



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 13, 2023 – 11:03 AM EDT

PDB ID : 4RES
Title : Crystal structure of the Na,K-ATPase E2P-bufalin complex with bound potassium
Authors : Laursen, M.; Yatime, L.; Gregersen, J.L.; Nissen, P.; Fedosova, N.U.
Deposited on : 2014-09-23
Resolution : 3.41 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

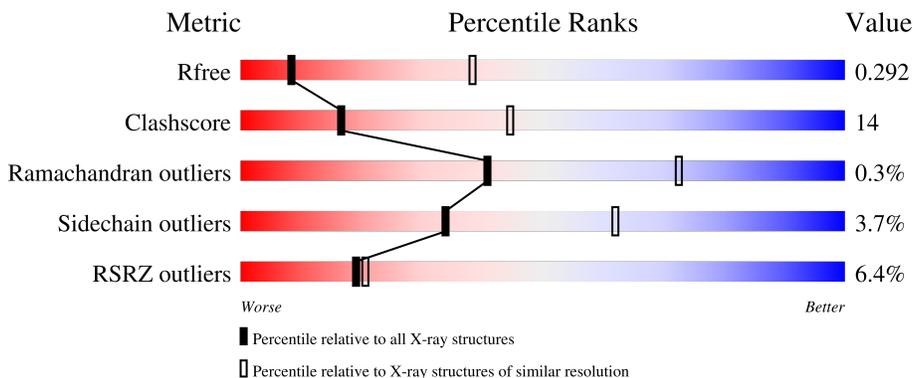
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.41 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.



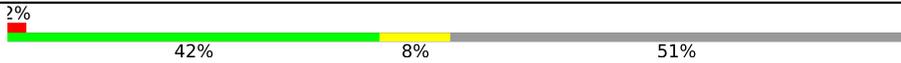
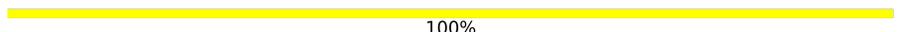
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	1021	
1	C	1021	
2	B	303	
2	D	303	
3	E	65	

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Mol	Chain	Length	Quality of chain
3	G	65	 2% 42% 8% 51%
4	F	2	 50% 50%
5	H	2	 50% 50%
5	I	2	 100%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 20881 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	P				S
1	A	996	7730	4922	1301	1459	1	47	0	0	0
1	C	996	7730	4922	1301	1459	1	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	288	2357	1525	385	434	13	0	0	0
2	D	285	2327	1504	380	430	13	0	0	0

- Molecule 3 is a protein called Na⁺/K⁺ ATPase gamma subunit transcript variant a.

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



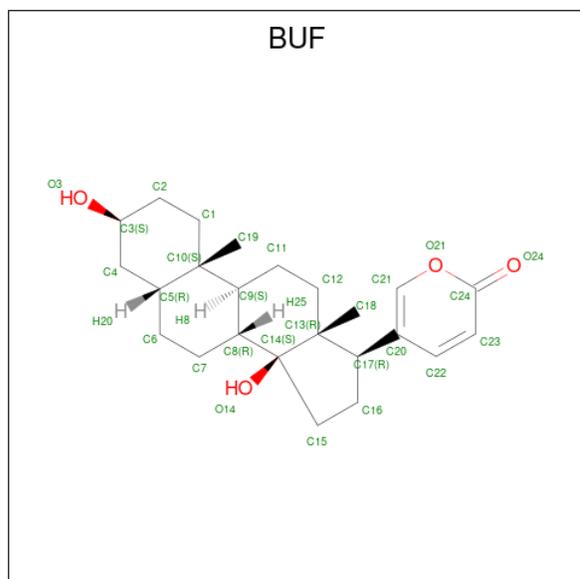
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	F	2	28	16	2	10	0	0	0

- Molecule 5 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



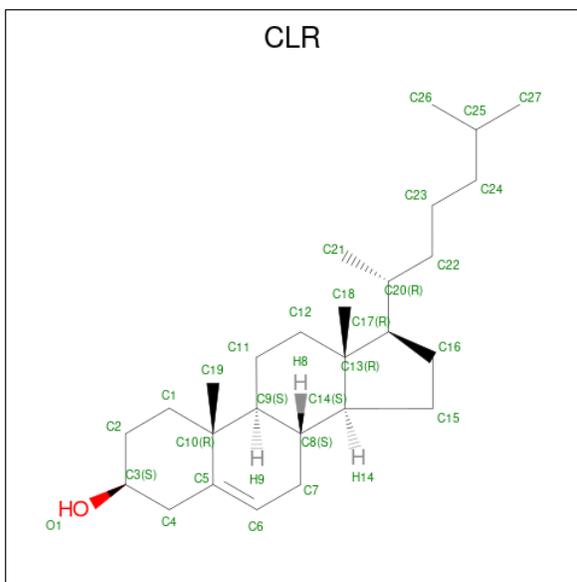
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
5	H	2	Total	C	O	0	0	0
			23	12	11			
5	I	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 6 is bufalin (three-letter code: BUF) (formula: $C_{24}H_{34}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			28	24	4		
6	C	1	Total	C	O	0	0
			28	24	4		

- Molecule 7 is CHOLESTEROL (three-letter code: CLR) (formula: $C_{27}H_{46}O$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	C O	0	0
			28	27 1		
7	E	1	Total	C O	0	0
			28	27 1		

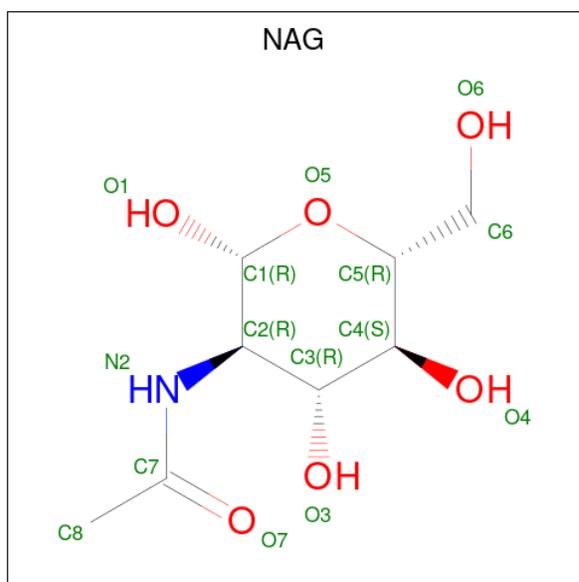
- Molecule 8 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	3	Total	K	0	0
			3	3		
8	C	3	Total	K	0	0
			3	3		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

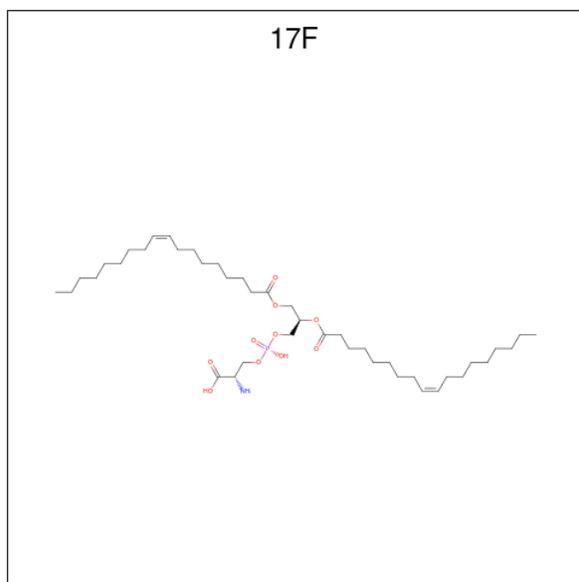
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Mg	0	0
			1	1		
9	C	1	Total	Mg	0	0
			1	1		

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 11 is O-[(S)-({(2R)-2,3-bis[(9Z)-octadec-9-enoyloxy]propyl}oxy)(hydroxy)phosphoryl]-L-serine (three-letter code: 17F) (formula: $C_{42}H_{78}NO_{10}P$).

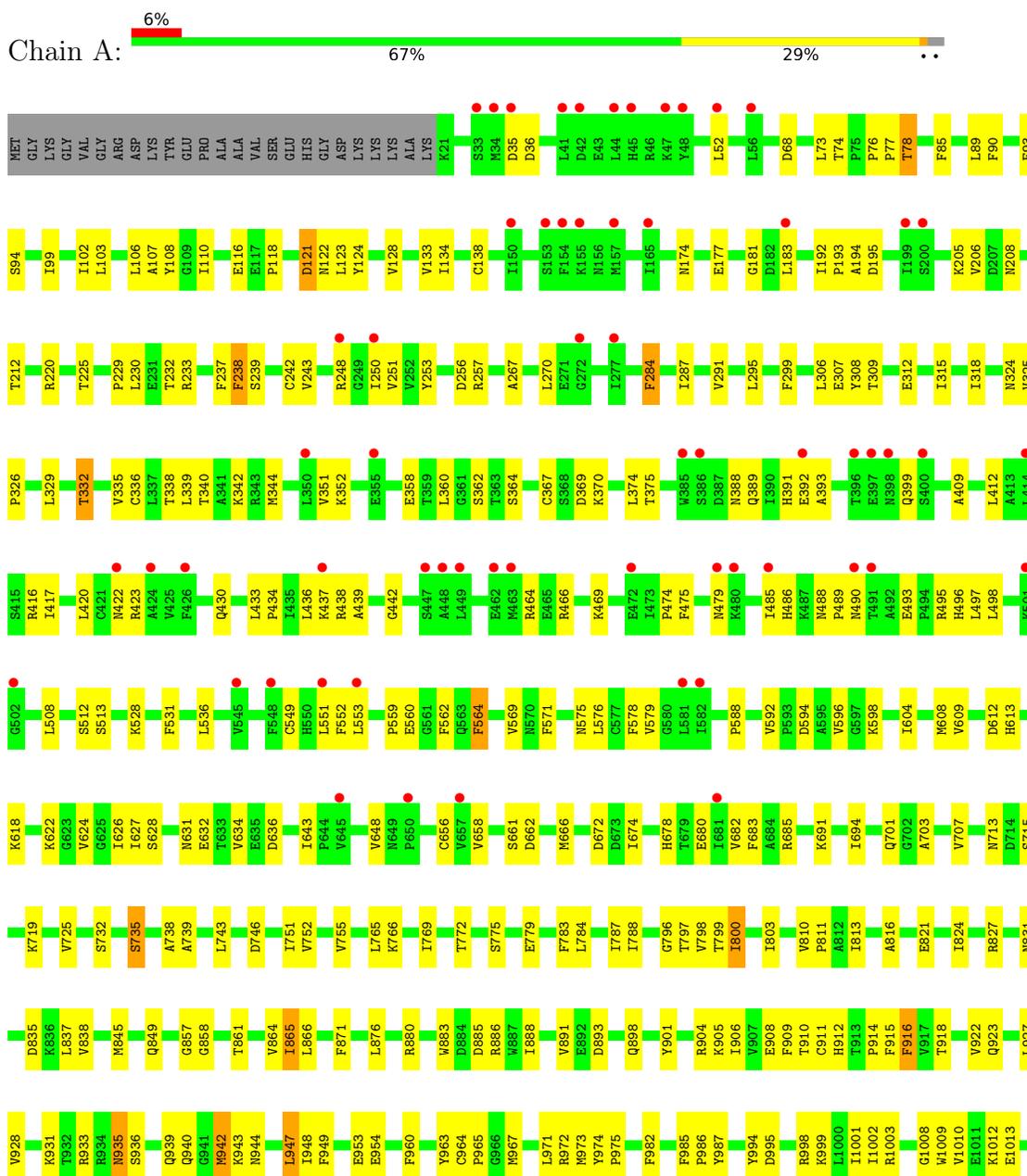


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
11	G	1	19	8	1	9	1	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

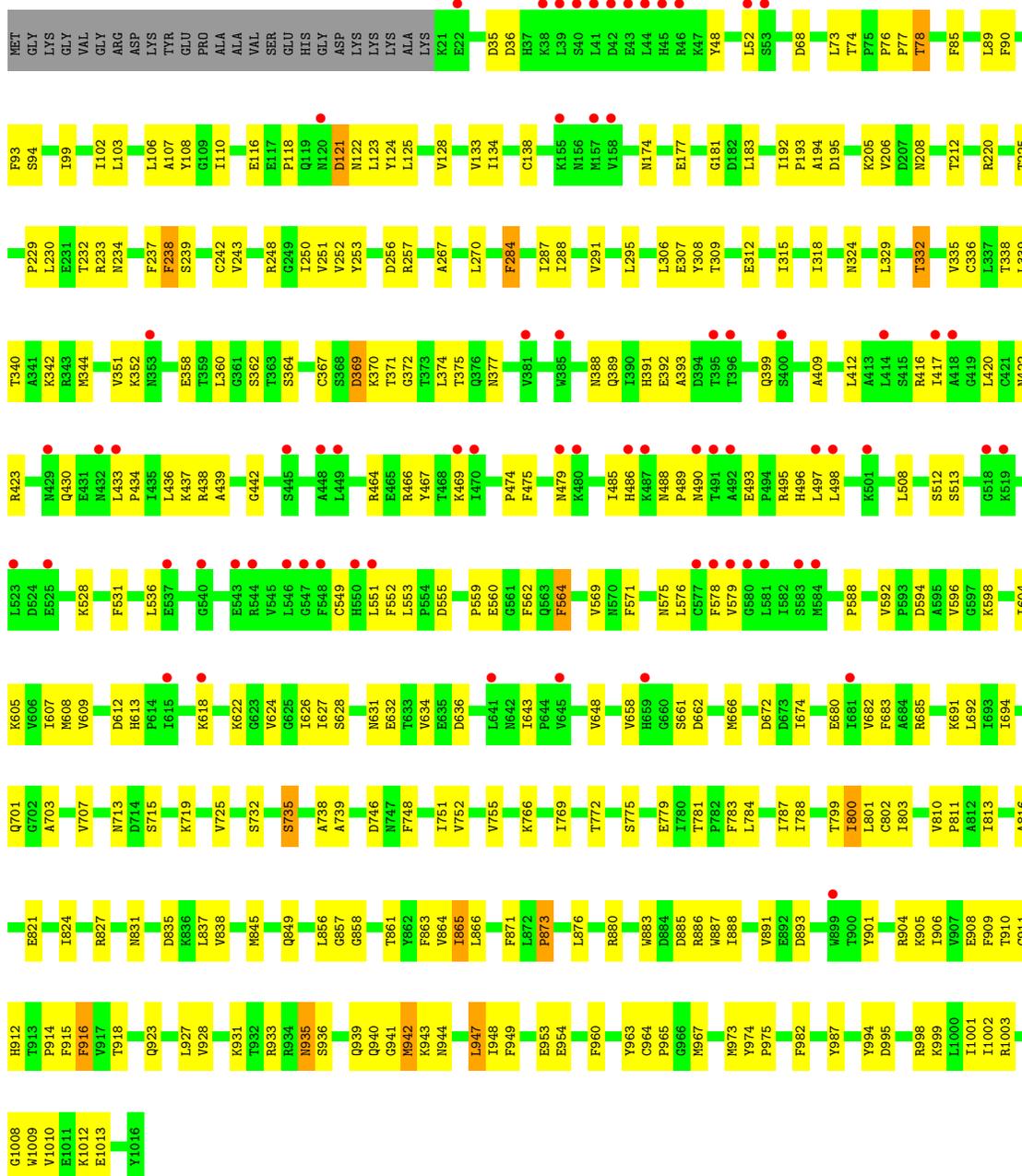
- Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1



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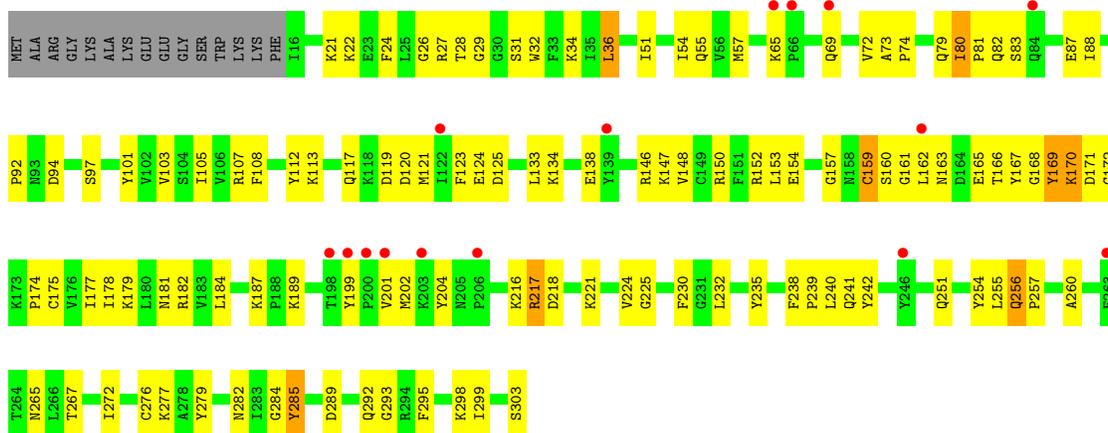
- Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

Chain C: 7% 67% 29% ..

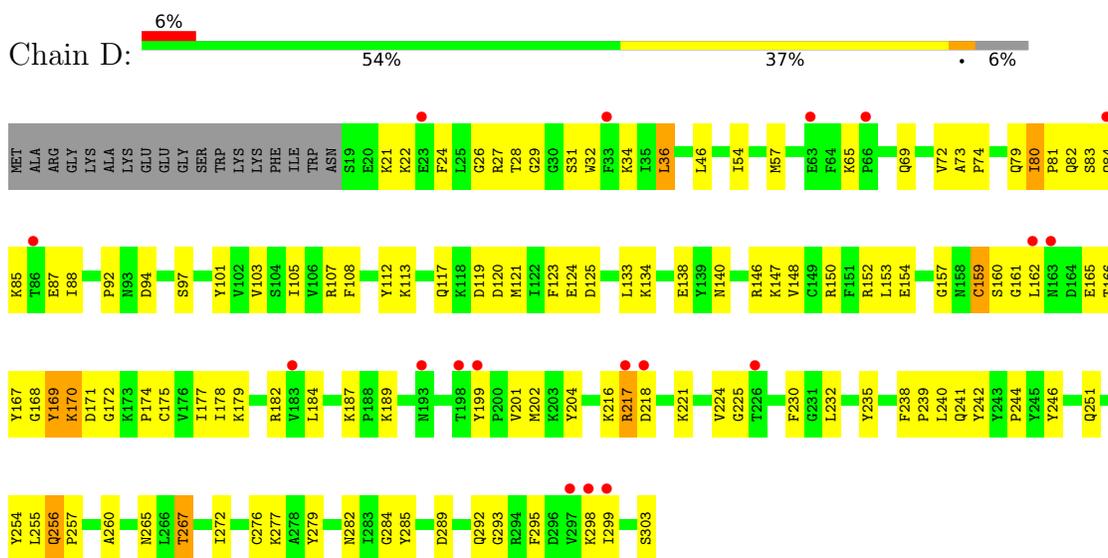


- Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1

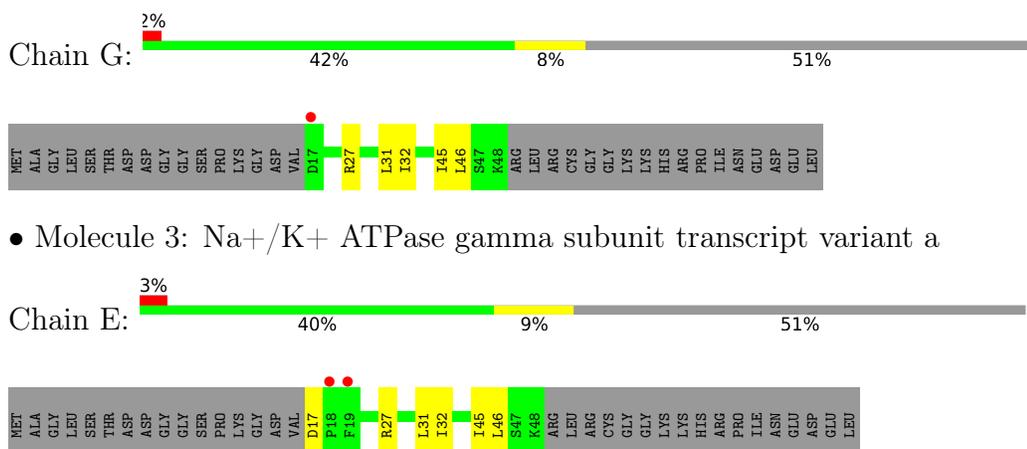
Chain B: 5% 56% 36% 5%



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



- Molecule 3: Na⁺/K⁺ ATPase gamma subunit transcript variant a



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

Chain F:  50% 50%

HA61
HA62

- Molecule 5: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain H:  50% 50%

GLC1
FRU2

- Molecule 5: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain I:  100%

GLC1
FRU2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.91Å 240.27Å 152.70Å 90.00° 102.28° 90.00°	Depositor
Resolution (Å)	49.90 – 3.41 54.59 – 3.41	Depositor EDS
% Data completeness (in resolution range)	49.9 (49.90-3.41) 50.2 (54.59-3.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 3.40Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.245 , 0.288 0.248 , 0.292	Depositor DCC
R_{free} test set	1634 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	92.8	Xtrriage
Anisotropy	0.064	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	0.368 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	20881	wwPDB-VP
Average B, all atoms (Å ²)	125.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CLR, MG, BUF, K, GLC, NAG, PHD, FRU, 17F

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	0/7867	0.54	0/10674
1	C	0.34	0/7867	0.54	0/10674
2	B	0.36	0/2419	0.59	0/3263
2	D	0.35	0/2387	0.59	0/3218
3	E	0.36	0/261	0.51	0/354
3	G	0.33	0/261	0.52	0/354
All	All	0.34	0/21062	0.55	0/28537

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

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	7730	0	7776	211	0
1	C	7730	0	7776	219	0
2	B	2357	0	2328	83	0
2	D	2327	0	2301	83	0
3	E	255	0	259	5	0
3	G	255	0	259	4	0
4	F	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	23	0	21	3	0
5	I	23	0	21	2	0
6	A	28	0	34	2	0
6	C	28	0	34	4	0
7	A	28	0	46	4	0
7	E	28	0	46	4	0
8	A	3	0	0	0	0
8	C	3	0	0	0	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
10	B	14	0	13	1	0
11	G	19	0	10	0	0
All	All	20881	0	20949	595	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 595 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:HG13	2:B:81:PRO:HD3	1.44	0.97
2:D:80:ILE:HG13	2:D:81:PRO:HD3	1.45	0.97
2:B:79:GLN:HB3	2:B:295:PHE:HZ	1.33	0.93
2:D:79:GLN:HB3	2:D:295:PHE:HZ	1.34	0.91
2:D:80:ILE:HD12	2:D:105:ILE:HD12	1.52	0.91

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	993/1021 (97%)	939 (95%)	53 (5%)	1 (0%)	51	82
1	C	993/1021 (97%)	937 (94%)	55 (6%)	1 (0%)	51	82
2	B	286/303 (94%)	265 (93%)	18 (6%)	3 (1%)	15	46
2	D	283/303 (93%)	263 (93%)	17 (6%)	3 (1%)	14	44
3	E	30/65 (46%)	30 (100%)	0	0	100	100
3	G	30/65 (46%)	30 (100%)	0	0	100	100
All	All	2615/2778 (94%)	2464 (94%)	143 (6%)	8 (0%)	41	72

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	170	LYS
2	B	217	ARG
2	D	170	LYS
2	D	217	ARG
1	A	78	THR

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	846/864 (98%)	819 (97%)	27 (3%)	39	67
1	C	846/864 (98%)	818 (97%)	28 (3%)	38	66
2	B	258/269 (96%)	245 (95%)	13 (5%)	24	54
2	D	255/269 (95%)	242 (95%)	13 (5%)	24	54
3	E	26/52 (50%)	25 (96%)	1 (4%)	33	61
3	G	26/52 (50%)	25 (96%)	1 (4%)	33	61
All	All	2257/2370 (95%)	2174 (96%)	83 (4%)	34	62

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	569	VAL

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Mol	Chain	Res	Type
2	D	80	ILE
1	C	746	ASP
1	C	935	ASN
2	D	175	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	399	GLN
1	C	488	ASN
1	C	898	GLN
1	C	889	ASN
1	A	898	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](#)

2 non-standard protein/DNA/RNA residues 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
1	PHD	C	369	1,9	9,11,12	1.38	1 (11%)	10,15,17	1.47	2 (20%)
1	PHD	A	369	1,9	9,11,12	1.37	1 (11%)	10,15,17	1.44	2 (20%)

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
1	PHD	C	369	1,9	-	1/8/11/13	-
1	PHD	A	369	1,9	-	1/8/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	369	PHD	CB-CA	-2.39	1.48	1.53
1	A	369	PHD	CB-CA	-2.30	1.48	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	369	PHD	OD2-CG-CB	-3.22	117.62	124.73
1	A	369	PHD	OD2-CG-CB	-3.20	117.66	124.73
1	A	369	PHD	OD1-CG-CB	2.28	117.39	111.11
1	C	369	PHD	OD1-CG-CB	2.21	117.19	111.11

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	369	PHD	CA-CB-CG-OD2
1	C	369	PHD	CA-CB-CG-OD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	369	PHD	1	0

5.5 Carbohydrates [i](#)

6 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	F	1	4,2	14,14,15	0.53	0	17,19,21	0.62	0
4	NAG	F	2	4	14,14,15	0.34	0	17,19,21	0.39	0
5	GLC	H	1	5	11,11,12	0.54	0	15,15,17	1.95	3 (20%)
5	FRU	H	2	5	11,12,12	0.72	1 (9%)	10,18,18	0.81	0
5	GLC	I	1	5	11,11,12	0.55	0	15,15,17	1.34	1 (6%)
5	FRU	I	2	5	11,12,12	0.65	0	10,18,18	1.08	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	F	1	4,2	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
5	GLC	H	1	5	-	0/2/19/22	0/1/1/1
5	FRU	H	2	5	-	2/5/24/24	0/1/1/1
5	GLC	I	1	5	-	1/2/19/22	0/1/1/1
5	FRU	I	2	5	-	2/5/24/24	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	2	FRU	O2-C2	2.05	1.44	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	1	GLC	C1-O5-C5	5.23	119.28	112.19
5	I	1	GLC	C1-O5-C5	3.38	116.77	112.19
5	H	1	GLC	C1-C2-C3	2.98	113.33	109.67
5	H	1	GLC	O5-C5-C6	2.09	110.49	107.20

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	2	FRU	C4-C5-C6-O6
5	I	2	FRU	C4-C5-C6-O6
5	H	2	FRU	O5-C5-C6-O6

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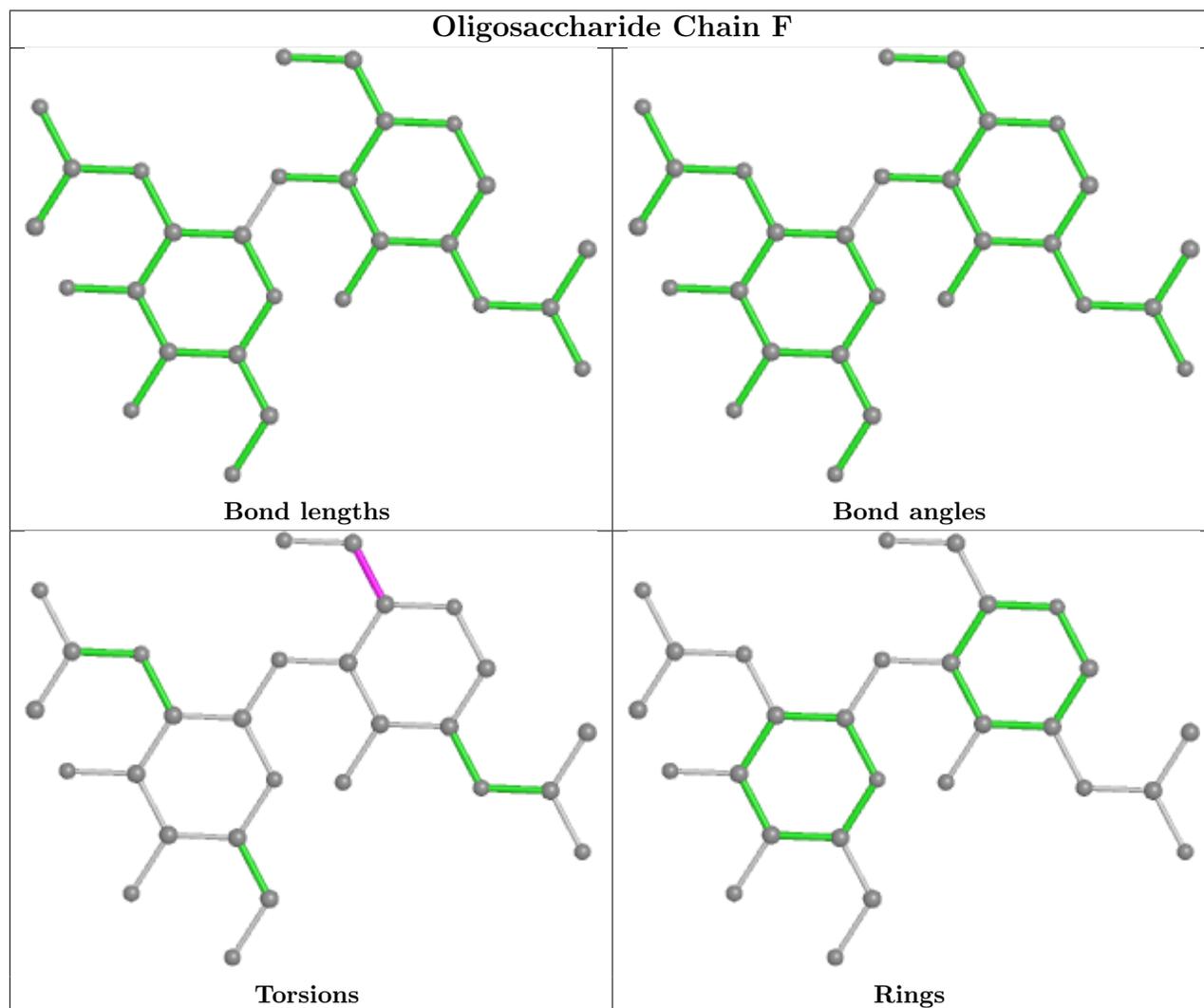
Mol	Chain	Res	Type	Atoms
5	I	2	FRU	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6

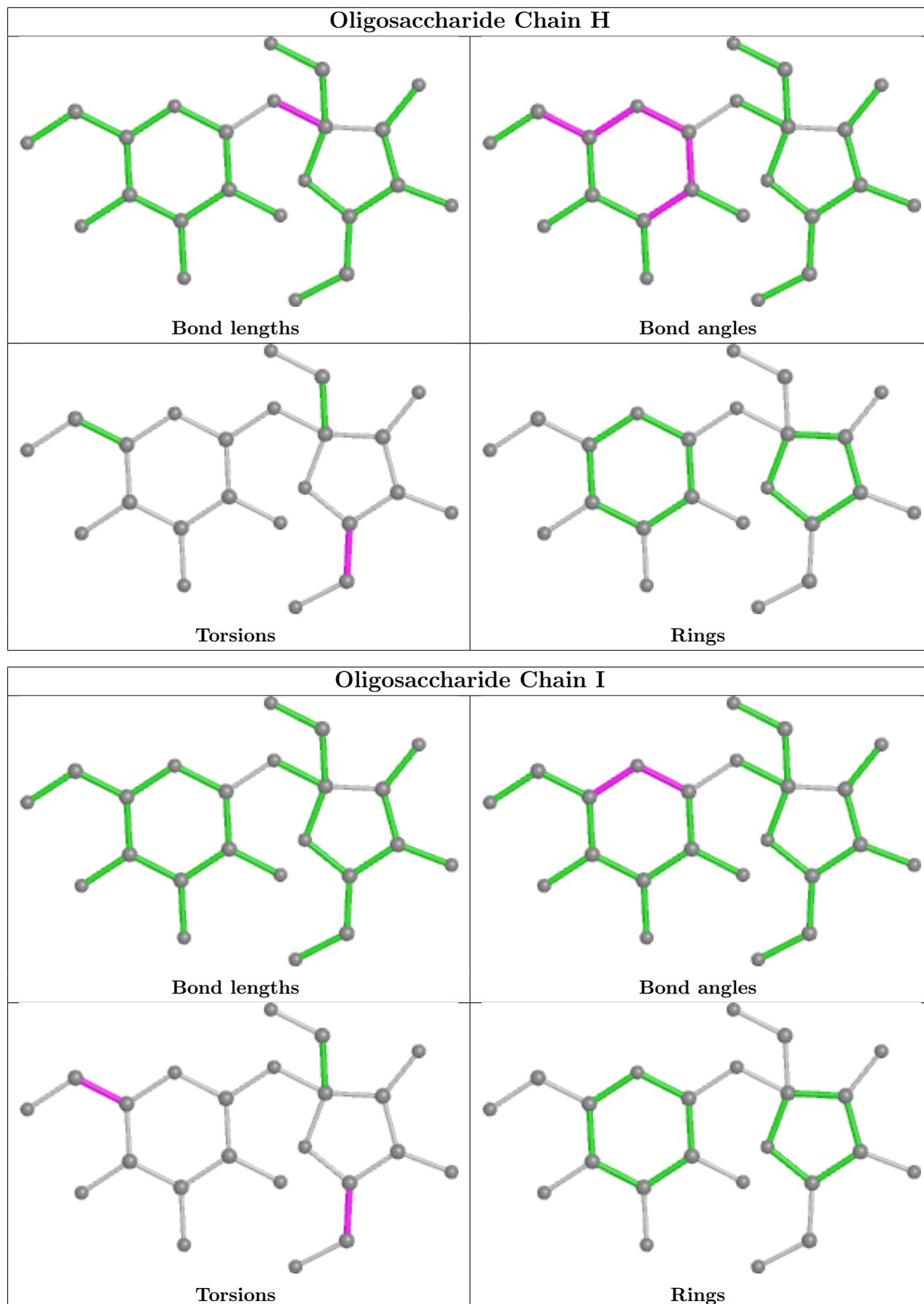
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	2	FRU	3	0
5	I	2	FRU	2	0
4	F	1	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

Of 14 ligands modelled in this entry, 8 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
11	17F	G	1001	-	17,18,53	1.74	3 (17%)	20,24,60	1.91	2 (10%)
10	NAG	B	1001	2	14,14,15	0.40	0	17,19,21	0.55	0
7	CLR	E	101	-	31,31,31	2.49	9 (29%)	48,48,48	2.83	20 (41%)
6	BUF	C	1102	8	32,32,32	0.97	3 (9%)	52,52,52	1.44	7 (13%)
6	BUF	A	2001	8	32,32,32	0.90	2 (6%)	52,52,52	1.36	8 (15%)
7	CLR	A	2002	-	31,31,31	2.52	12 (38%)	48,48,48	2.81	21 (43%)

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
11	17F	G	1001	-	-	16/21/21/59	-
10	NAG	B	1001	2	-	2/6/23/26	0/1/1/1
7	CLR	E	101	-	-	3/10/68/68	0/4/4/4
6	BUF	C	1102	8	-	0/4/68/68	0/5/5/5
6	BUF	A	2001	8	-	0/4/68/68	0/5/5/5
7	CLR	A	2002	-	-	3/10/68/68	0/4/4/4

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	2002	CLR	C6-C5	9.12	1.53	1.33
7	E	101	CLR	C6-C5	9.07	1.53	1.33
7	A	2002	CLR	C11-C9	4.74	1.61	1.53
7	E	101	CLR	C11-C9	4.65	1.61	1.53
11	G	1001	17F	P1-O6	4.50	1.77	1.59

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	2002	CLR	C4-C5-C6	-7.59	109.67	120.61
7	E	101	CLR	C4-C5-C6	-7.45	109.87	120.61
7	E	101	CLR	C7-C6-C5	-7.14	111.89	125.06
11	G	1001	17F	O3-C1-C2	7.08	114.23	108.06
7	A	2002	CLR	C7-C6-C5	-6.82	112.48	125.06

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

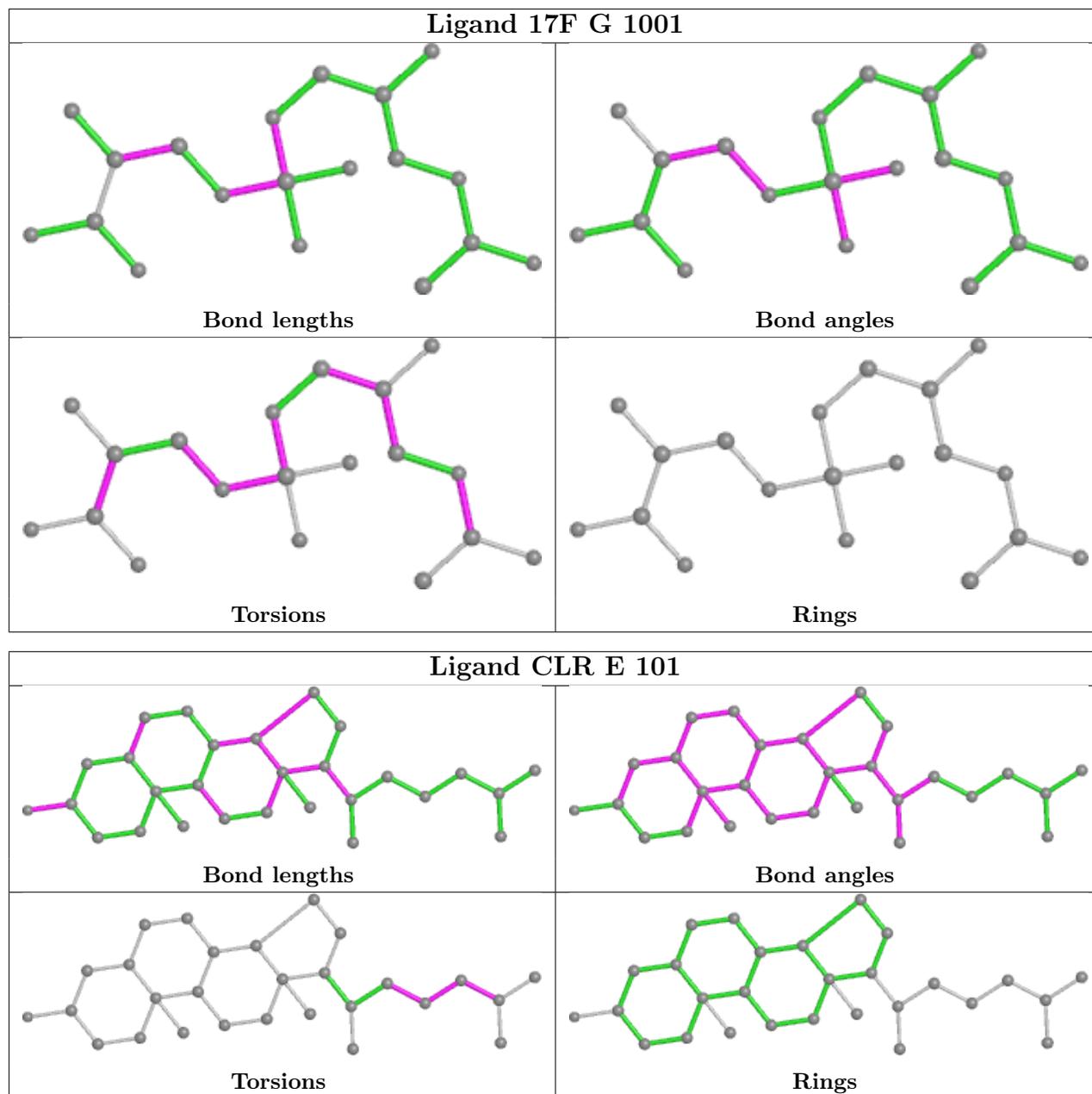
Mol	Chain	Res	Type	Atoms
11	G	1001	17F	C4-O6-P1-O1
11	G	1001	17F	C4-O6-P1-O2
11	G	1001	17F	C4-O6-P1-O3
11	G	1001	17F	C1-C2-C3-O4
11	G	1001	17F	C1-C2-C3-O5

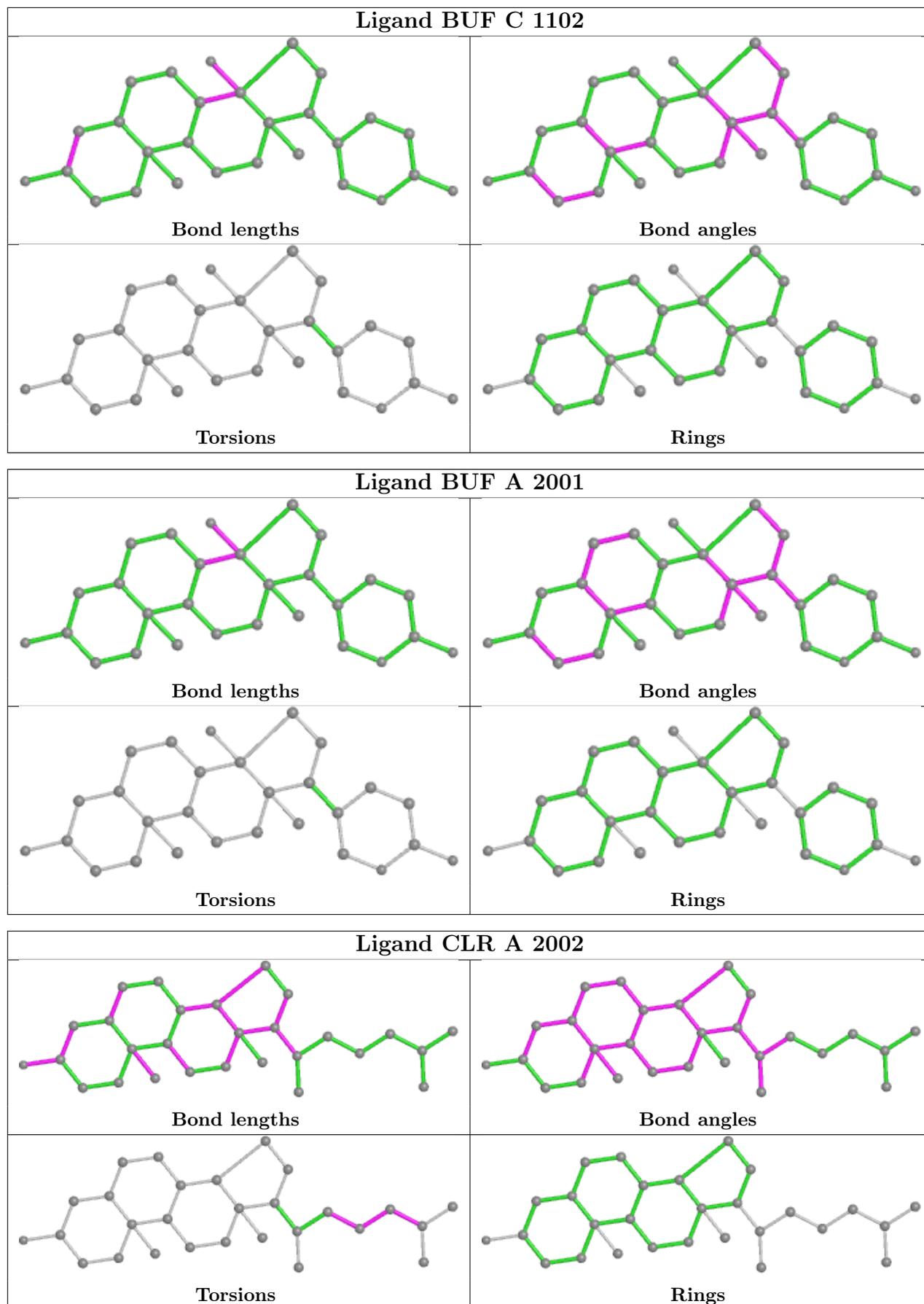
There are no ring outliers.

5 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	1001	NAG	1	0
7	E	101	CLR	4	0
6	C	1102	BUF	4	0
6	A	2001	BUF	2	0
7	A	2002	CLR	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	995/1021 (97%)	0.18	61 (6%) 21 22	40, 119, 201, 295	0
1	C	995/1021 (97%)	0.28	70 (7%) 16 18	41, 124, 212, 292	0
2	B	288/303 (95%)	0.25	15 (5%) 27 27	53, 124, 205, 248	0
2	D	285/303 (94%)	0.16	18 (6%) 20 21	56, 120, 199, 326	0
3	E	32/65 (49%)	0.13	2 (6%) 20 21	51, 80, 158, 178	0
3	G	32/65 (49%)	0.25	1 (3%) 49 48	56, 86, 144, 172	0
All	All	2627/2778 (94%)	0.23	167 (6%) 19 20	40, 121, 206, 326	0

The worst 5 of 167 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	547	GLY	11.6
2	B	198	THR	11.4
1	C	491	THR	9.0
2	B	199	TYR	8.7
1	C	550	HIS	7.3

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	PHD	C	369	12/13	0.97	0.23	102,103,105,105	0
1	PHD	A	369	12/13	0.98	0.18	116,118,121,121	0

6.3 Carbohydrates

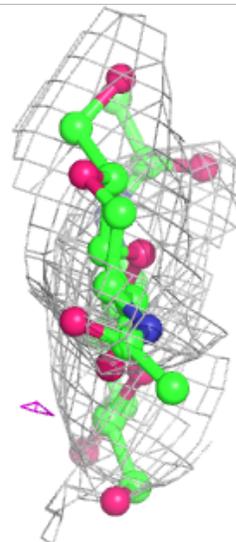
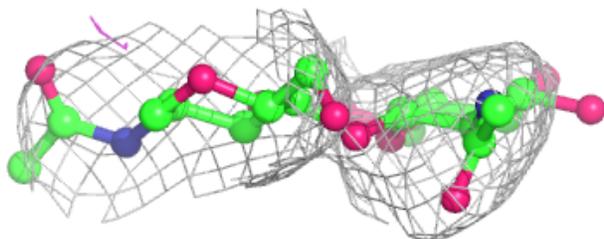
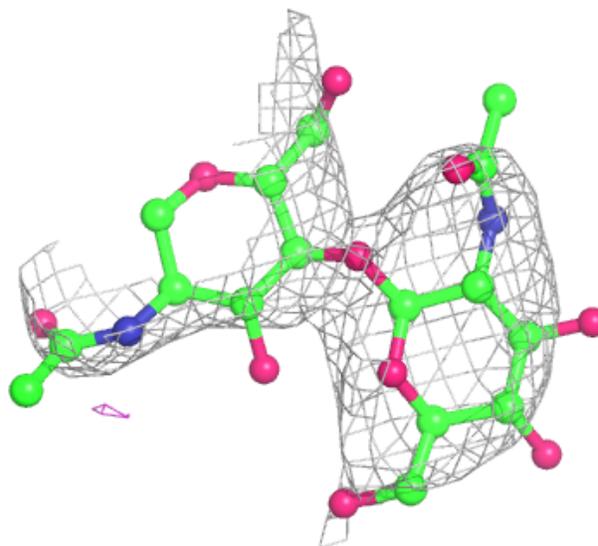
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	F	1	14/15	0.78	0.33	157,166,174,177	0
4	NAG	F	2	14/15	0.84	0.38	168,173,183,184	0
5	GLC	H	1	11/12	0.95	0.17	113,115,118,120	0
5	GLC	I	1	11/12	0.96	0.15	104,105,108,109	0
5	FRU	I	2	12/12	0.96	0.20	101,104,105,106	0
5	FRU	H	2	12/12	0.98	0.18	110,113,115,116	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.

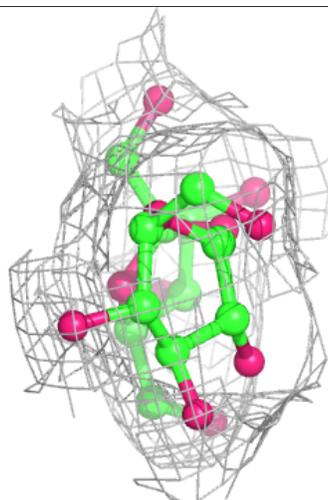
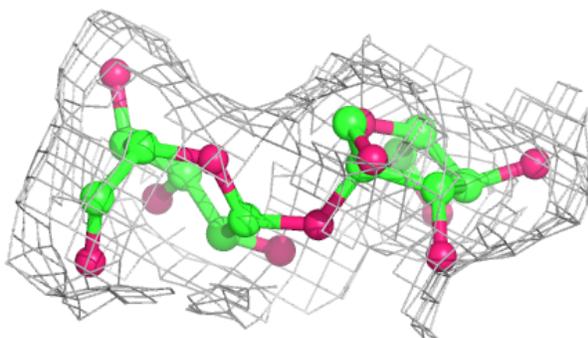
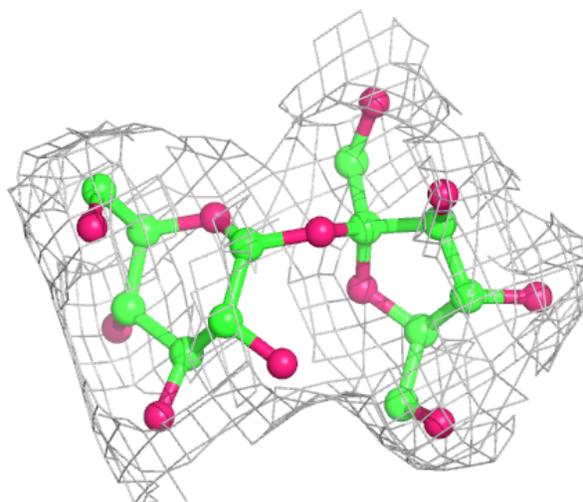
Electron density around Chain F:

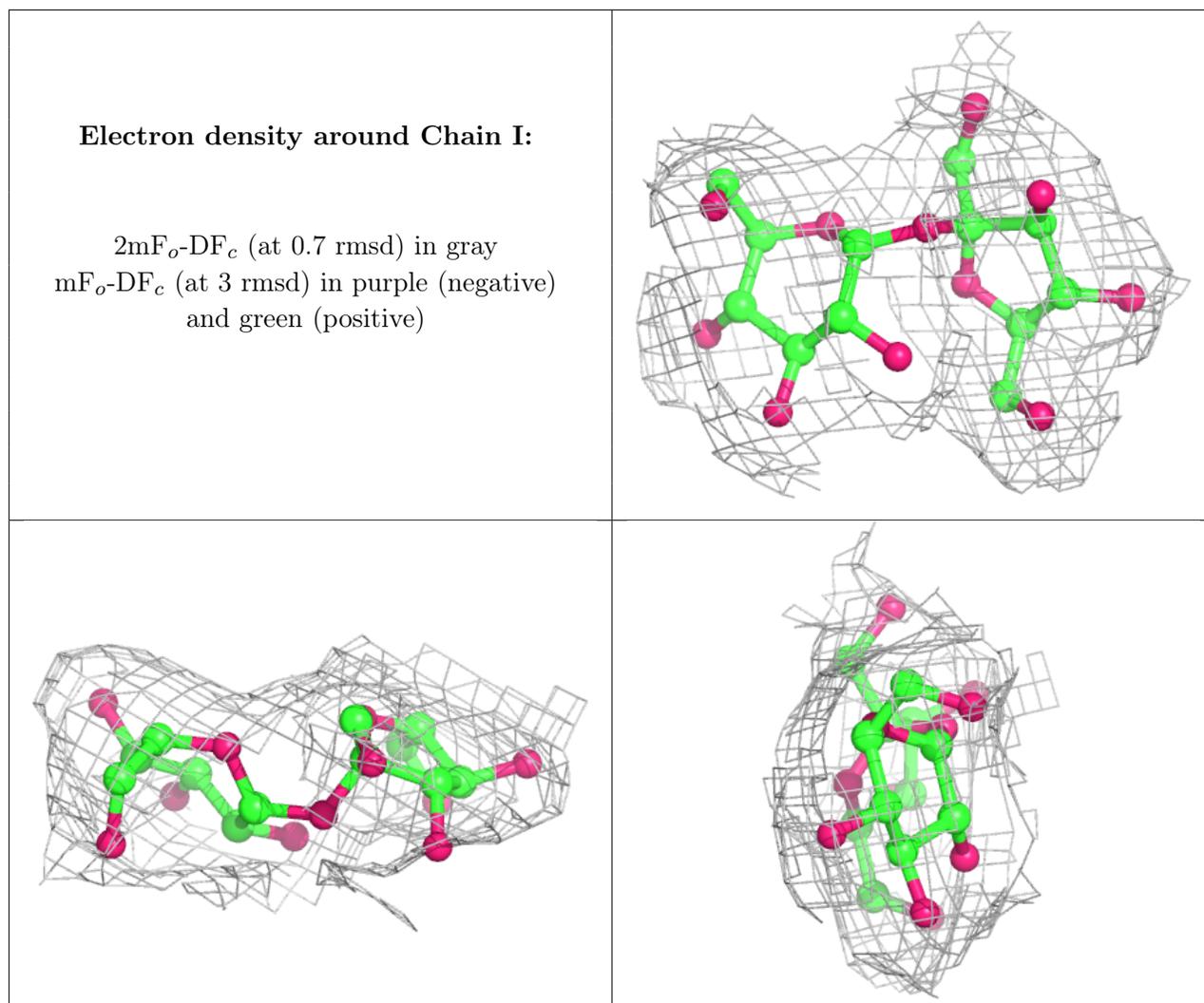
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

$2mF_o-DF_c$ (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.

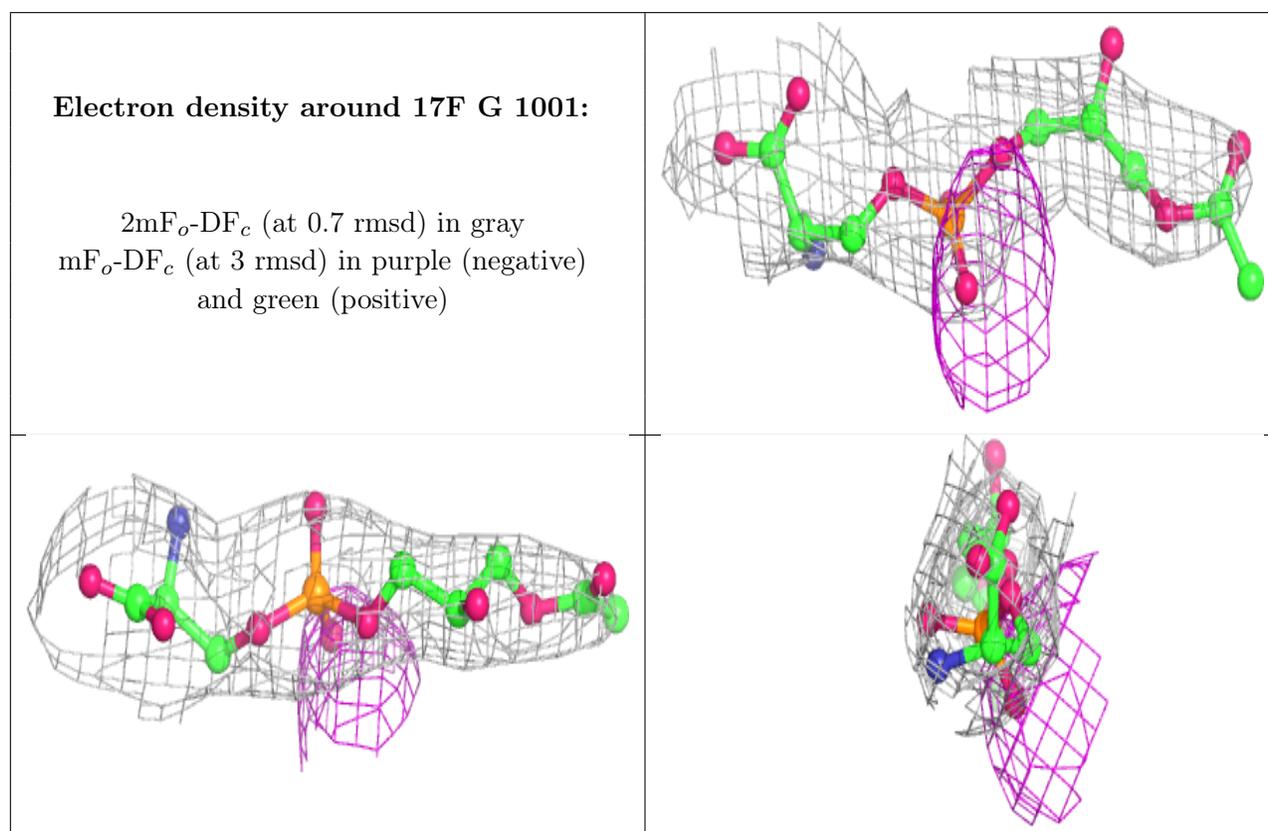
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
11	17F	G	1001	19/54	0.81	0.44	136,142,150,152	0
10	NAG	B	1001	14/15	0.87	0.16	138,146,152,154	0
8	K	A	2003	1/1	0.94	0.20	121,121,121,121	0
8	K	C	1104	1/1	0.96	0.18	92,92,92,92	0
6	BUF	A	2001	28/28	0.96	0.25	93,97,101,102	0
8	K	A	2005	1/1	0.96	0.28	121,121,121,121	0
6	BUF	C	1102	28/28	0.97	0.28	90,94,99,100	0
8	K	C	1105	1/1	0.98	0.13	60,60,60,60	0

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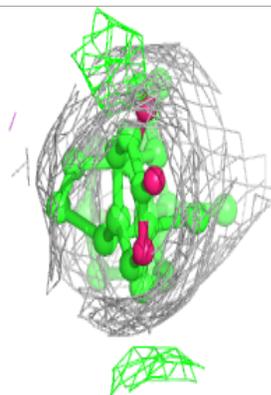
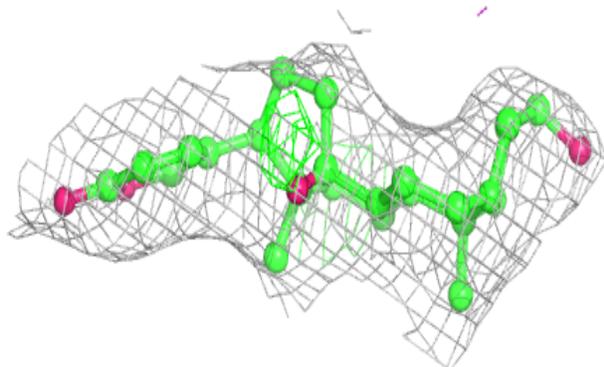
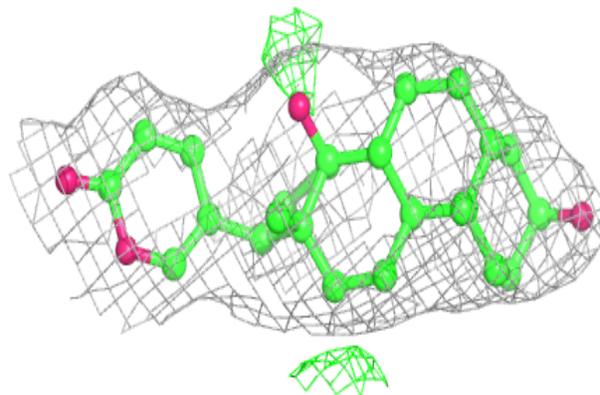
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	K	C	1106	1/1	0.98	0.13	69,69,69,69	0
7	CLR	E	101	28/28	0.98	0.31	56,60,65,67	0
7	CLR	A	2002	28/28	0.98	0.36	40,44,51,53	0
8	K	A	2004	1/1	0.99	0.14	54,54,54,54	0
9	MG	C	1107	1/1	0.99	0.18	106,106,106,106	0
9	MG	A	2006	1/1	1.00	0.20	71,71,71,71	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.

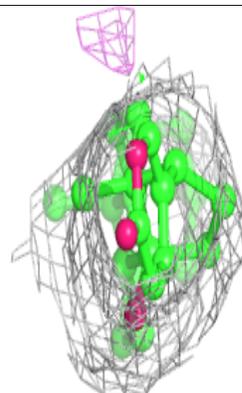
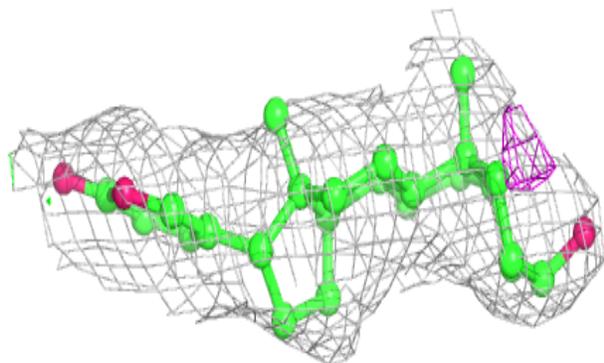
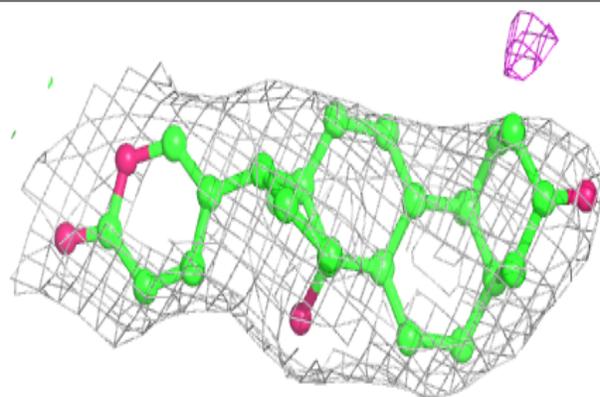


Electron density around BUF A 2001:

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

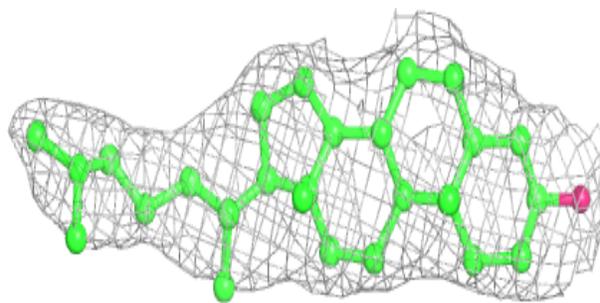
**Electron density around BUF C 1102:**

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

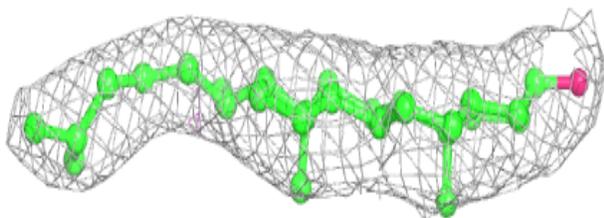


Electron density around CLR E 101:

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



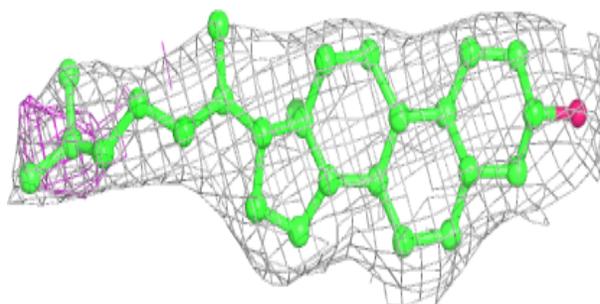
7



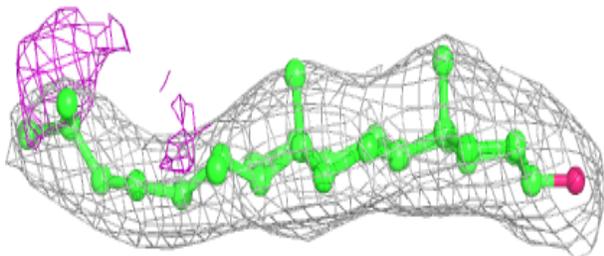
7

Electron density around CLR A 2002:

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



7



6.5 Other polymers [i](#)

There are no such residues in this entry.