



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:05 PM UTC

PDB ID : 3WGV / pdb_00003wgv
Title : Crystal structure of a Na⁺-bound Na⁺,K⁺-ATPase preceding the E1P state with oligomycin
Authors : Kanai, R.; Ogawa, H.; Vilsen, B.; Cornelius, F.; Toyoshima, C.
Deposited on : 2013-08-09
Resolution : 2.80 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

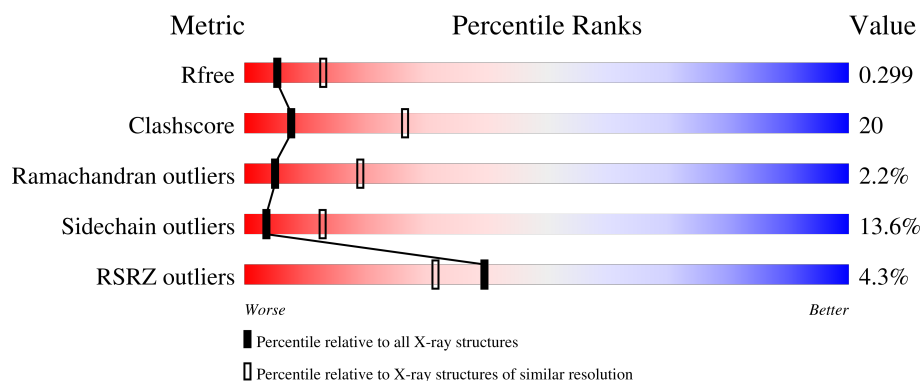
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



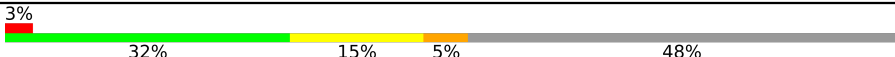
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	1016	0% 53% 36% 8% .
1	C	1016	3% 57% 34% 6% .
2	B	303	10% 52% 39% 9%
2	D	303	14% 53% 37% 9% .
3	E	65	2% 20% 28% 5% . 46%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	G	65	 A horizontal bar chart showing the distribution of quality metrics for chain G. The bar is divided into five segments: a small red segment at the start labeled '3%', followed by a green segment labeled '32%', a yellow segment labeled '15%', an orange segment labeled '5%', and a long grey segment at the end labeled '48%'.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	ALF	C	2002	-	-	X	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 21909 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
1	A	994	Total	C	N	O	S	0	0	0
			7714	4918	1300	1449	47			
1	C	994	Total	C	N	O	S	0	0	0
			7714	4918	1300	1449	47			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	303	Total	C	N	O	S	0	0	0
			2479	1603	408	454	14			
2	D	303	Total	C	N	O	S	0	0	0
			2479	1603	408	454	14			

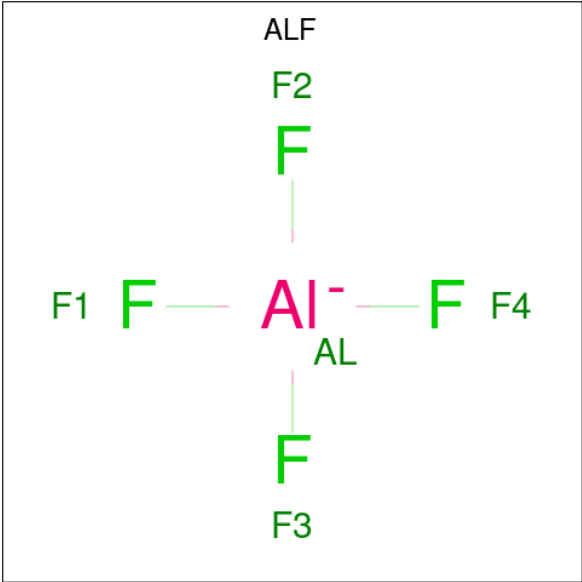
- Molecule 3 is a protein called Na⁺/K⁺ ATPase gamma subunit transcript variant a.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	34	Total	C	N	O	0	0	0
			270	183	39	48			
3	E	35	Total	C	N	O	0	0	0
			281	189	43	49			

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

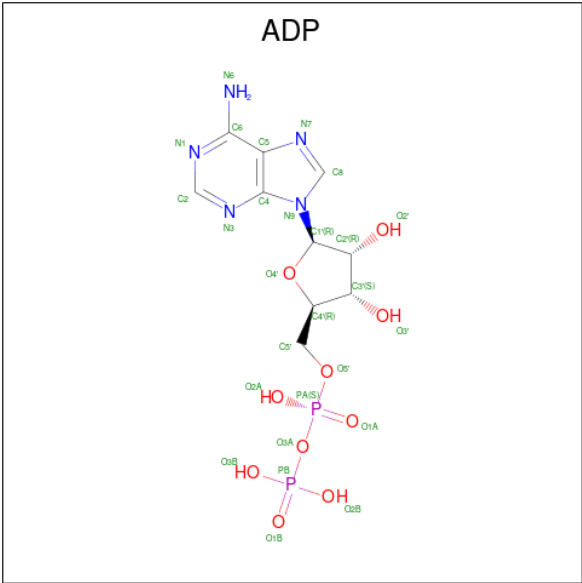
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	C	2	Total	Mg	0	0
			2	2		

- Molecule 5 is TETRAFLUOROALUMINATE ION (CCD ID: ALF) (formula: AlF₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Al	F	0	0
			5	1	4		
5	C	1	Total	Al	F	0	0
			5	1	4		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

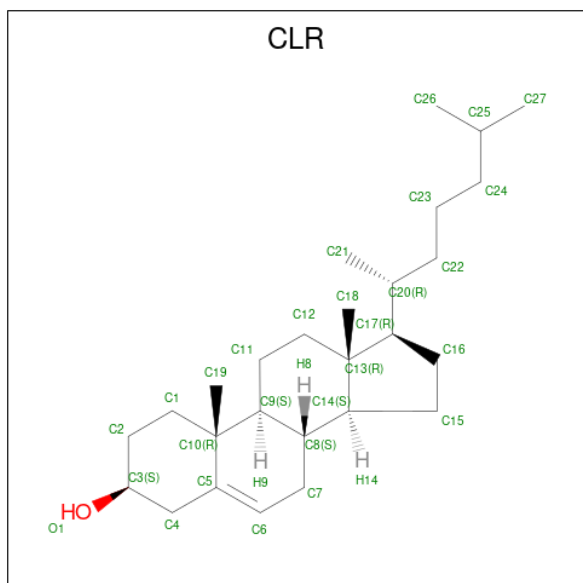


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
6	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

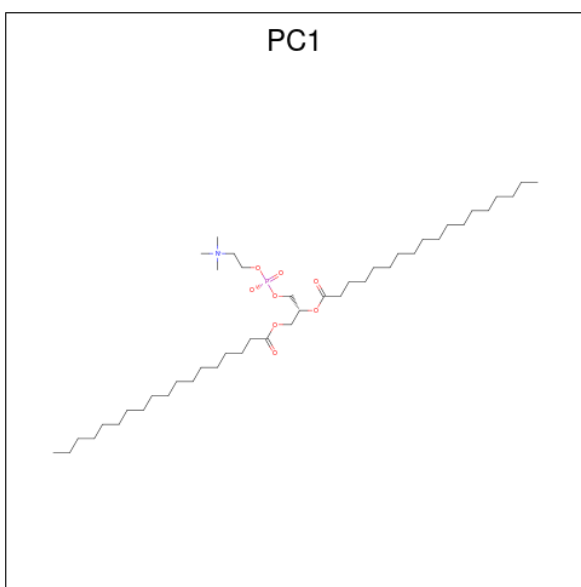
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	4	Total	Na	0	0
			4	4		
7	C	4	Total	Na	0	0
			4	4		

- Molecule 8 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



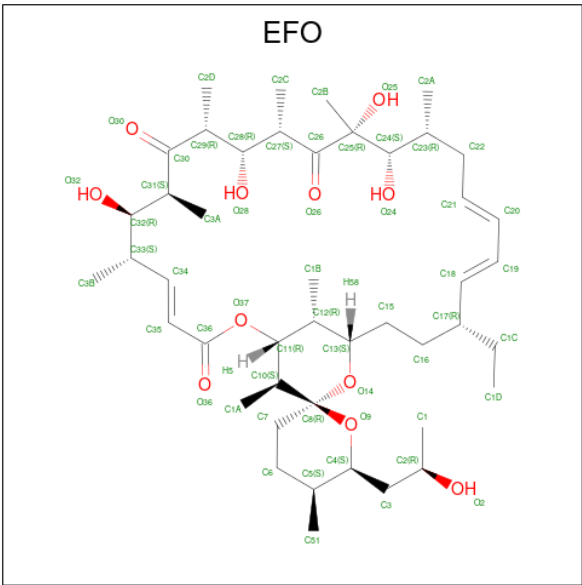
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			28	27	1		
8	A	1	Total	C	O	0	0
			28	27	1		
8	G	1	Total	C	O	0	0
			28	27	1		
8	D	1	Total	C	O	0	0
			28	27	1		
8	D	1	Total	C	O	0	0
			28	27	1		
8	E	1	Total	C	O	0	0
			28	27	1		

- Molecule 9 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



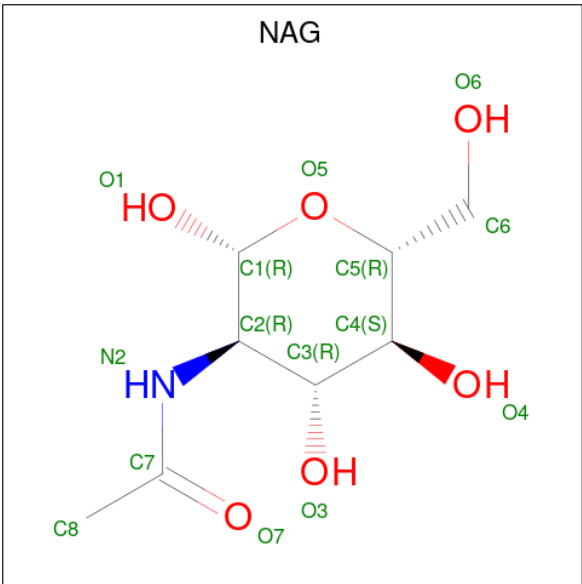
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	B	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	C	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
9	D	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 10 is Oligomycin A (CCD ID: EFO) (formula: C₄₅H₇₄O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			56	45	11		
10	C	1	Total	C	O	0	0
			56	45	11		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	D	1	Total	C	N	O	0	0
			14	8	1	5		

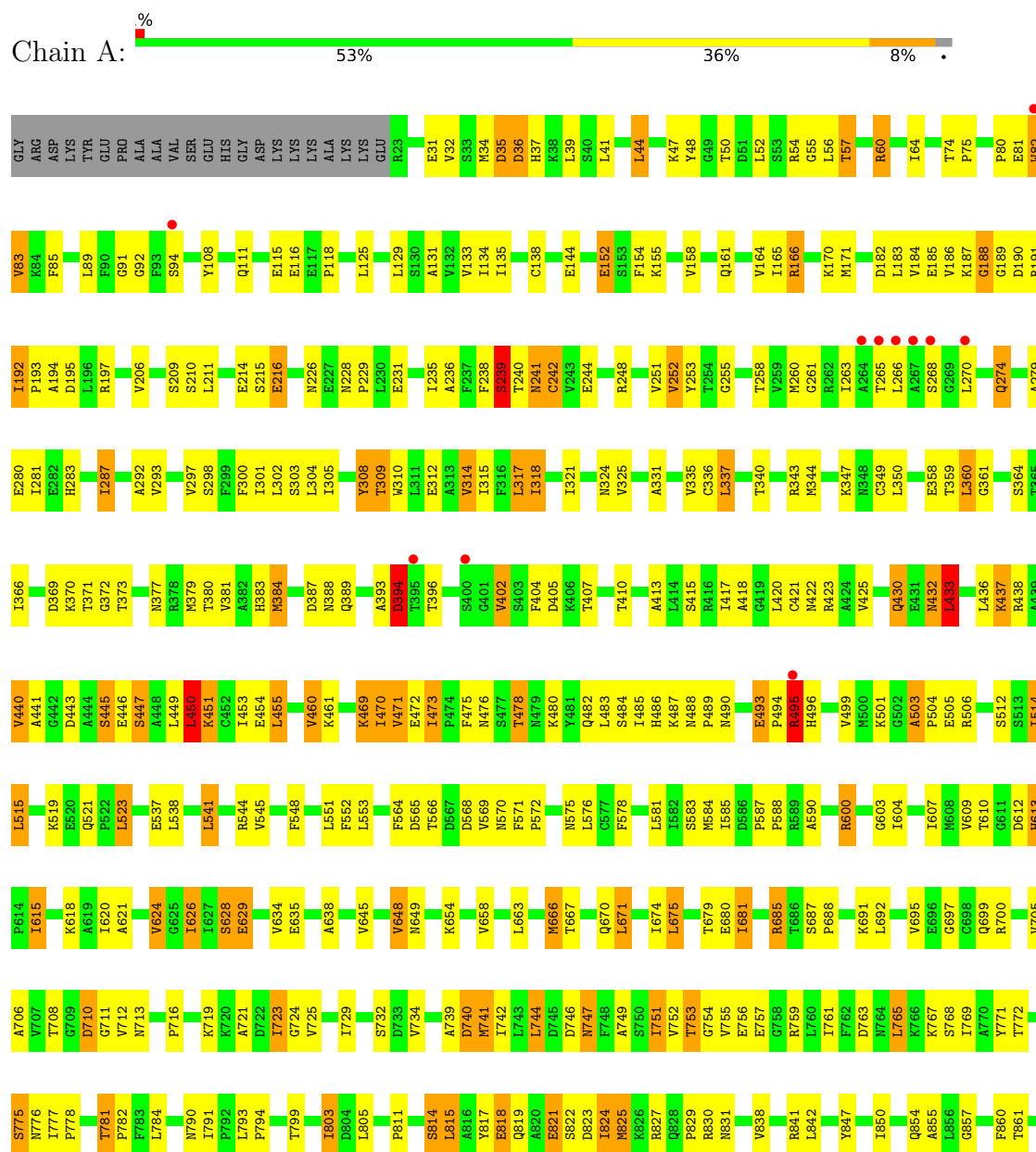
- Molecule 12 is water.

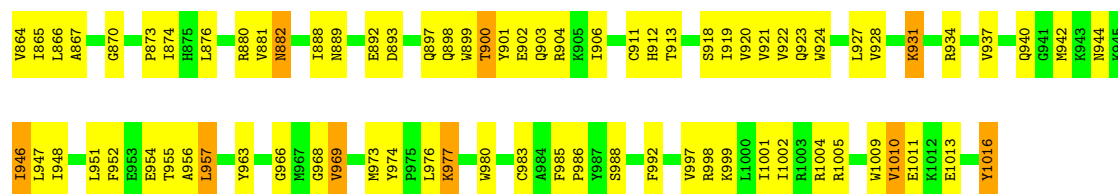
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	24	Total	O	0	0
			24	24		
12	B	2	Total	O	0	0
			2	2		
12	C	20	Total	O	0	0
			20	20		
12	D	2	Total	O	0	0
			2	2		

3 Residue-property plots

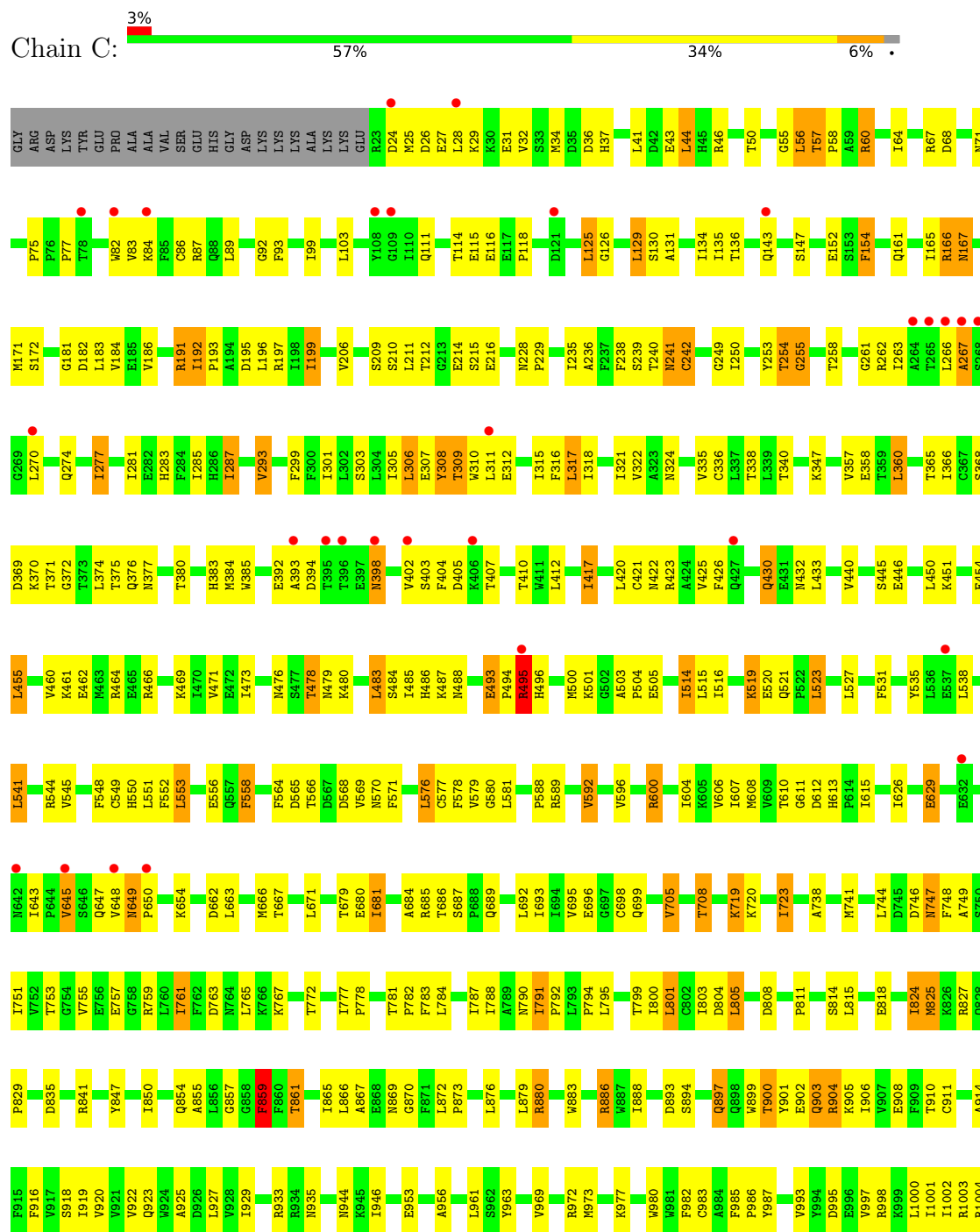
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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



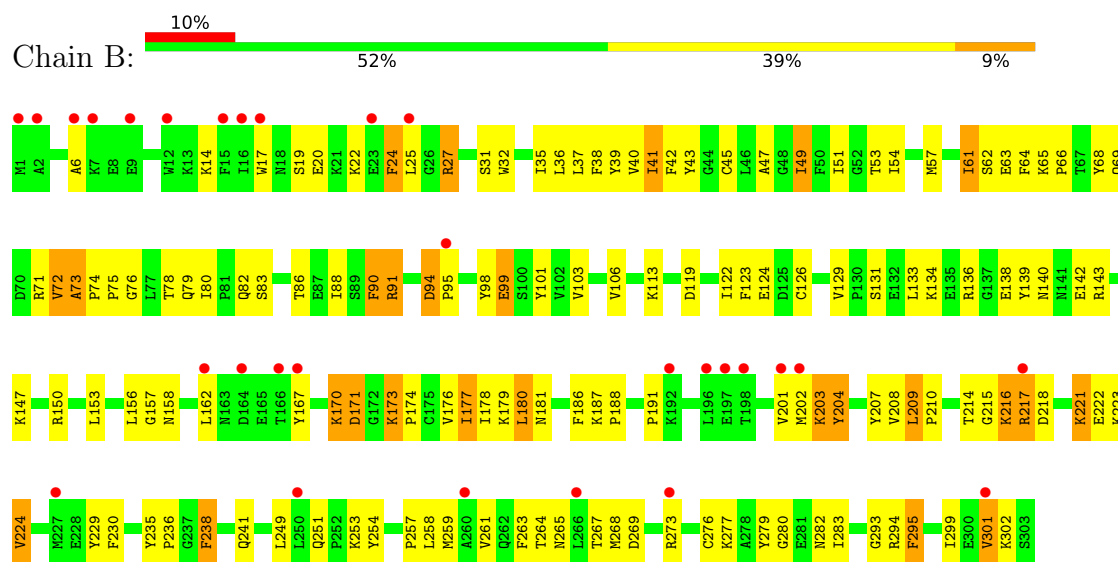


• Molecule 1: Sodium/potassium-transporting ATPase subunit alpha-1

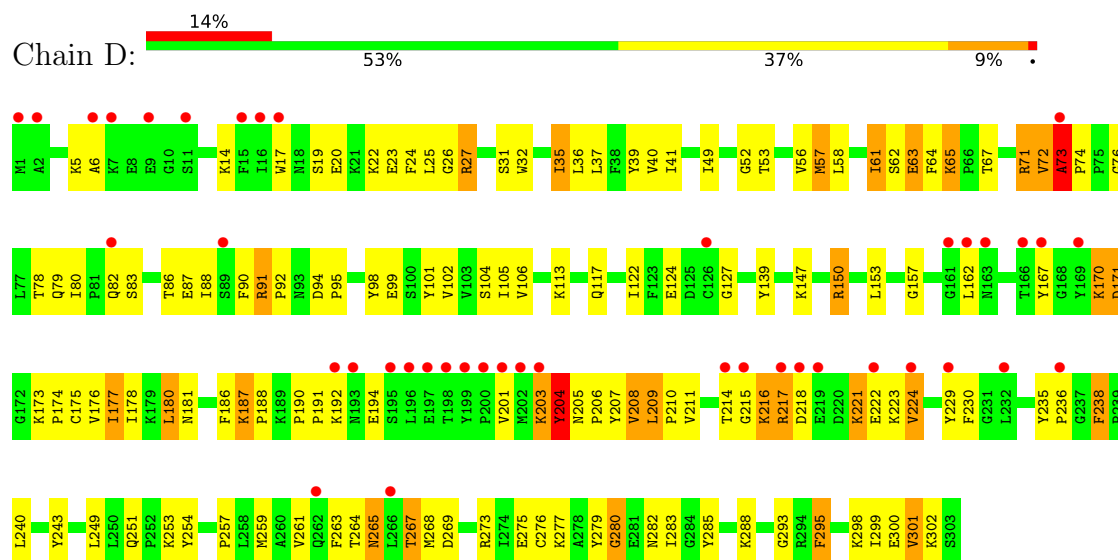




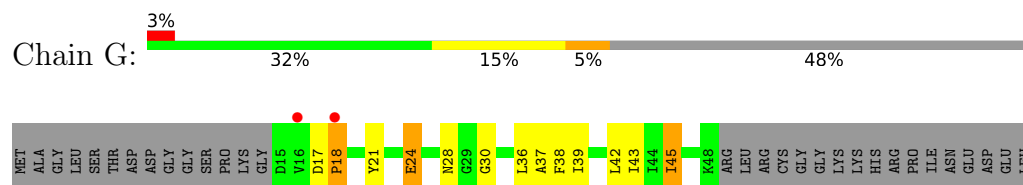
• Molecule 2: Sodium/potassium-transporting ATPase subunit beta-1



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



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



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





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.28Å 210.18Å 256.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.99 – 2.80 15.99 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.4 (15.99-2.80) 93.8 (15.99-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.270 , 0.298 0.272 , 0.299	Depositor DCC
R_{free} test set	3965 reflections (2.82%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.15 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	21909	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: NA, ALF, NAG, EFO, PC1, CLR, ADP, 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	0.60	0/7864	1.01	26/10671 (0.2%)
1	C	0.51	0/7864	0.92	15/10671 (0.1%)
2	B	0.42	0/2544	0.92	11/3426 (0.3%)
2	D	0.44	0/2544	0.92	11/3426 (0.3%)
3	E	0.49	0/287	0.94	0/389
3	G	0.46	0/276	0.85	0/375
All	All	0.53	0/21379	0.95	63/28958 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	E	0	1

There are no bond length outliers.

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	495	ARG	CB-CA-C	-18.33	91.69	109.83
2	B	73	ALA	CA-C-N	-12.49	107.52	120.38
2	B	73	ALA	C-N-CA	-12.49	107.52	120.38
2	D	73	ALA	CA-C-N	-11.36	108.68	120.38
2	D	73	ALA	C-N-CA	-11.36	108.68	120.38

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	17	ASP	Peptide

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	7714	0	7770	314	0
1	C	7714	0	7769	283	0
2	B	2479	0	2458	103	0
2	D	2479	0	2458	101	0
3	E	281	0	285	14	0
3	G	270	0	272	12	0
4	A	2	0	0	0	0
4	C	2	0	0	0	0
5	A	5	0	0	1	0
5	C	5	0	0	3	0
6	A	27	0	12	3	0
6	C	27	0	12	6	0
7	A	4	0	0	0	0
7	C	4	0	0	0	0
8	A	56	0	92	27	0
8	D	56	0	92	29	0
8	E	28	0	45	13	0
8	G	28	0	45	9	0
9	A	216	0	352	14	0
9	B	54	0	88	2	0
9	C	216	0	352	15	0
9	D	54	0	88	2	0
10	A	56	0	74	0	0
10	C	56	0	74	0	0
11	B	14	0	13	0	0
11	D	14	0	13	0	0
12	A	24	0	0	0	0
12	B	2	0	0	0	0
12	C	20	0	0	2	0
12	D	2	0	0	0	0
All	All	21909	0	22364	883	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 20.

The worst 5 of 883 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2009:CLR:C11	8:A:2009:CLR:C9	1.77	1.62
8:D:3002:CLR:C12	8:D:3002:CLR:C11	1.74	1.60
8:A:2010:CLR:C11	8:A:2010:CLR:C9	1.76	1.59
8:D:3001:CLR:C11	8:D:3001:CLR:C9	1.78	1.57
8:E:101:CLR:C11	8:E:101:CLR:C9	1.78	1.56

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	992/1016 (98%)	859 (87%)	114 (12%)	19 (2%)	6	22
1	C	992/1016 (98%)	884 (89%)	91 (9%)	17 (2%)	7	25
2	B	301/303 (99%)	238 (79%)	55 (18%)	8 (3%)	4	15
2	D	301/303 (99%)	231 (77%)	59 (20%)	11 (4%)	2	9
3	E	33/65 (51%)	31 (94%)	1 (3%)	1 (3%)	3	12
3	G	32/65 (49%)	27 (84%)	4 (12%)	1 (3%)	3	12
All	All	2651/2768 (96%)	2270 (86%)	324 (12%)	57 (2%)	5	19

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	388	ASN
1	A	402	VAL
2	B	82	GLN
2	B	139	TYR
3	G	18	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	844/861 (98%)	707 (84%)	137 (16%)	2	8
1	C	844/861 (98%)	749 (89%)	95 (11%)	5	19
2	B	269/269 (100%)	233 (87%)	36 (13%)	4	13
2	D	269/269 (100%)	236 (88%)	33 (12%)	4	16
3	E	29/52 (56%)	23 (79%)	6 (21%)	1	4
3	G	28/52 (54%)	25 (89%)	3 (11%)	6	21
All	All	2283/2364 (97%)	1973 (86%)	310 (14%)	3	13

5 of 310 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	523	LEU
2	D	175	CYS
1	C	667	THR
1	C	886	ARG
2	D	263	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	324	ASN
1	C	854	GLN
1	C	399	GLN
1	C	570	ASN
1	C	889	ASN

5.3.3 RNA ⓘ

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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 12 are monoatomic - leaving 24 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$
9	PC1	A	2012	-	53,53,53	0.95	3 (5%)	59,61,61	1.42	7 (11%)
9	PC1	C	2012	-	53,53,53	0.93	4 (7%)	59,61,61	1.28	4 (6%)
9	PC1	C	2010	-	53,53,53	0.92	3 (5%)	59,61,61	1.39	5 (8%)
9	PC1	A	2014	-	53,53,53	0.94	3 (5%)	59,61,61	1.35	4 (6%)
8	CLR	G	101	-	31,31,31	4.80	13 (41%)	48,48,48	2.73	15 (31%)
6	ADP	C	2004	-	28,29,29	1.36	5 (17%)	43,45,45	1.84	10 (23%)
8	CLR	A	2010	-	31,31,31	4.59	11 (35%)	48,48,48	2.29	16 (33%)
8	CLR	D	3001	-	31,31,31	4.63	12 (38%)	48,48,48	2.22	15 (31%)
9	PC1	C	2009	-	53,53,53	0.95	4 (7%)	59,61,61	1.29	6 (10%)
9	PC1	D	3003	-	53,53,53	0.95	5 (9%)	59,61,61	1.21	5 (8%)
9	PC1	A	2013	-	53,53,53	0.93	4 (7%)	59,61,61	1.19	5 (8%)
6	ADP	A	2004	4	28,29,29	1.43	3 (10%)	43,45,45	2.02	9 (20%)
8	CLR	D	3002	-	31,31,31	4.69	12 (38%)	48,48,48	2.00	15 (31%)
9	PC1	B	401	-	53,53,53	0.93	4 (7%)	59,61,61	1.31	5 (8%)
11	NAG	D	3004	-	14,14,15	0.23	0	17,19,21	0.52	0
5	ALF	A	2002	-	4,4,4	1.40	0	-	-	-
9	PC1	C	2011	-	53,53,53	0.98	5 (9%)	59,61,61	1.32	5 (8%)
8	CLR	A	2009	-	31,31,31	4.62	12 (38%)	48,48,48	2.24	16 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	EFO	A	2015	-	57,58,58	2.21	20 (35%)	72,85,85	3.79	25 (34%)
11	NAG	B	402	-	14,14,15	0.21	0	17,19,21	0.45	0
10	EFO	C	2013	-	57,58,58	2.29	21 (36%)	72,85,85	3.77	26 (36%)
8	CLR	E	101	-	31,31,31	4.80	14 (45%)	48,48,48	2.49	15 (31%)
9	PC1	A	2011	-	53,53,53	0.94	4 (7%)	59,61,61	1.32	6 (10%)
5	ALF	C	2002	-	4,4,4	1.33	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
9	PC1	A	2012	-	-	29/57/57/57	-
9	PC1	C	2012	-	-	24/57/57/57	-
9	PC1	C	2010	-	-	33/57/57/57	-
9	PC1	A	2014	-	-	30/57/57/57	-
8	CLR	G	101	-	-	1/10/68/68	0/4/4/4
6	ADP	C	2004	-	-	1/16/32/32	0/3/3/3
8	CLR	A	2010	-	-	1/10/68/68	0/4/4/4
8	CLR	D	3001	-	-	0/10/68/68	0/4/4/4
9	PC1	D	3003	-	-	29/57/57/57	-
9	PC1	C	2009	-	-	27/57/57/57	-
9	PC1	A	2013	-	-	29/57/57/57	-
6	ADP	A	2004	4	-	6/16/32/32	0/3/3/3
8	CLR	D	3002	-	-	1/10/68/68	0/4/4/4
9	PC1	B	401	-	-	32/57/57/57	-
11	NAG	D	3004	-	-	1/6/23/26	0/1/1/1
9	PC1	C	2011	-	-	32/57/57/57	-
8	CLR	A	2009	-	-	0/10/68/68	0/4/4/4
10	EFO	A	2015	-	-	9/72/110/110	0/2/3/3
11	NAG	B	402	-	-	0/6/23/26	0/1/1/1
10	EFO	C	2013	-	-	11/72/110/110	0/2/3/3
8	CLR	E	101	-	-	0/10/68/68	0/4/4/4
9	PC1	A	2011	-	-	23/57/57/57	-

The worst 5 of 162 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	G	101	CLR	C11-C9	15.69	1.79	1.53
8	D	3002	CLR	C11-C9	15.09	1.78	1.53
8	E	101	CLR	C11-C9	14.94	1.78	1.53
8	D	3001	CLR	C11-C9	14.82	1.78	1.53
8	A	2009	CLR	C11-C9	14.36	1.77	1.53

The worst 5 of 214 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	2015	EFO	O9-C8-O14	21.09	161.70	109.73
10	C	2013	EFO	O9-C8-O14	20.49	160.24	109.73
10	A	2015	EFO	O14-C8-C7	-12.65	63.03	107.36
10	C	2013	EFO	O14-C8-C7	-12.17	64.72	107.36
10	C	2013	EFO	O9-C4-C3	9.91	118.41	105.95

There are no chirality outliers.

5 of 319 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2004	ADP	C5'-O5'-PA-O1A
6	A	2004	ADP	C5'-O5'-PA-O2A
6	A	2004	ADP	C5'-O5'-PA-O3A
6	A	2004	ADP	O4'-C4'-C5'-O5'
9	A	2011	PC1	O13-C11-C12-N

There are no ring outliers.

19 monomers are involved in 117 short contacts:

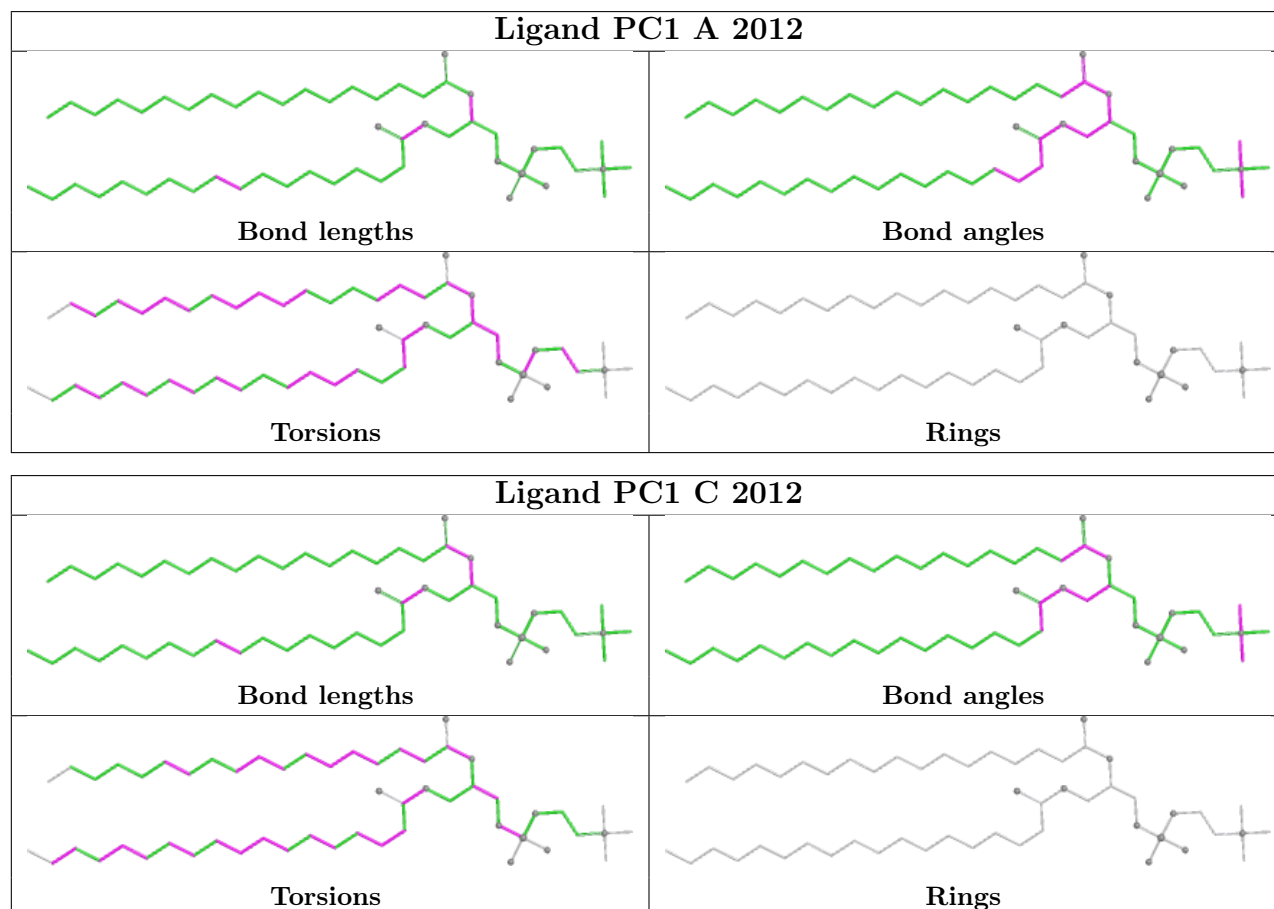
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	2012	PC1	2	0
9	C	2012	PC1	6	0
9	A	2014	PC1	4	0
8	G	101	CLR	9	0
6	C	2004	ADP	6	0
8	A	2010	CLR	15	0
8	D	3001	CLR	12	0
9	C	2009	PC1	8	0
9	D	3003	PC1	2	0
9	A	2013	PC1	7	0
6	A	2004	ADP	3	0
8	D	3002	CLR	17	0
9	B	401	PC1	2	0

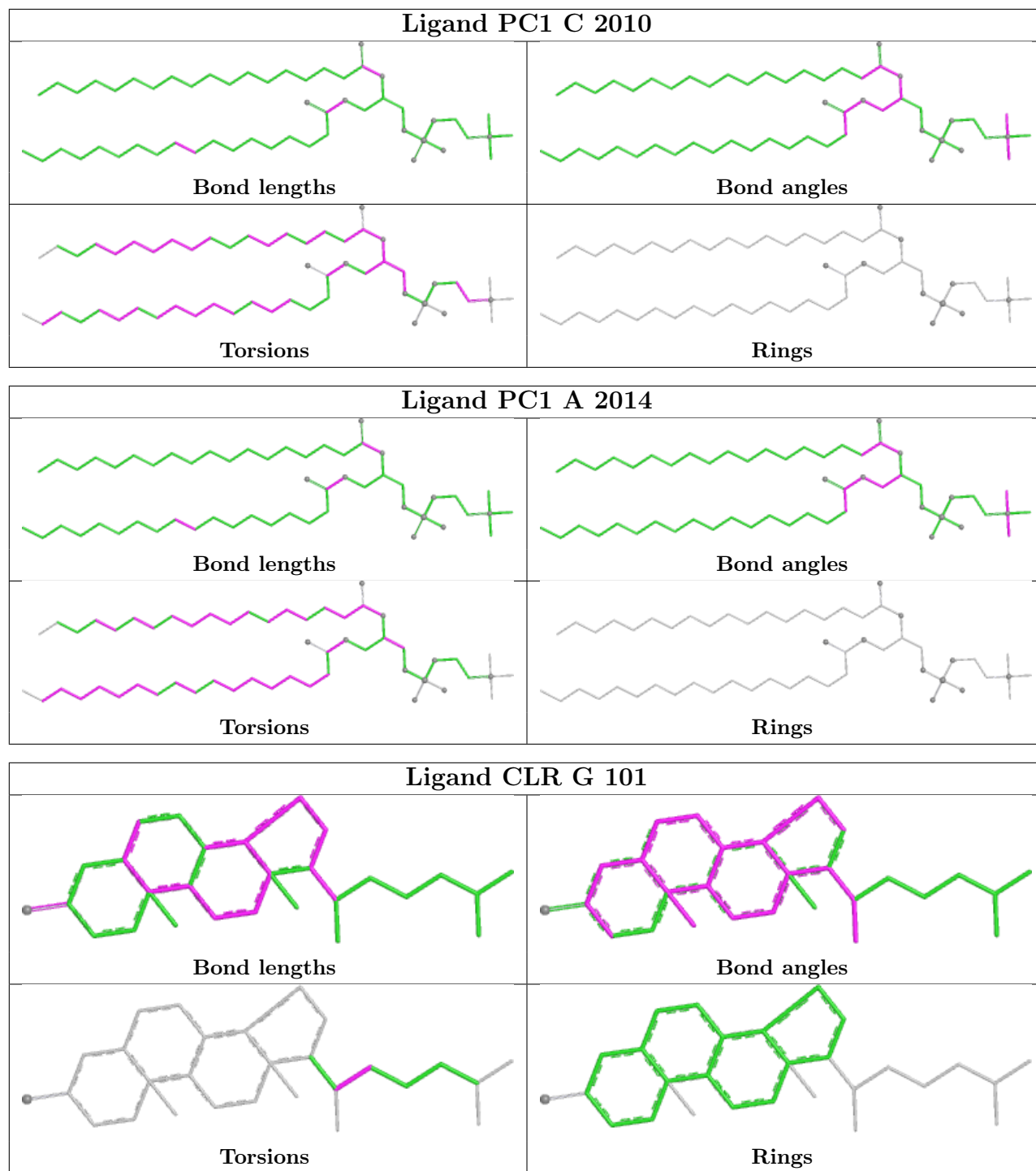
Continued on next page...

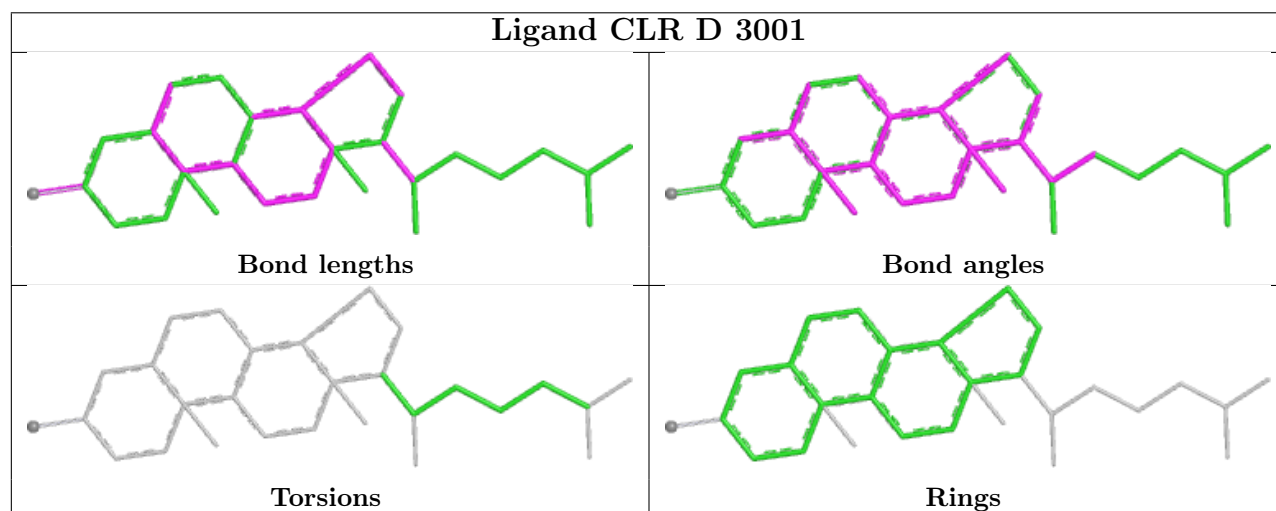
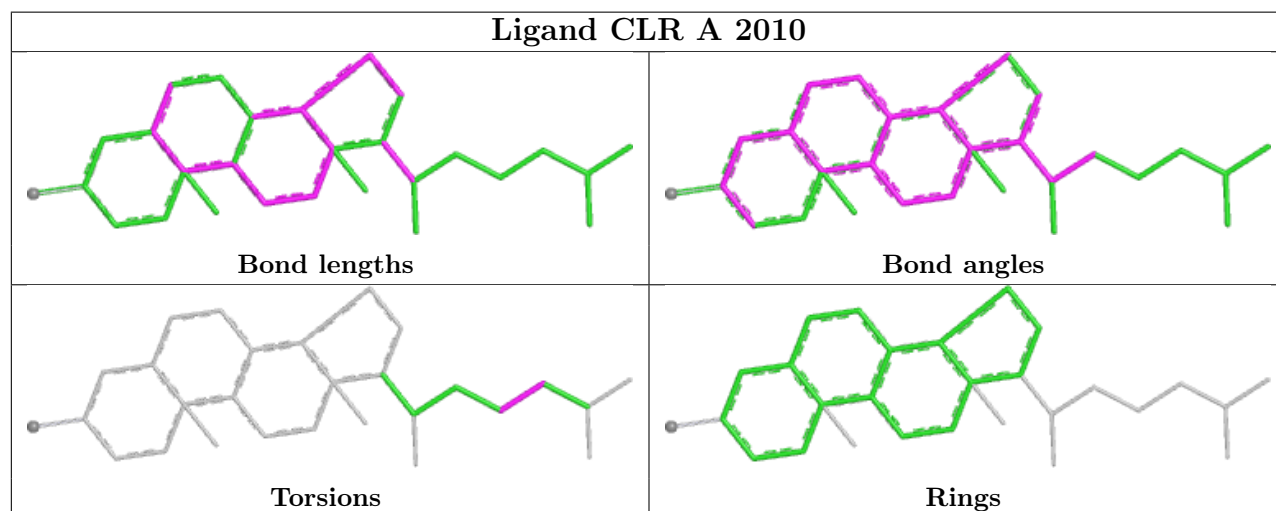
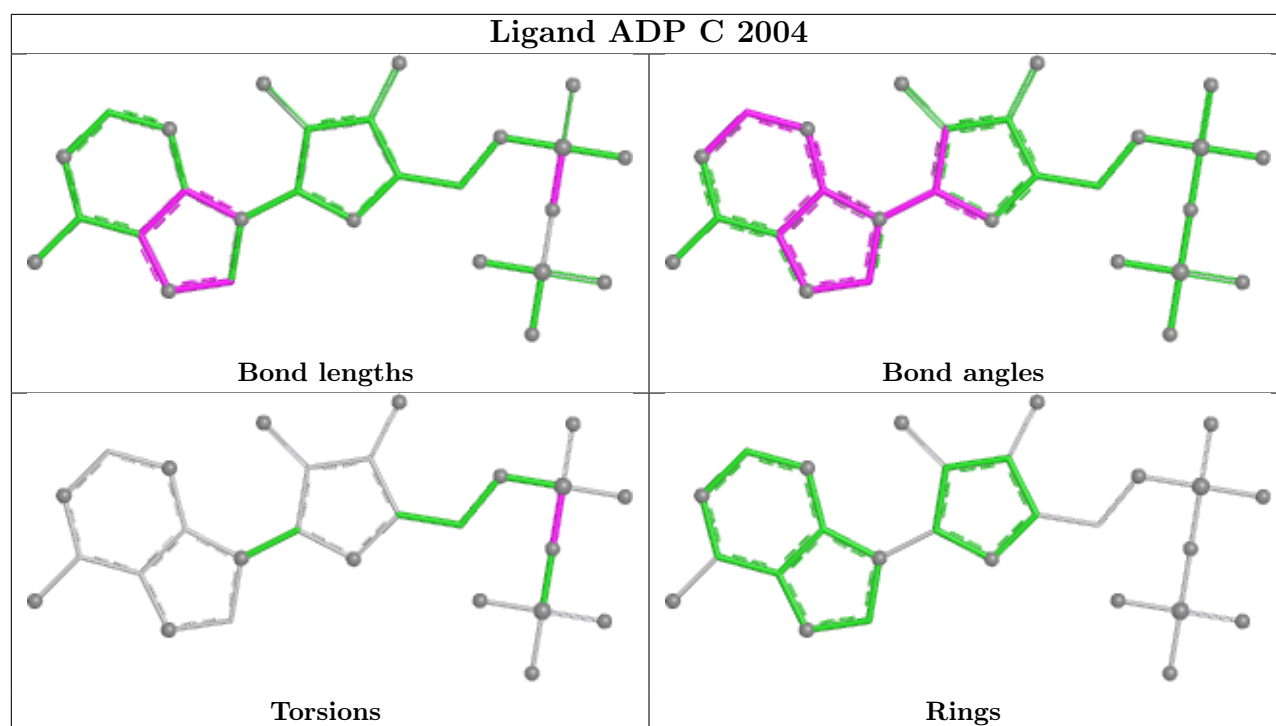
Continued from previous page...

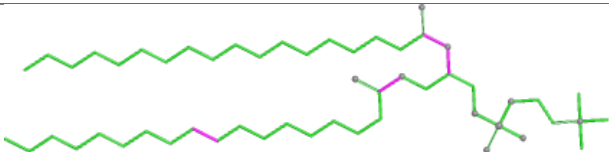
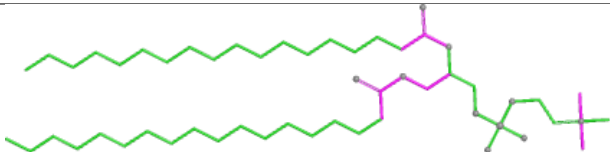
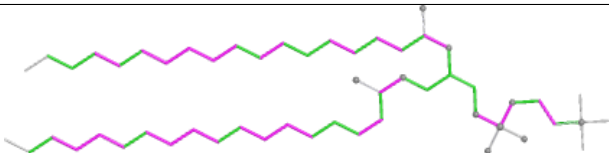
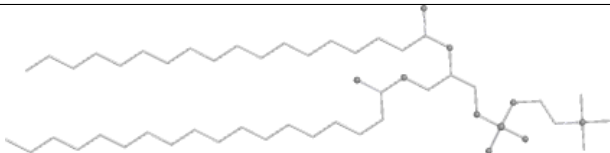
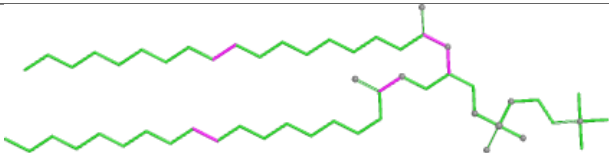
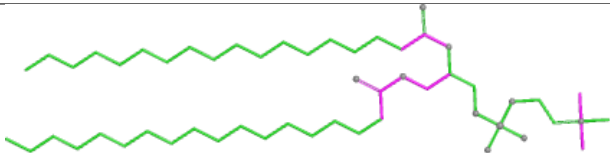
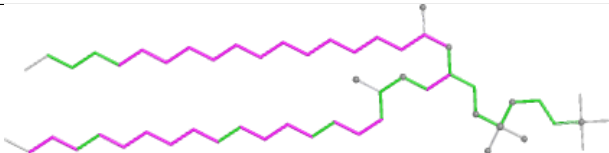
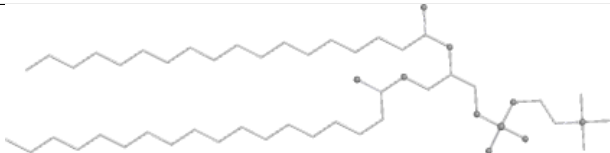
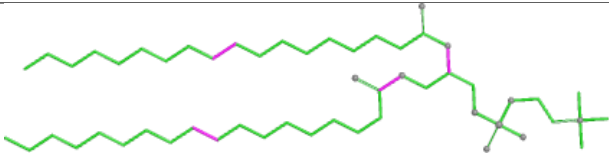
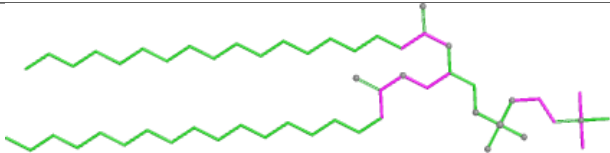
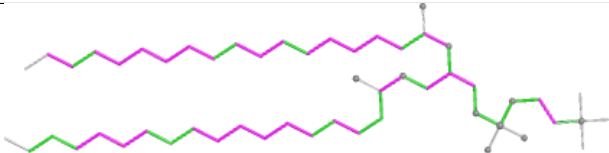
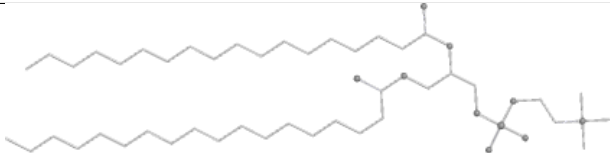
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2002	ALF	1	0
9	C	2011	PC1	3	0
8	A	2009	CLR	12	0
8	E	101	CLR	13	0
9	A	2011	PC1	1	0
5	C	2002	ALF	3	0

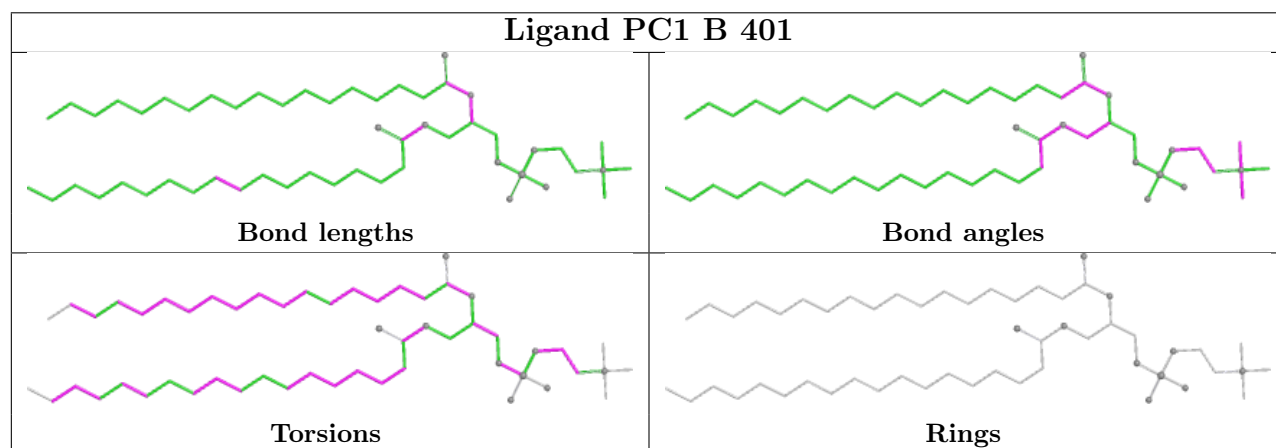
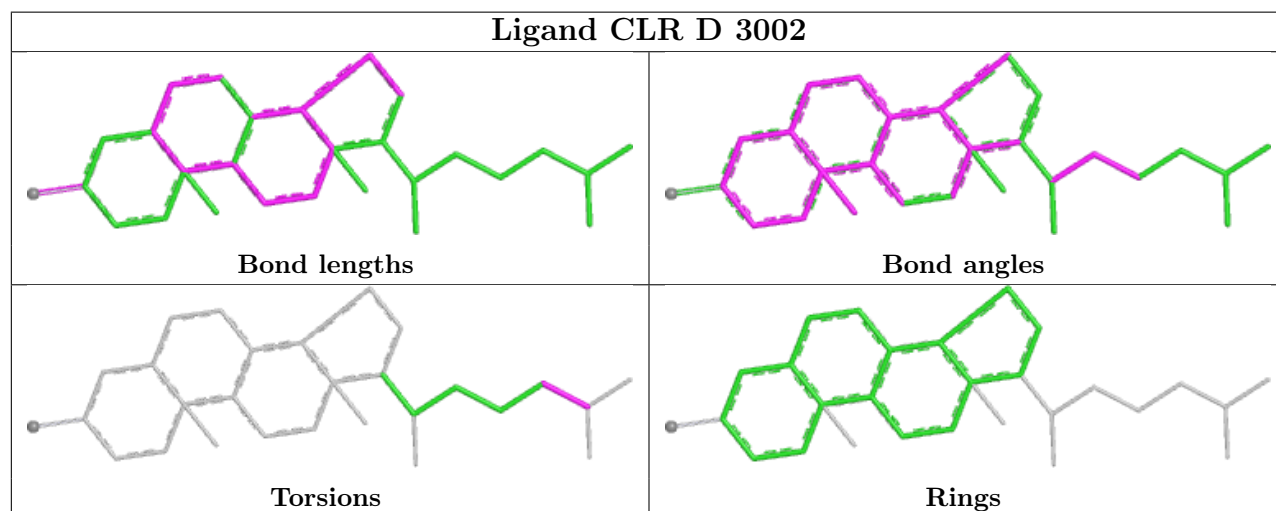
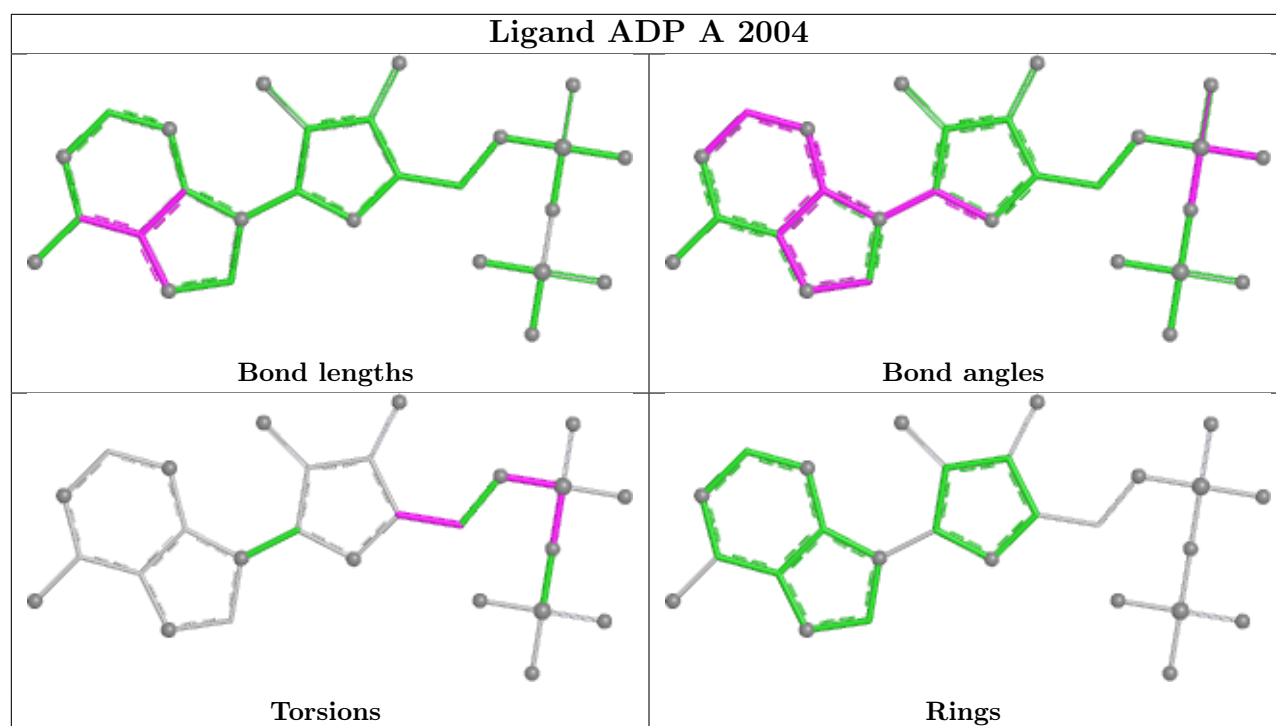
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

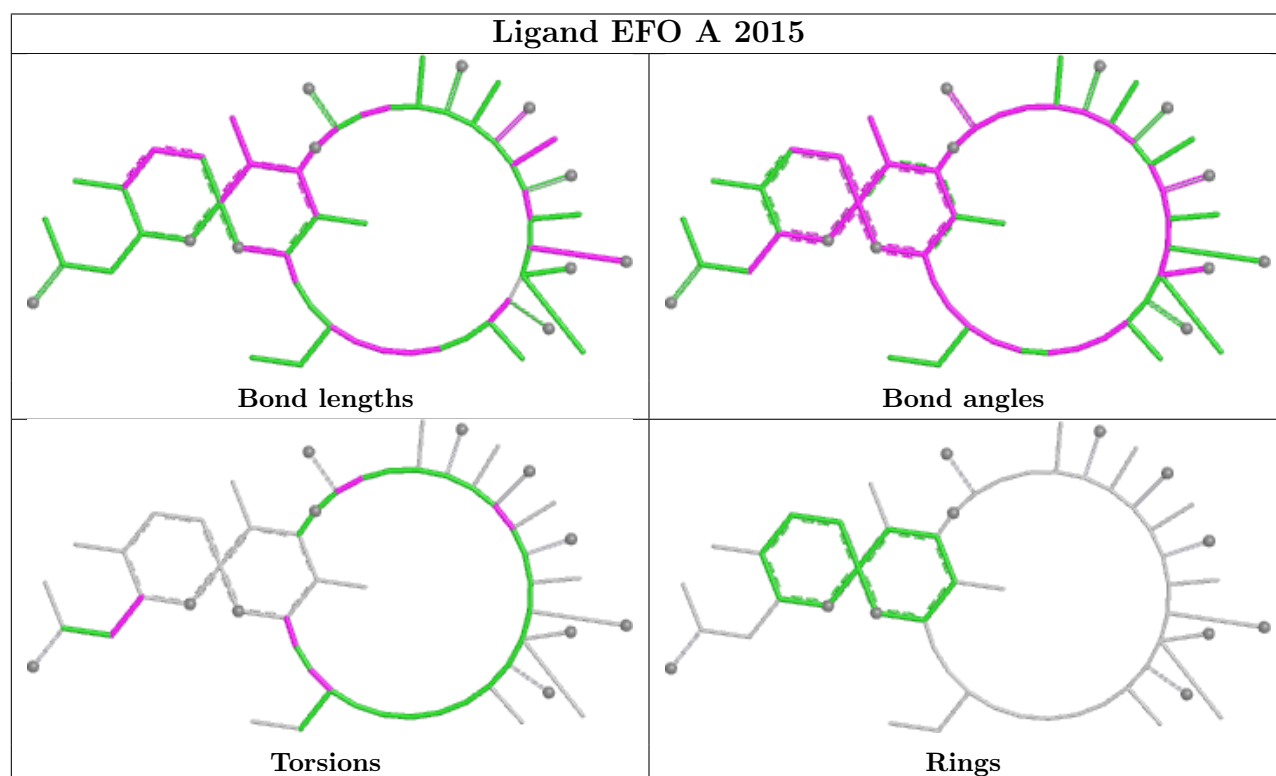
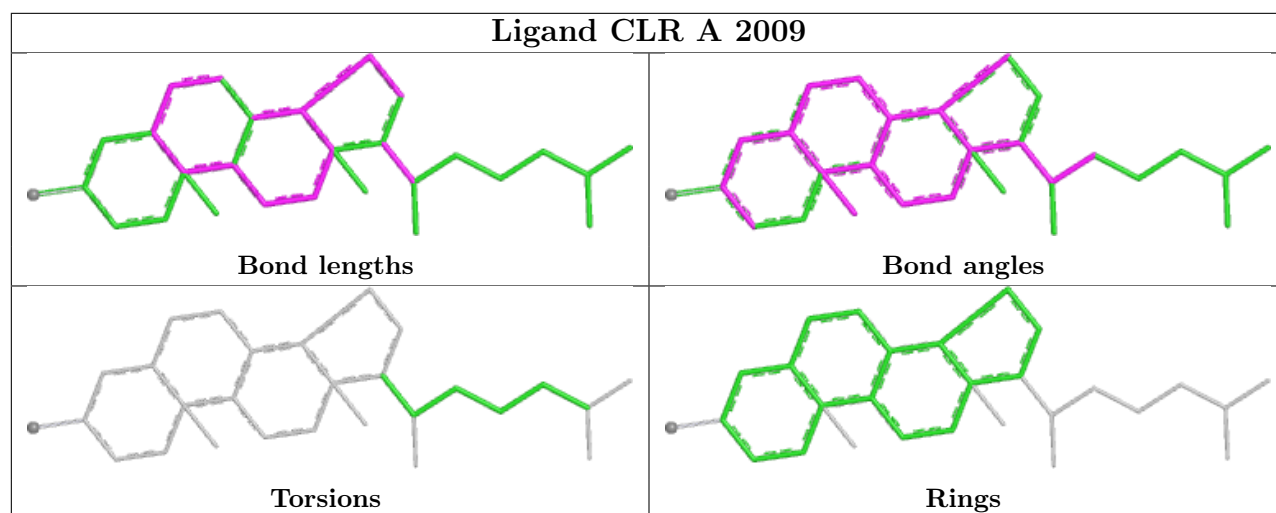
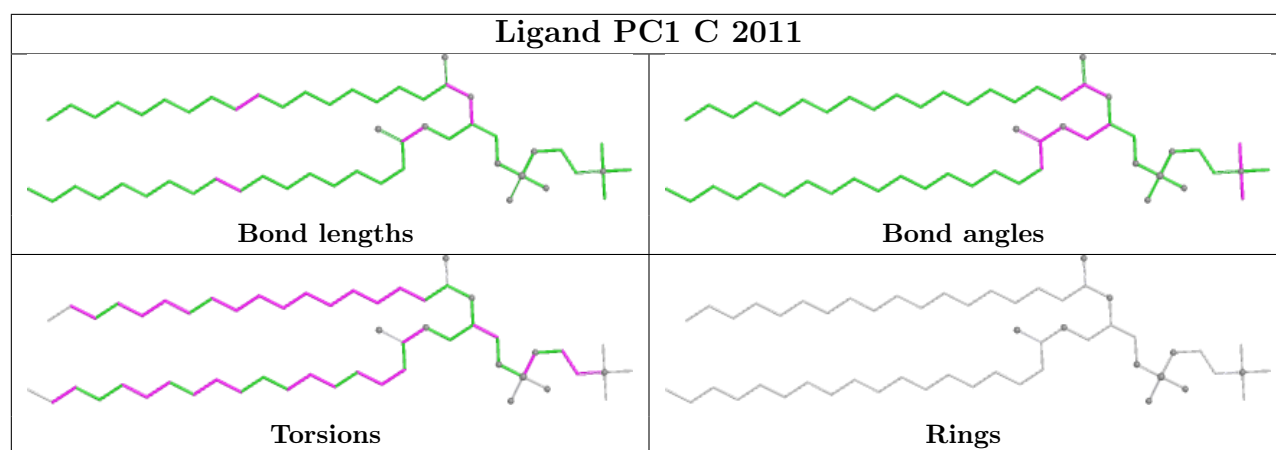


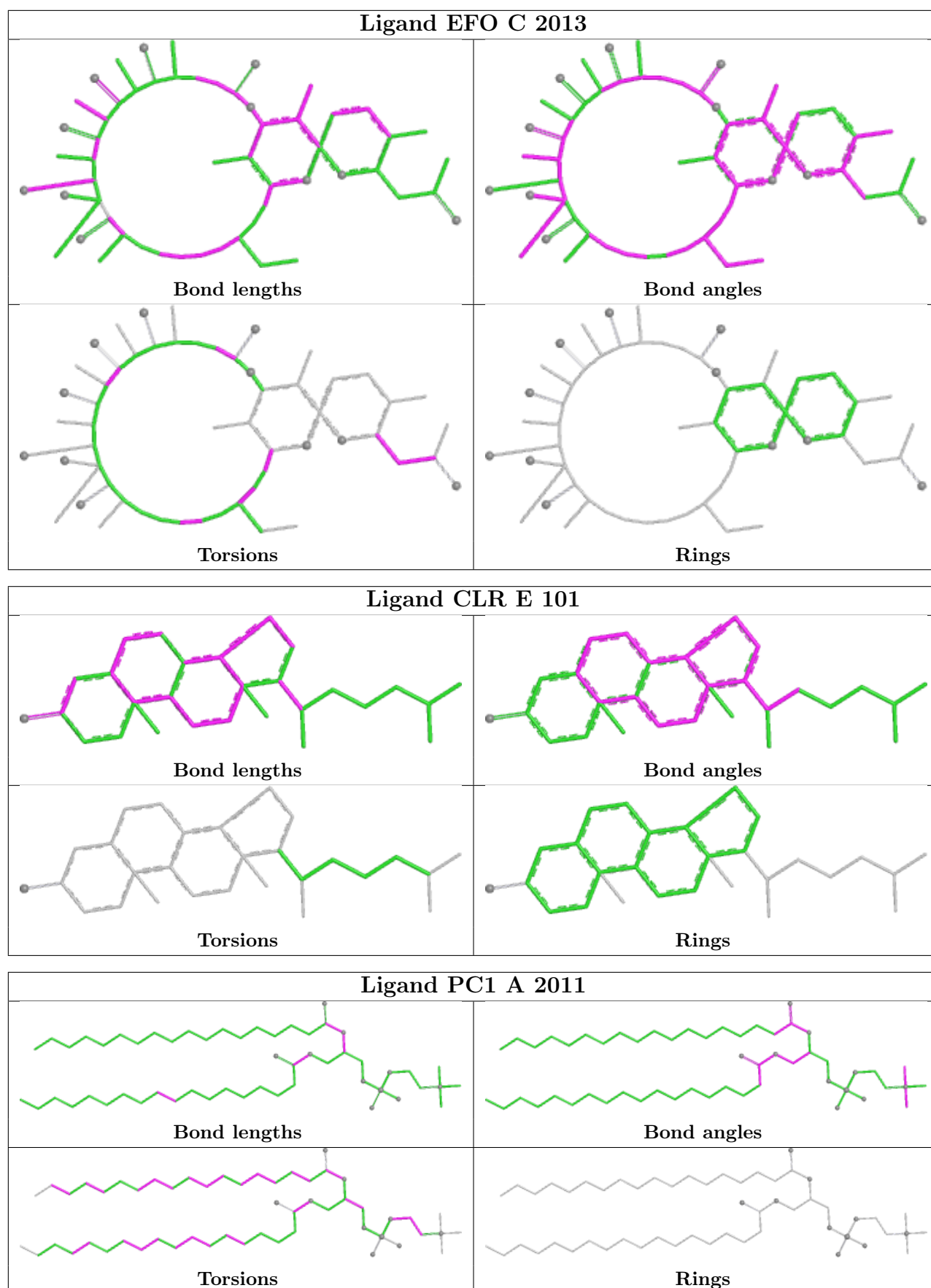




Ligand PC1 C 2009	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PC1 D 3003	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PC1 A 2013	
 Bond lengths	 Bond angles
 Torsions	 Rings







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	994/1016 (97%)	-0.55	11 (1%) 78 70	17, 57, 117, 181	0
1	C	994/1016 (97%)	-0.24	30 (3%) 52 42	34, 74, 143, 199	0
2	B	303/303 (100%)	0.68	29 (9%) 13 10	59, 130, 199, 229	0
2	D	303/303 (100%)	0.76	42 (13%) 6 5	68, 127, 205, 239	0
3	E	35/65 (53%)	0.14	1 (2%) 53 43	70, 88, 165, 168	0
3	G	34/65 (52%)	0.06	2 (5%) 28 21	75, 91, 164, 175	0
All	All	2663/2768 (96%)	-0.13	115 (4%) 40 31	17, 77, 161, 239	0

The worst 5 of 115 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	201	VAL	7.1
2	D	218	ASP	7.0
1	C	395	THR	6.6
2	D	166	THR	6.1
2	D	196	LEU	5.6

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](#)

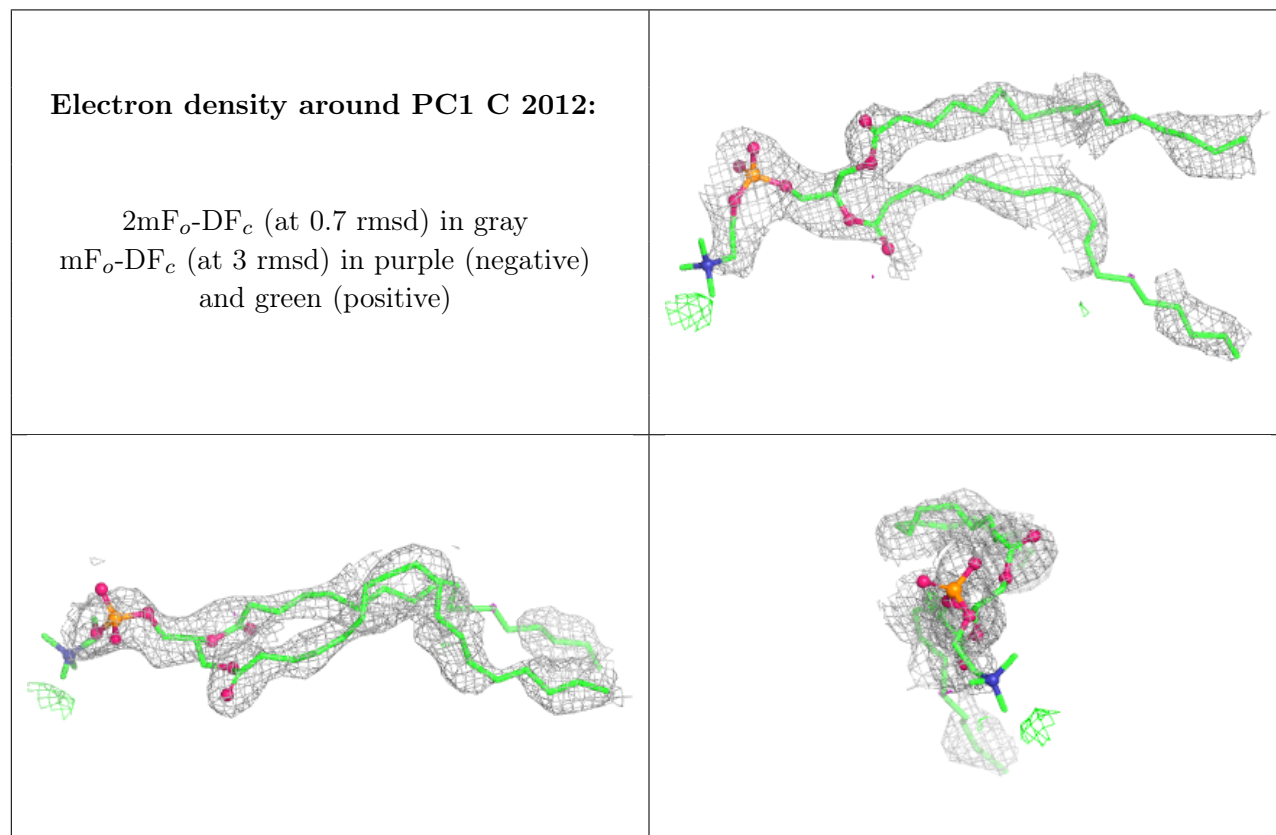
There are no oligosaccharides in this entry.

6.4 Ligands

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

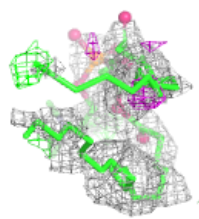
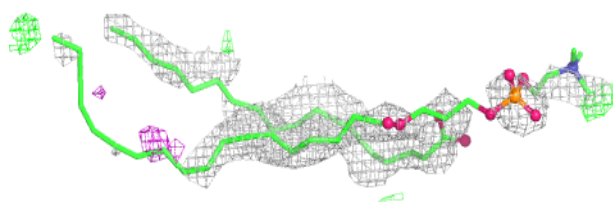
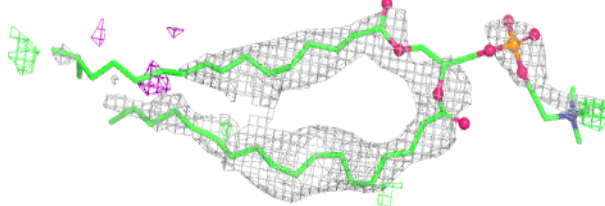
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	NAG	B	402	14/15	0.66	0.15	126,137,144,146	0
9	PC1	C	2012	54/54	0.68	0.16	79,133,162,185	0
9	PC1	A	2014	54/54	0.69	0.18	86,123,160,189	0
9	PC1	A	2012	54/54	0.76	0.17	61,117,163,176	0
11	NAG	D	3004	14/15	0.78	0.12	96,123,132,133	0
9	PC1	C	2010	54/54	0.79	0.14	68,101,143,205	0
7	NA	C	2006	1/1	0.80	0.08	83,83,83,83	0
10	EFO	C	2013	56/56	0.81	0.18	49,150,194,195	0
9	PC1	C	2011	54/54	0.81	0.20	77,117,163,173	0
9	PC1	B	401	54/54	0.81	0.15	61,90,146,170	0
9	PC1	A	2013	54/54	0.85	0.16	71,103,124,174	0
9	PC1	C	2009	54/54	0.86	0.14	59,107,140,145	0
7	NA	A	2006	1/1	0.86	0.08	65,65,65,65	0
9	PC1	D	3003	54/54	0.86	0.11	44,80,121,142	0
7	NA	A	2007	1/1	0.87	0.14	98,98,98,98	0
8	CLR	A	2010	28/28	0.87	0.14	60,98,131,138	0
10	EFO	A	2015	56/56	0.88	0.14	91,134,150,160	0
9	PC1	A	2011	54/54	0.89	0.14	57,97,128,130	0
8	CLR	G	101	28/28	0.89	0.11	54,91,100,131	0
8	CLR	A	2009	28/28	0.90	0.11	62,93,107,147	0
8	CLR	E	101	28/28	0.90	0.11	37,77,109,172	0
8	CLR	D	3002	28/28	0.91	0.13	13,97,131,141	0
7	NA	C	2008	1/1	0.92	0.08	46,46,46,46	0
7	NA	A	2008	1/1	0.92	0.11	59,59,59,59	0
8	CLR	D	3001	28/28	0.94	0.10	35,83,89,92	0
7	NA	A	2005	1/1	0.95	0.04	95,95,95,95	0
4	MG	A	2001	1/1	0.95	0.13	61,61,61,61	0
7	NA	C	2007	1/1	0.96	0.05	77,77,77,77	0
7	NA	C	2005	1/1	0.96	0.06	103,103,103,103	0
6	ADP	C	2004	27/27	0.98	0.05	31,47,57,60	0
6	ADP	A	2004	27/27	0.99	0.04	10,23,38,47	0
4	MG	A	2003	1/1	0.99	0.05	15,15,15,15	0
4	MG	C	2001	1/1	0.99	0.11	54,54,54,54	0
4	MG	C	2003	1/1	0.99	0.03	51,51,51,51	0
5	ALF	A	2002	5/5	0.99	0.04	14,14,28,29	0
5	ALF	C	2002	5/5	1.00	0.04	20,24,71,106	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.

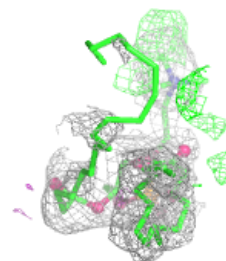
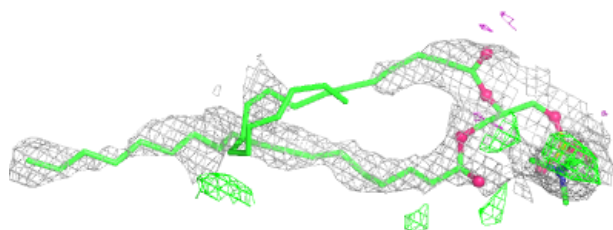
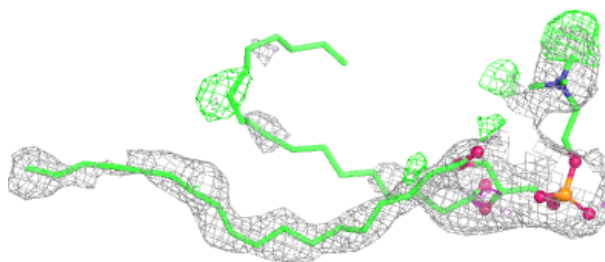


Electron density around PC1 A 2014:

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

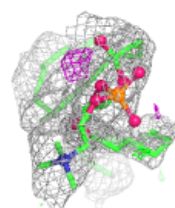
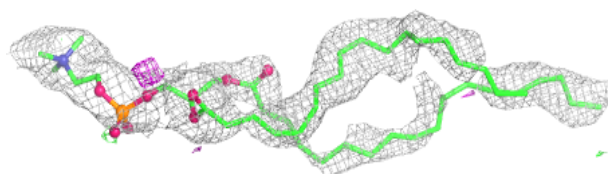
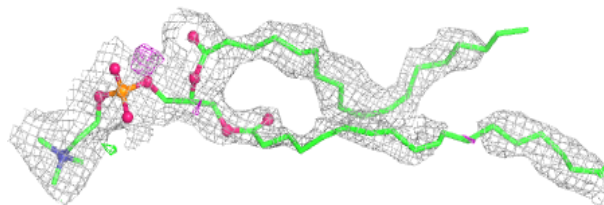
**Electron density around PC1 A 2012:**

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



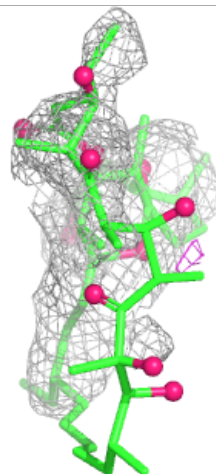
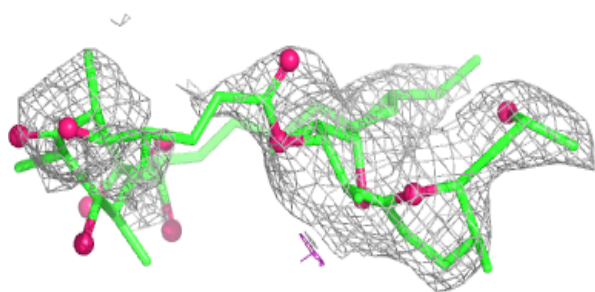
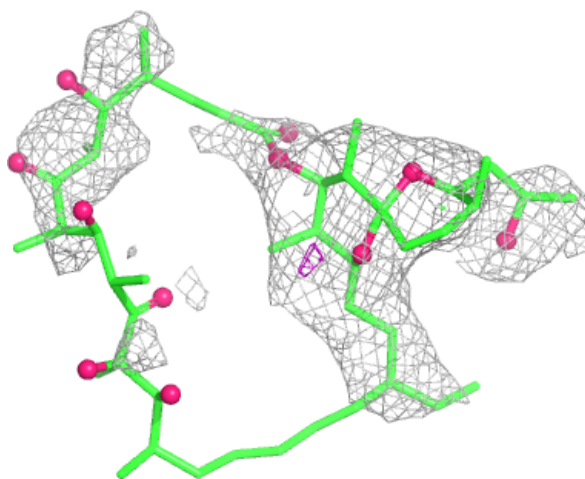
Electron density around PC1 C 2010:

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



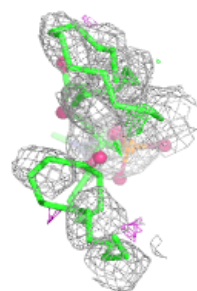
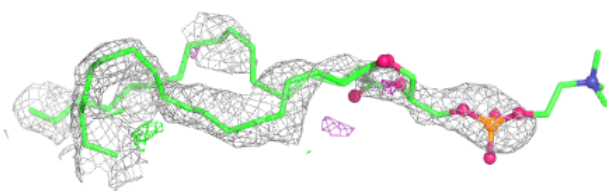
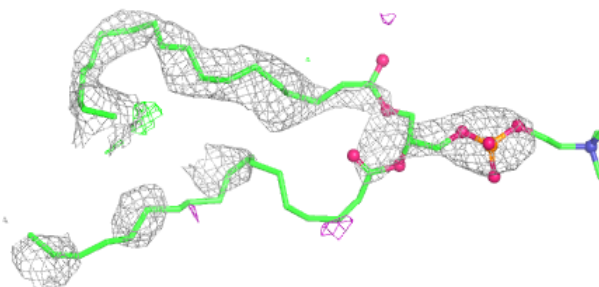
Electron density around EFO C 2013:

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

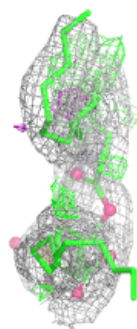
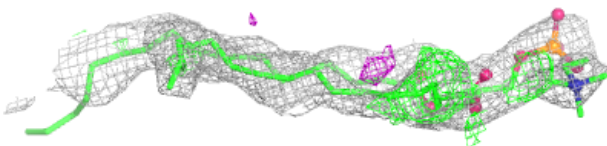
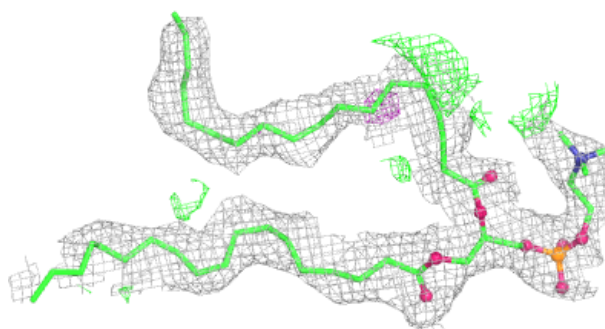


Electron density around PC1 C 2011:

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

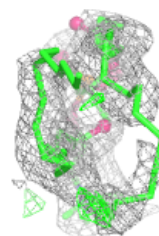
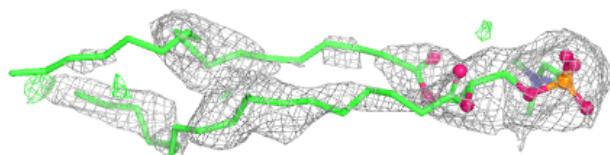
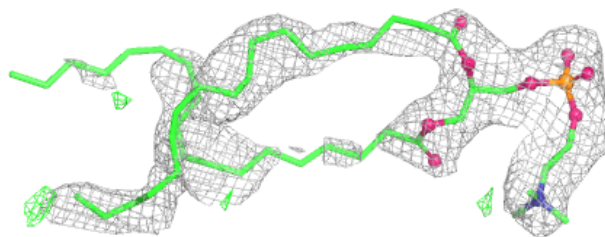
**Electron density around PC1 B 401:**

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

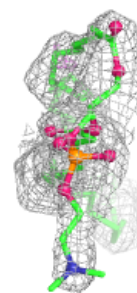
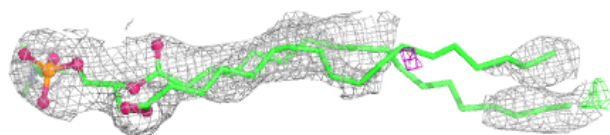
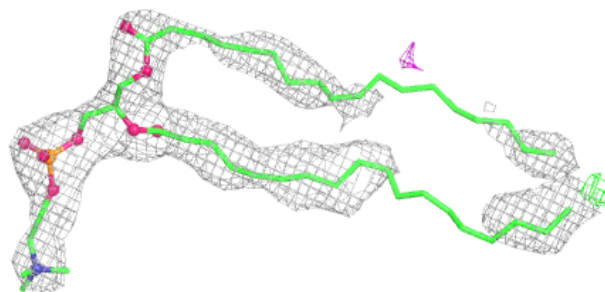


Electron density around PC1 A 2013:

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

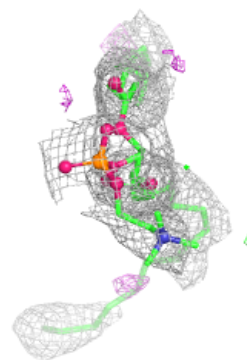
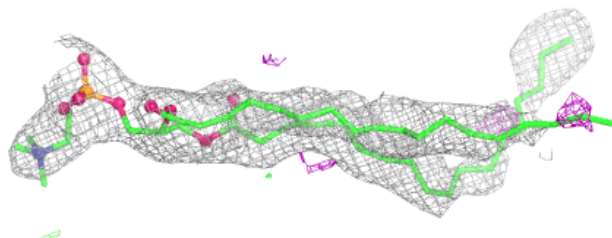
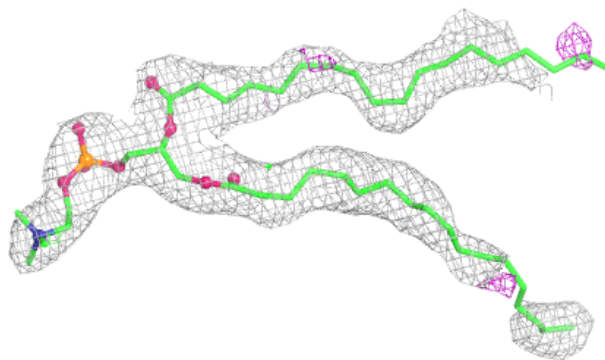
**Electron density around PC1 C 2009:**

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

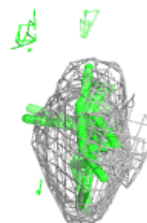
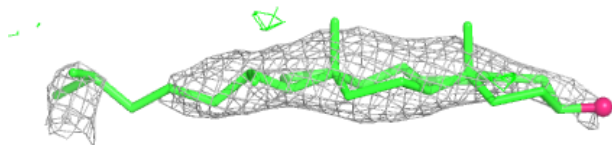


Electron density around PC1 D 3003:

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

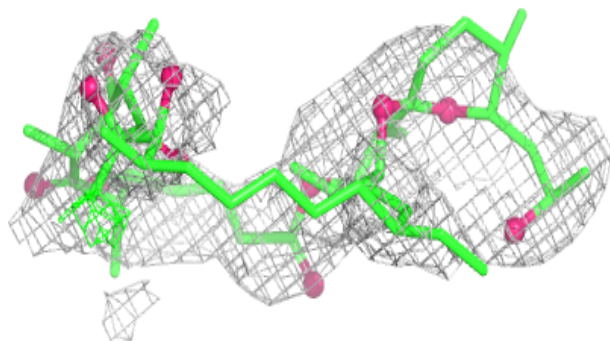
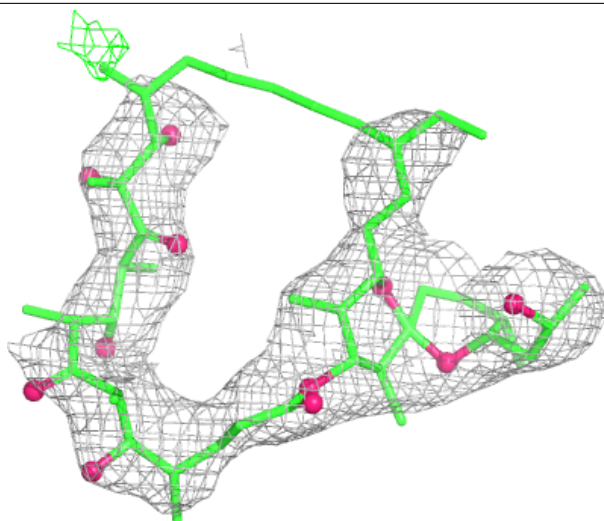
**Electron density around CLR A 2010:**

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



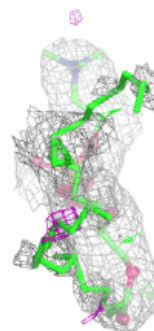
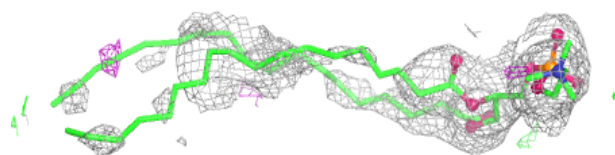
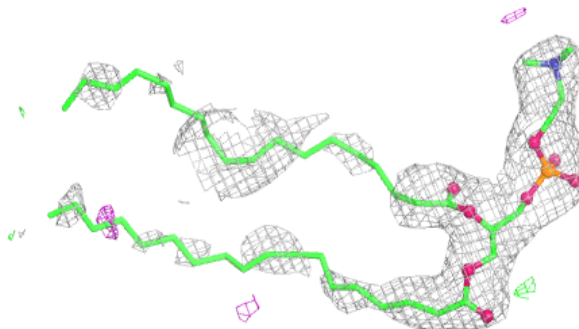
Electron density around EFO A 2015:

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

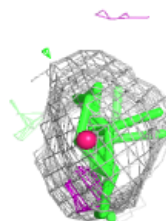
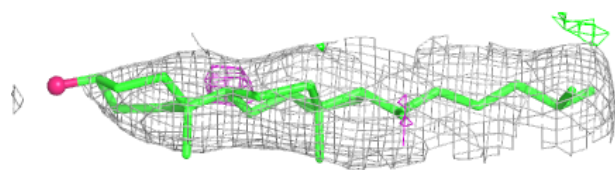
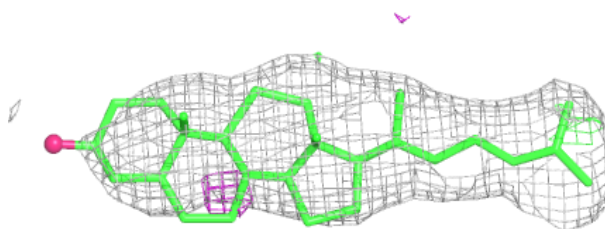


Electron density around PC1 A 2011:

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

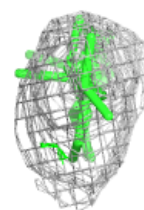
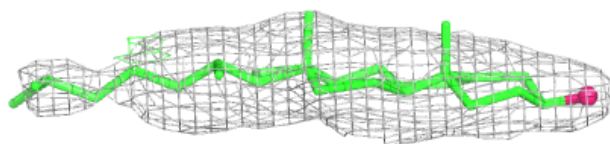
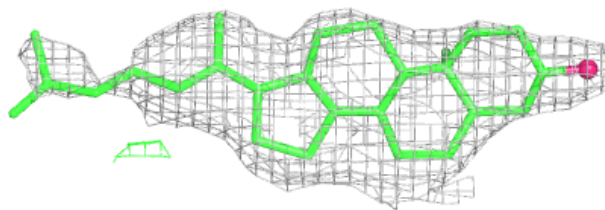
**Electron density around CLR G 101:**

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

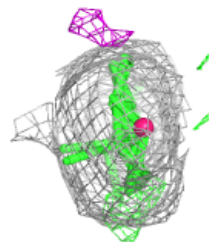
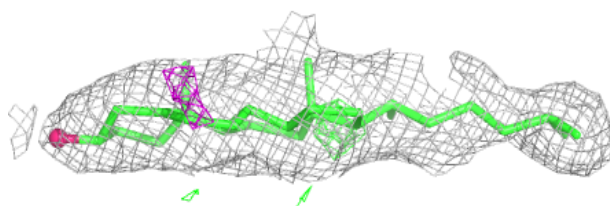
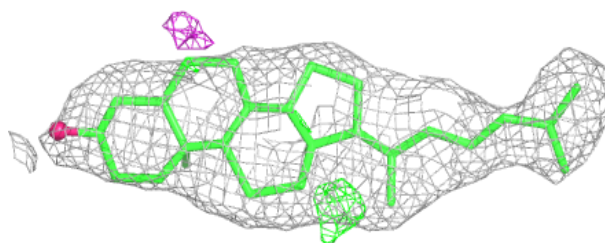


Electron density around CLR A 2009:

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

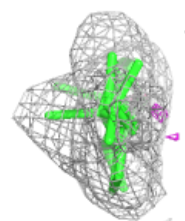
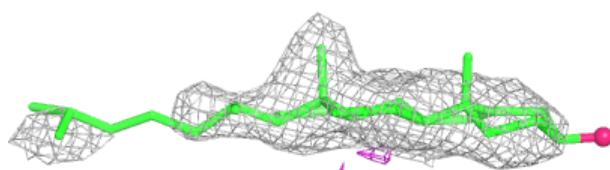
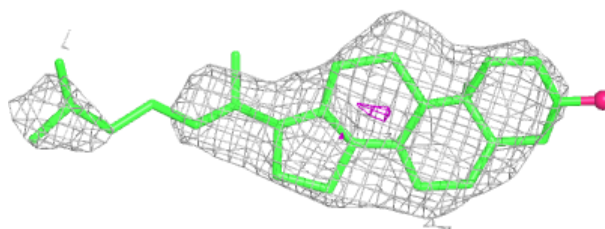
**Electron density around CLR E 101:**

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

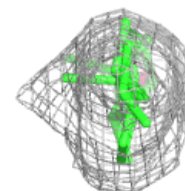
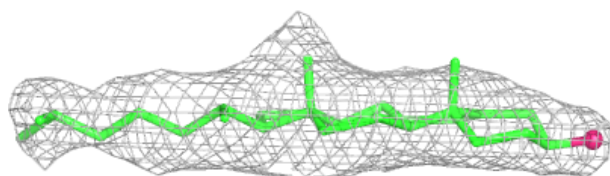
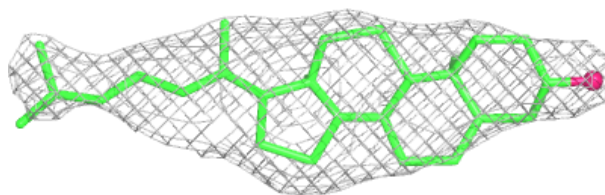


Electron density around CLR D 3002:

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

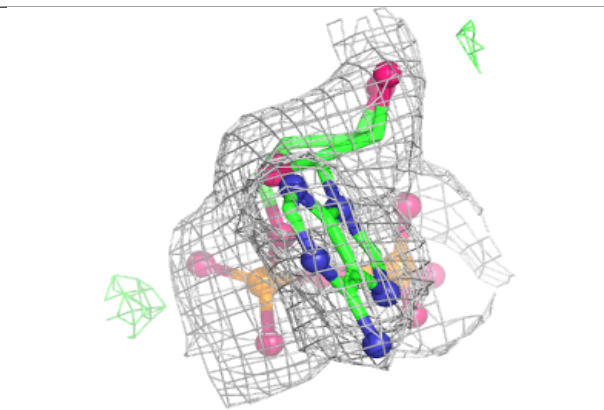
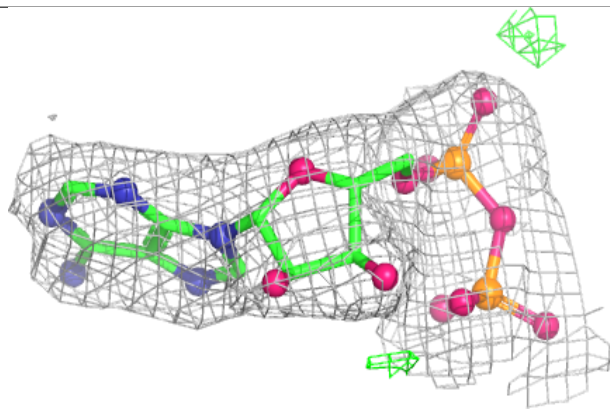
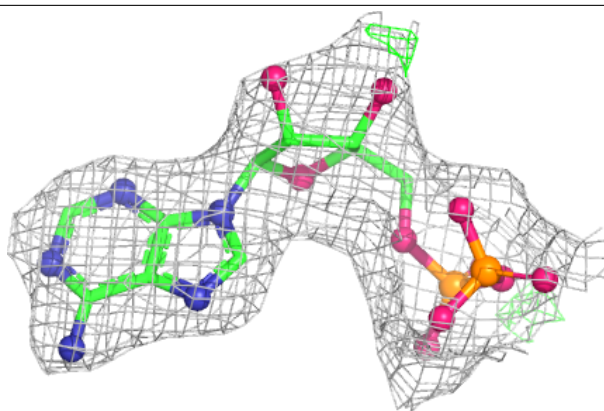
**Electron density around CLR D 3001:**

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

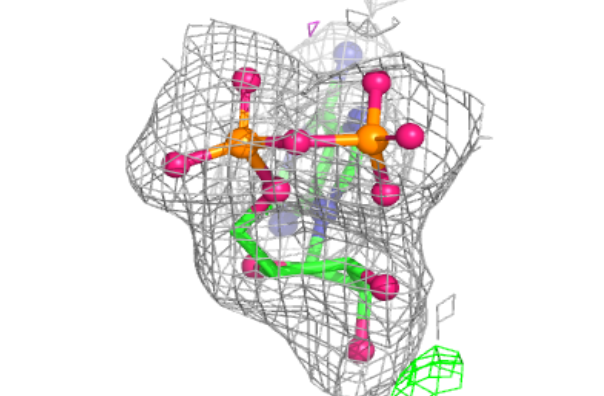
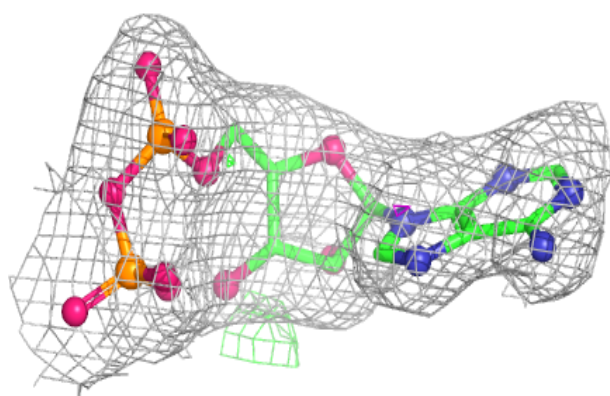
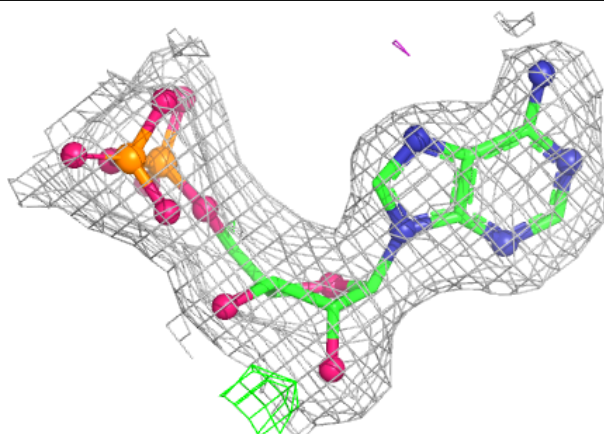


Electron density around ADP C 2004:

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

**Electron density around ADP A 2004:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.