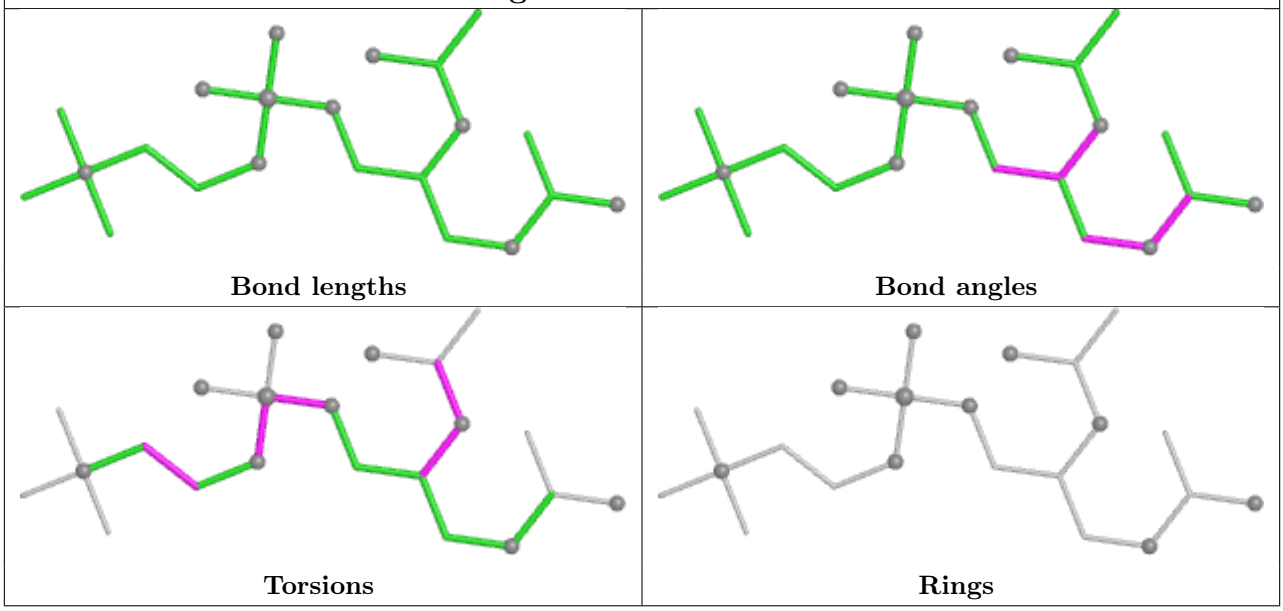

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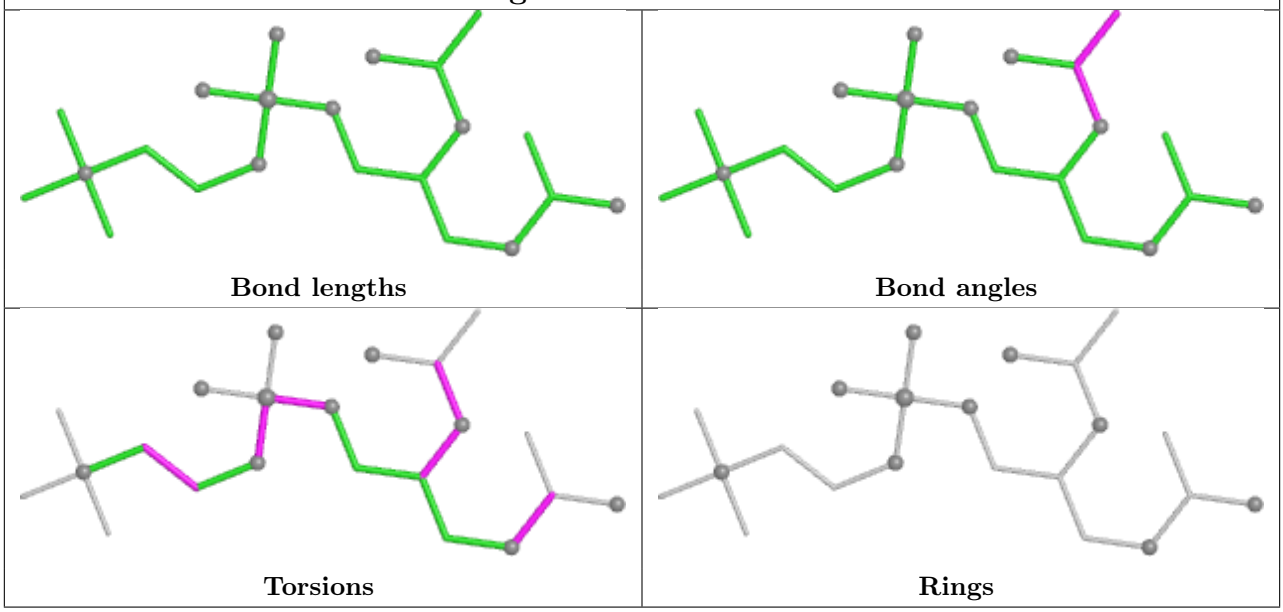
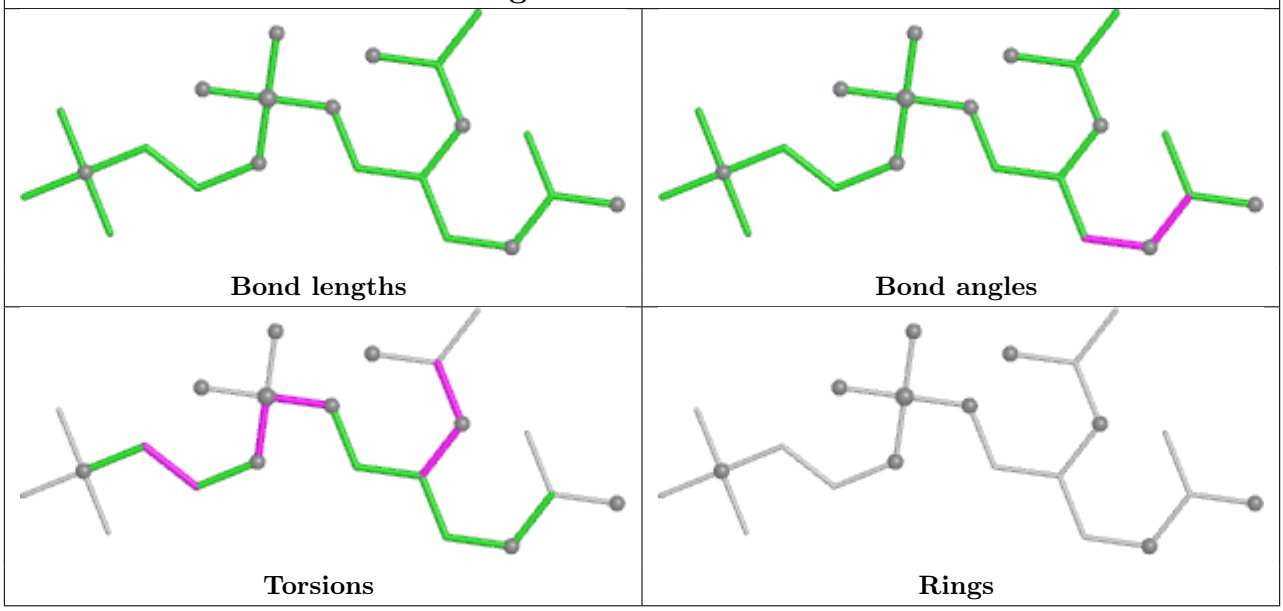
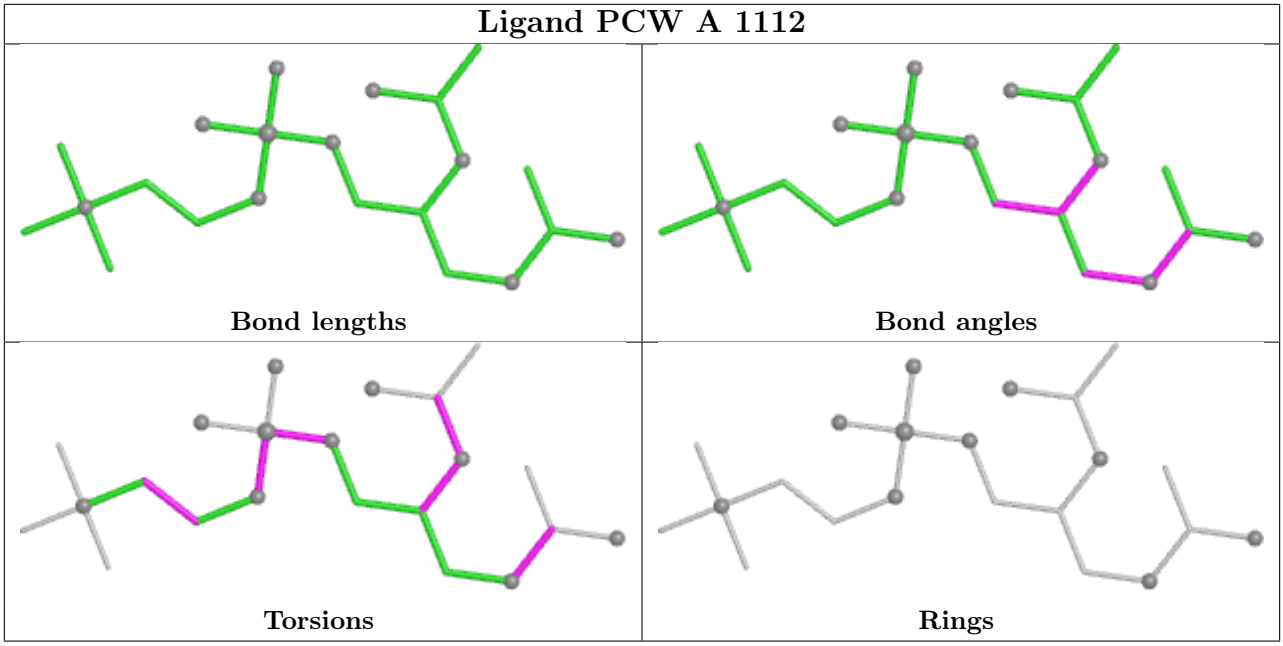


Ligand PCW A 1105





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	A	996/1016 (98%)	-0.31	2 (0%) 91 87	35, 76, 127, 163	0
2	B	291/303 (96%)	-0.16	0 100 100	46, 94, 138, 169	0
3	G	32/65 (49%)	-0.48	0 100 100	38, 66, 95, 109	0
All	All	1319/1384 (95%)	-0.28	2 (0%) 91 87	35, 80, 130, 169	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	432	ASN	2.2
1	A	213	GLY	2.1

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)

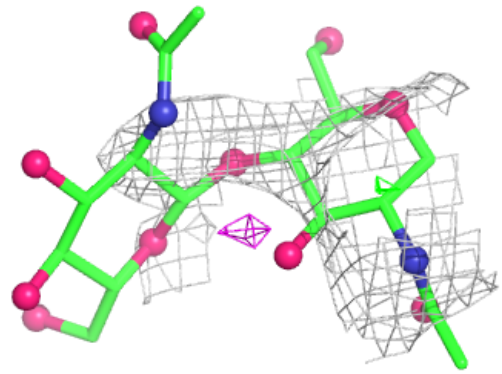
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

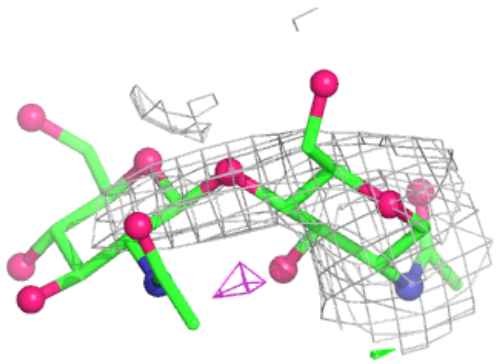
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	C	1	14/15	-	-	106,123,162,168	0
4	NAG	C	2	14/15	-	-	137,165,170,172	0

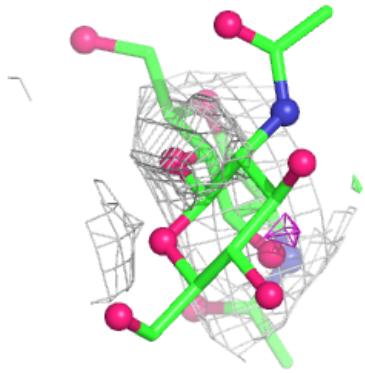
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

$2mF_o$-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
7	PCW	A	1114	22/54	0.42	0.18	84,124,157,160	0
7	PCW	A	1109	22/54	0.53	0.14	99,127,165,173	0
7	PCW	A	1112	22/54	0.63	0.16	91,136,161,162	0
7	PCW	A	1105	22/54	0.64	0.13	89,130,153,165	0
9	NAG	B	421	14/15	0.64	0.15	93,119,143,149	0
7	PCW	A	1115	22/54	0.65	0.12	97,135,155,172	0
7	PCW	A	1110	22/54	0.70	0.15	63,113,135,146	0
7	PCW	A	1107	22/54	0.71	0.12	76,130,171,181	0
7	PCW	A	1111	22/54	0.72	0.14	87,126,148,150	0
7	PCW	A	1113	22/54	0.77	0.14	87,125,166,176	0
7	PCW	A	1108	22/54	0.77	0.12	86,126,150,158	0
7	PCW	A	1106	22/54	0.78	0.11	72,107,134,159	0
6	CLR	A	1104	28/28	0.83	0.13	53,75,100,116	0

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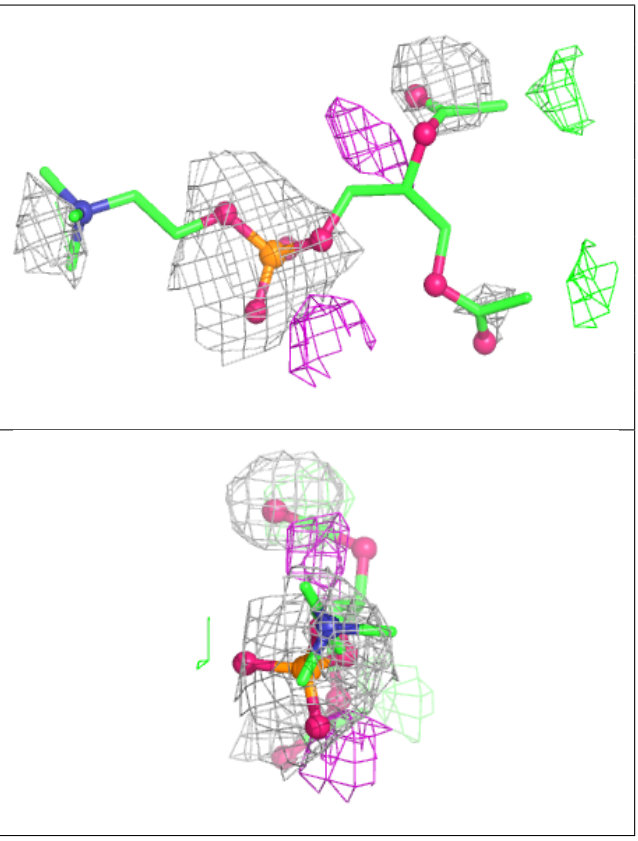
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	MG	A	1103	1/1	0.88	0.20	71,71,71,71	0
6	CLR	G	101	28/28	0.90	0.10	49,80,94,100	0
8	BEF	A	1116	4/4	0.93	0.08	67,71,76,87	0
5	MG	A	1101	1/1	0.98	0.03	54,54,54,54	0
5	MG	A	1102	1/1	0.98	0.07	38,38,38,38	0

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.

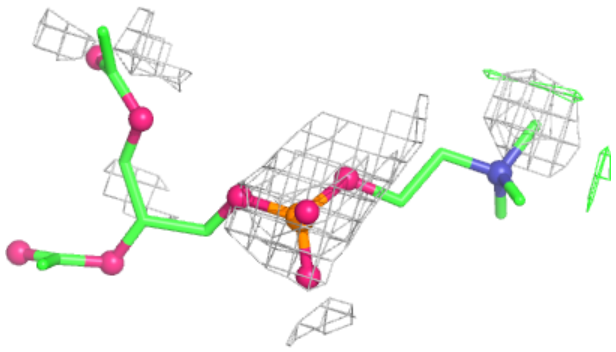
Electron density around PCW A 1114:

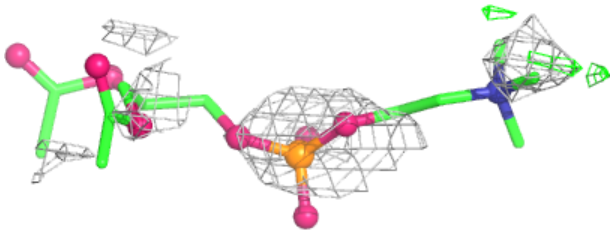
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

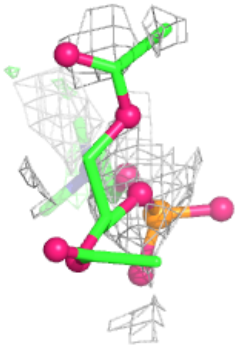


Electron density around PCW A 1109:

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

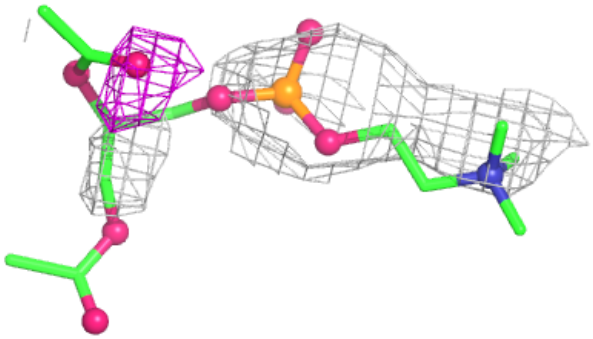


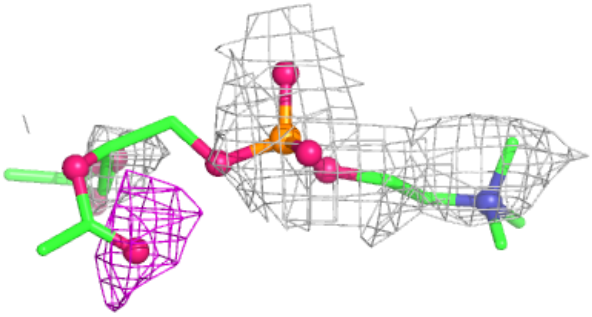


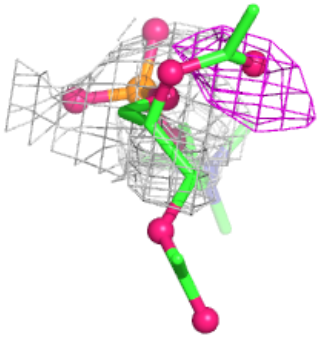


Electron density around PCW A 1112:

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

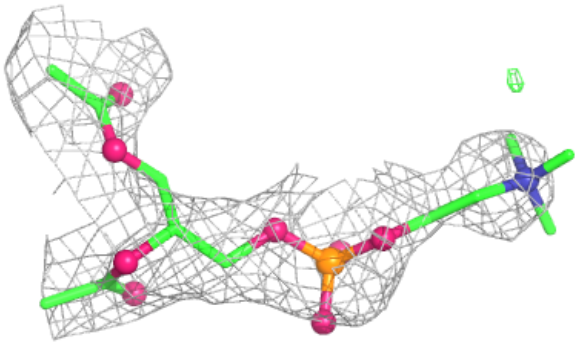


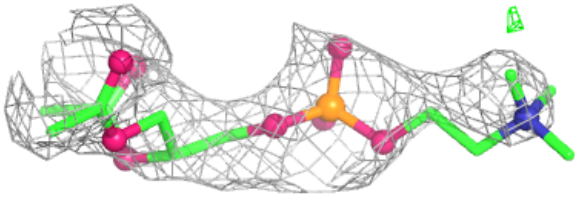


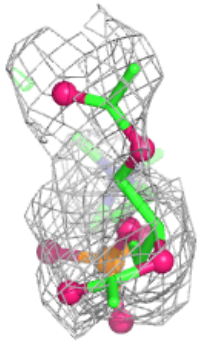


Electron density around PCW A 1105:

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

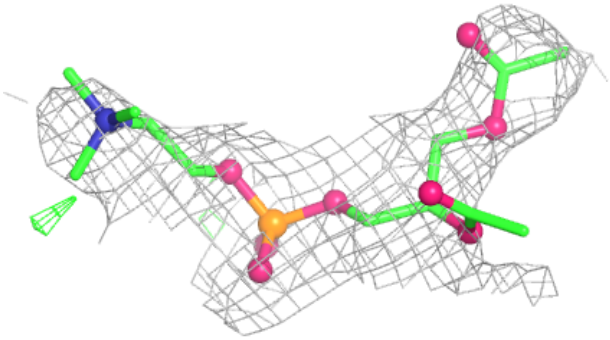


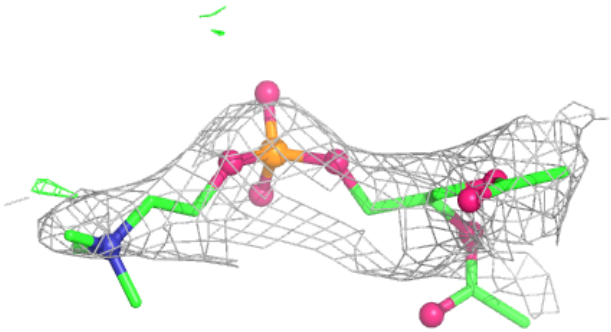


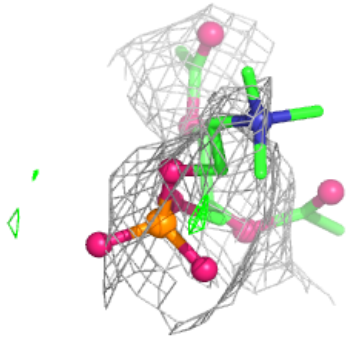


Electron density around PCW A 1115:

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

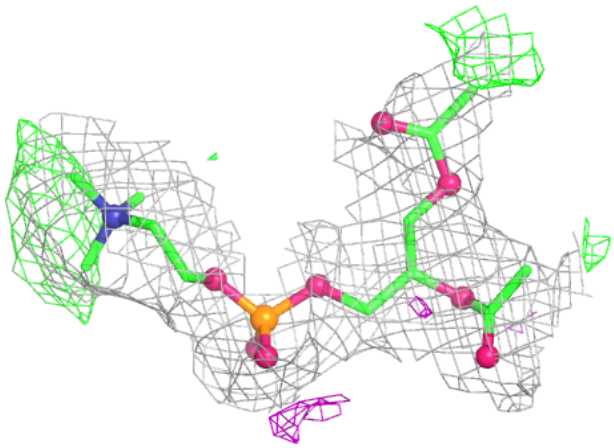


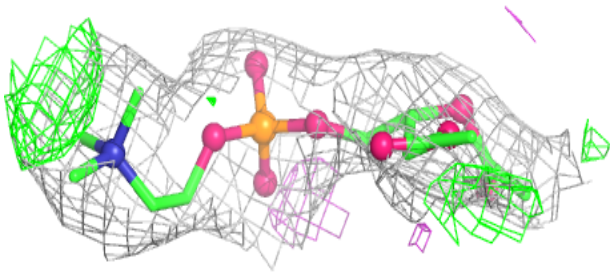


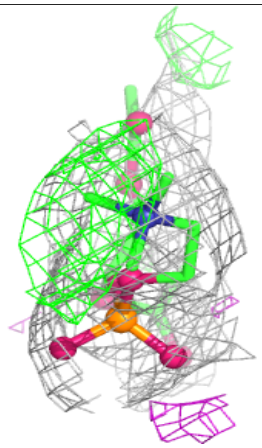


Electron density around PCW A 1110:

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

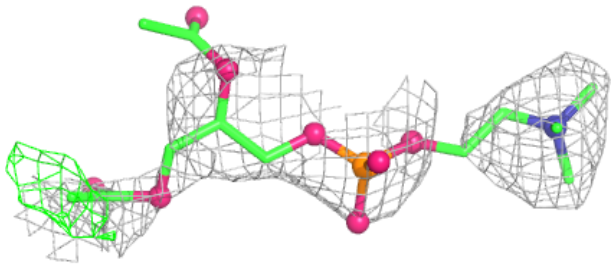


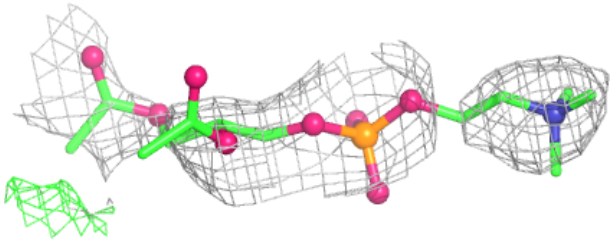


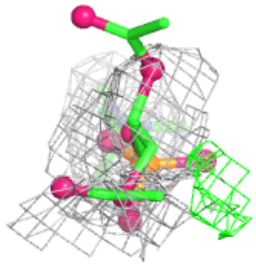


Electron density around PCW A 1107:

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

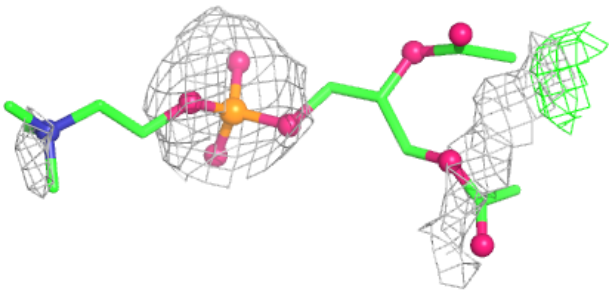


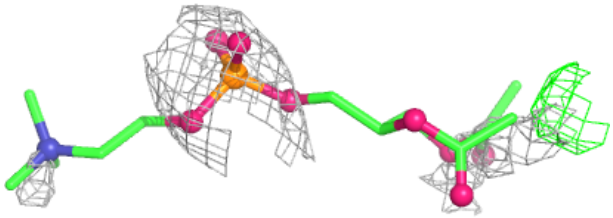


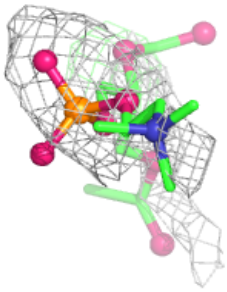


Electron density around PCW A 1111:

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

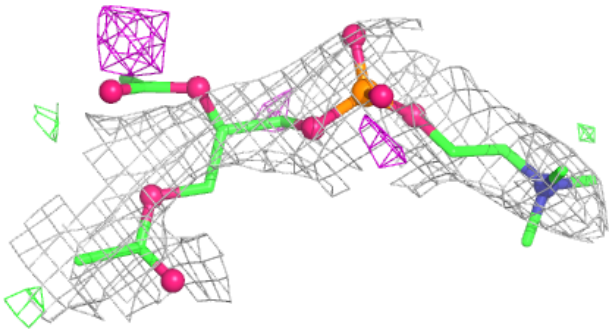


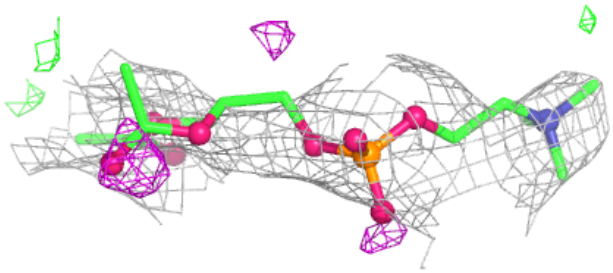


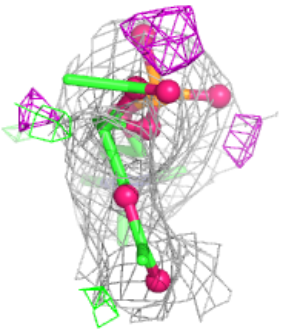


Electron density around PCW A 1113:

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

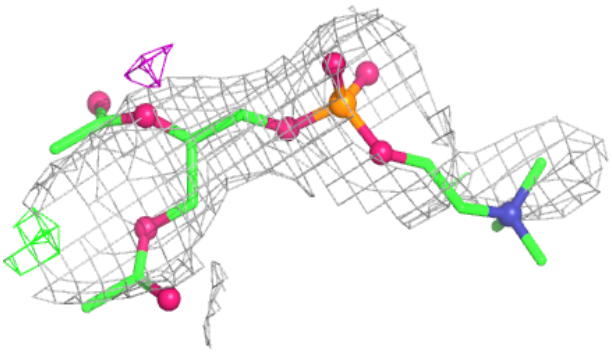


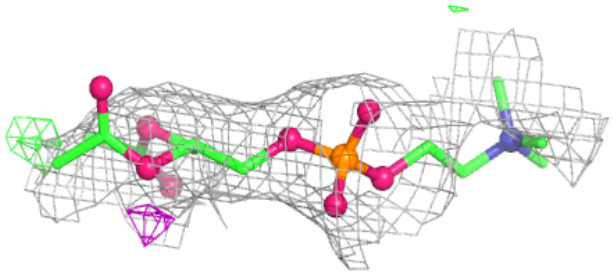


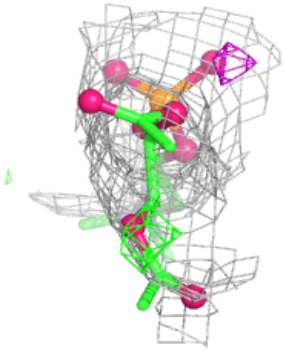


Electron density around PCW A 1108:

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

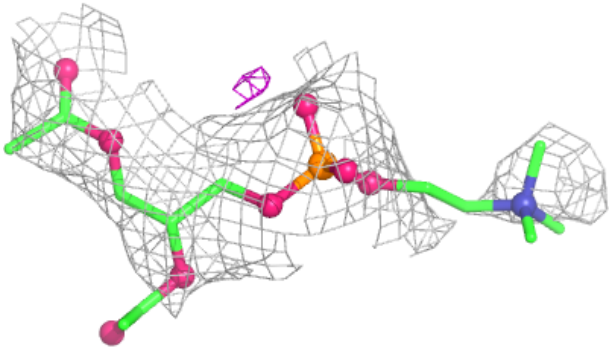


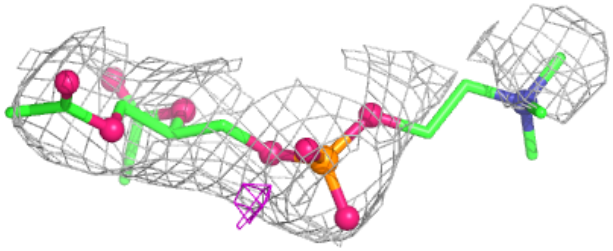


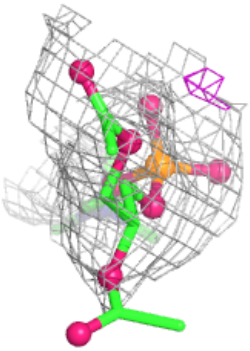


Electron density around PCW A 1106:

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

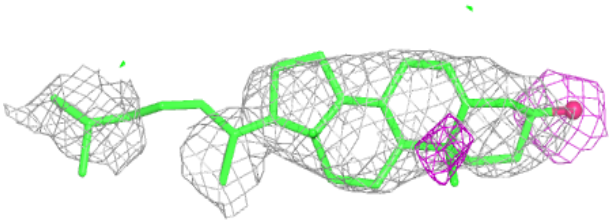


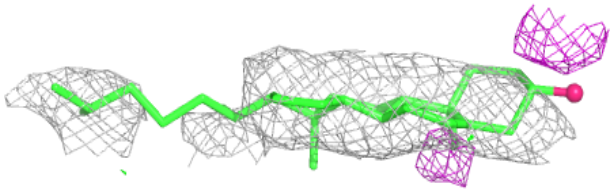


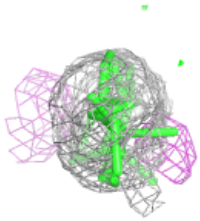


Electron density around CLR A 1104:

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







Electron density around CLR G 101:

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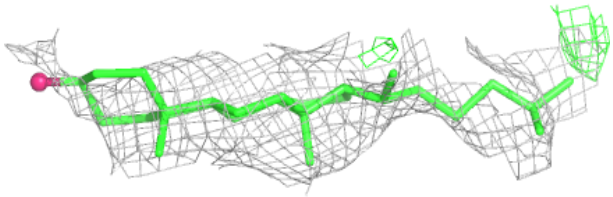
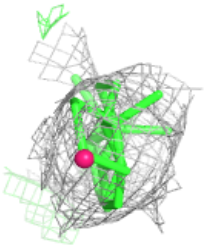
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers (i)

There are no such residues in this entry.