



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 03:41 PM EDT

PDB ID : 1WPG / pdb_00001wpg
Title : Crystal structure of the SR CA2+-ATPase with MGF4
Authors : Toyoshima, C.; Nomura, H.; Tsuda, T.
Deposited on : 2004-09-02
Resolution : 2.30 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

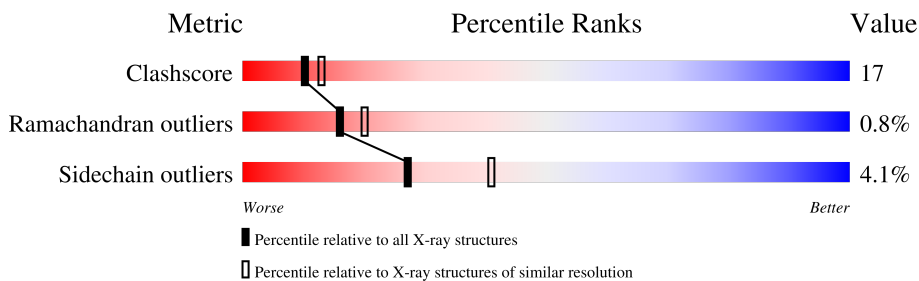
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	994	 66% 31% •
1	B	994	 66% 31% •
1	C	994	 66% 31% •
1	D	994	 65% 32% •

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 31698 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 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	994	Total	C	N	O	S	0	0	0
			7671	4876	1287	1451	57			
1	B	994	Total	C	N	O	S	0	0	0
			7671	4876	1287	1451	57			
1	C	994	Total	C	N	O	S	0	0	0
			7671	4876	1287	1451	57			
1	D	994	Total	C	N	O	S	0	0	0
			7671	4876	1287	1451	57			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	994	GLY	-	SEE REMARK 999	UNP P04191
B	994	GLY	-	SEE REMARK 999	UNP P04191
C	994	GLY	-	SEE REMARK 999	UNP P04191
D	994	GLY	-	SEE REMARK 999	UNP P04191

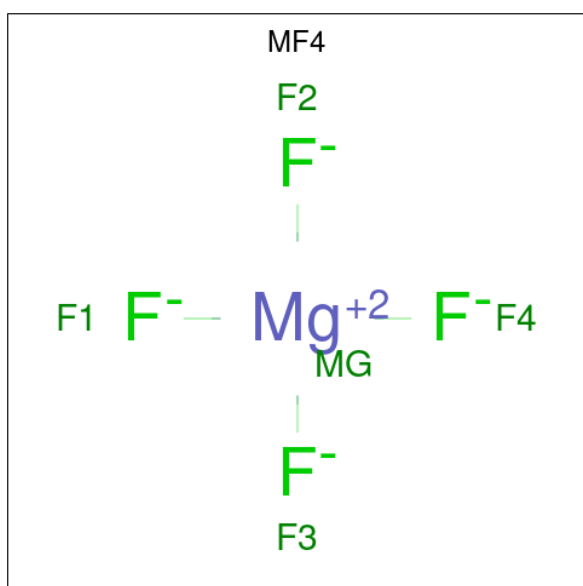
- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

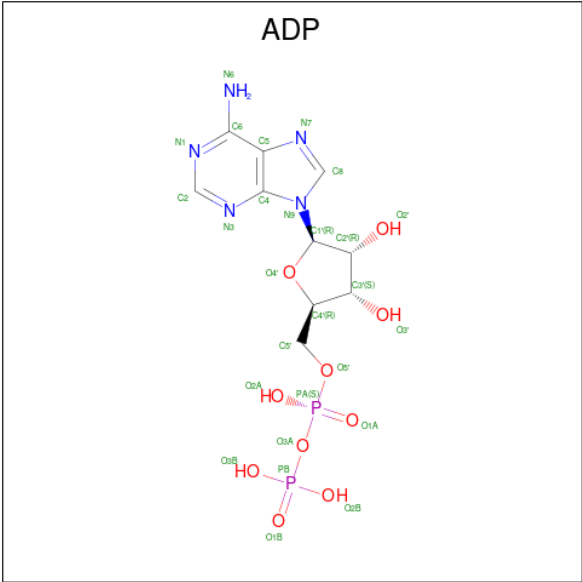
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Na 1	0	0
3	B	1	Total 1	Na 1	0	0
3	C	1	Total 1	Na 1	0	0
3	D	1	Total 1	Na 1	0	0

- Molecule 4 is TETRAFLUOROMAGNESATE(2-) (CCD ID: MF4) (formula: F_4Mg).



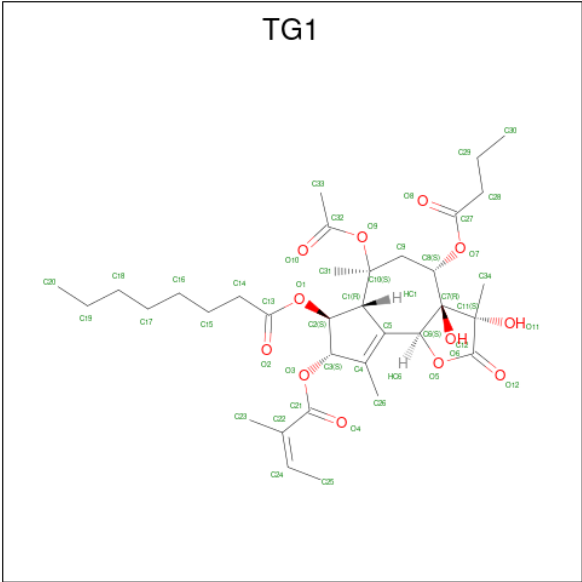
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 5	F 4	Mg 1	0	0
4	B	1	Total 5	F 4	Mg 1	0	0
4	C	1	Total 5	F 4	Mg 1	0	0
4	D	1	Total 5	F 4	Mg 1	0	0

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

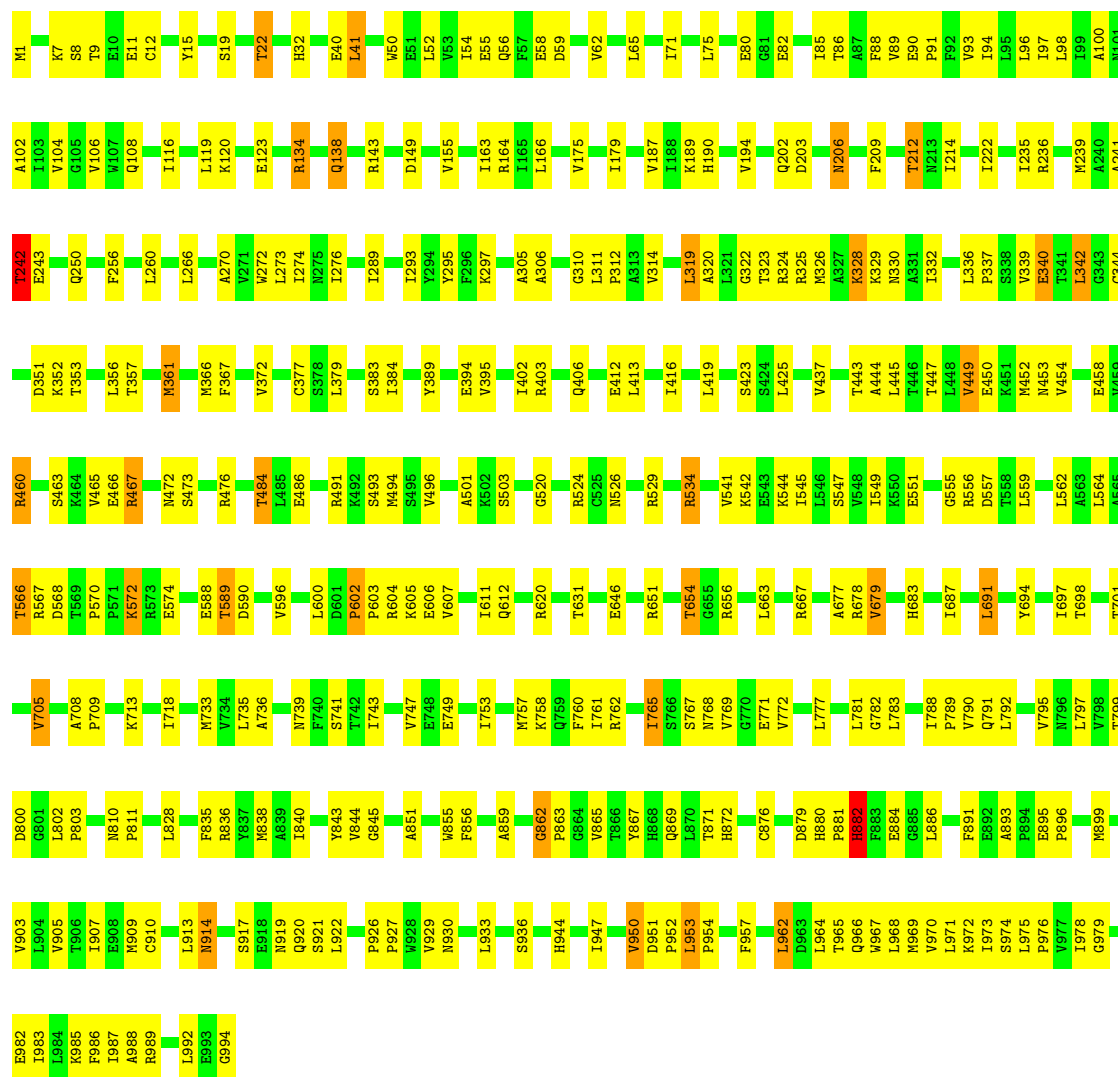
- Molecule 6 is OCTANOIC ACID [3S-[3ALPHA, 3ABETA, 4ALPHA, 6BETA, 6ABETA, 7BETA, 8ALPHA(Z), 9BALPHA]]-6-(ACETYLOXY)-2,3,-3A,4,5,6,6A,7,8,9B-DECAHYDRO-3,3A-DIHYDROXY-3,6,9-TRIMETHYL-8-[(2-METHYL-1-OXO-2-BUTENYL)OXY]-2-OXO-4-(1-OXOBUTOXY)-AZULENO[4,5-B]FURAN-7-YL ESTER (CCD ID: TG1) (formula: C₃₄H₅₀O₁₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			46	34	12		
6	B	1	Total	C	O	0	0
			46	34	12		
6	C	1	Total	C	O	0	0
			46	34	12		
6	D	1	Total	C	O	0	0
			46	34	12		

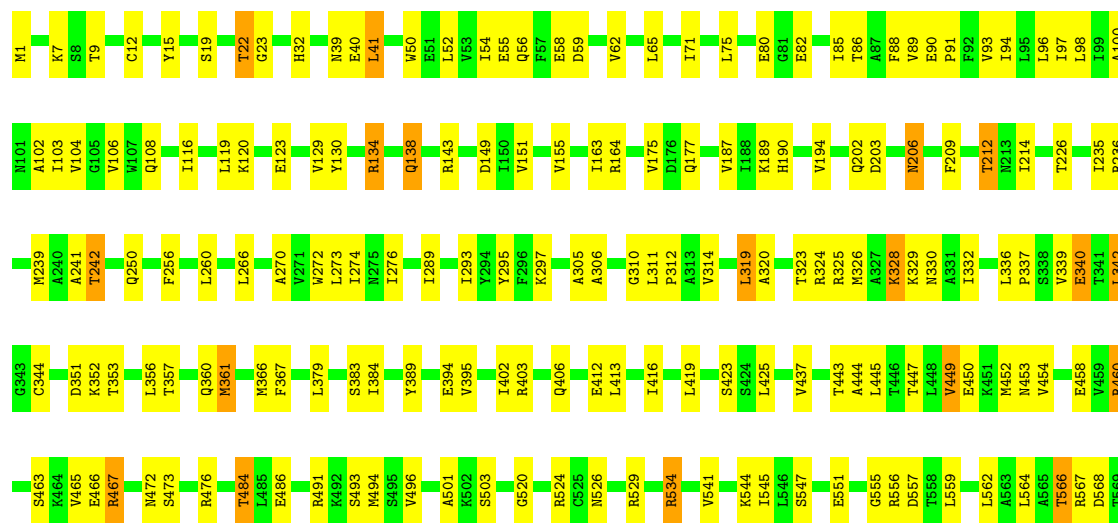
- Molecule 7 is water.

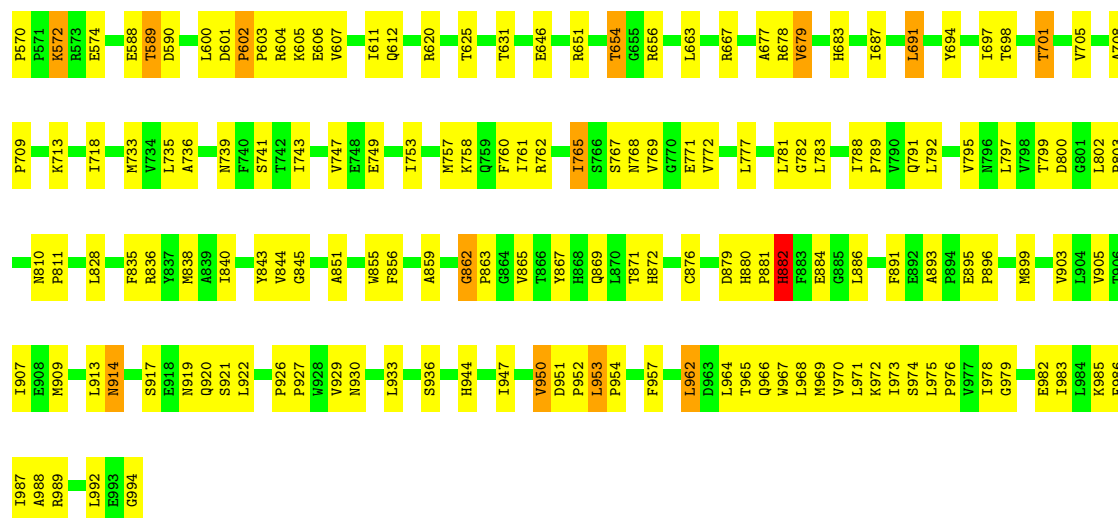
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	165	Total	O	0	0
			165	165		
7	B	180	Total	O	0	0
			180	180		
7	C	180	Total	O	0	0
			180	180		
7	D	165	Total	O	0	0
			165	165		



• Molecule 1: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1

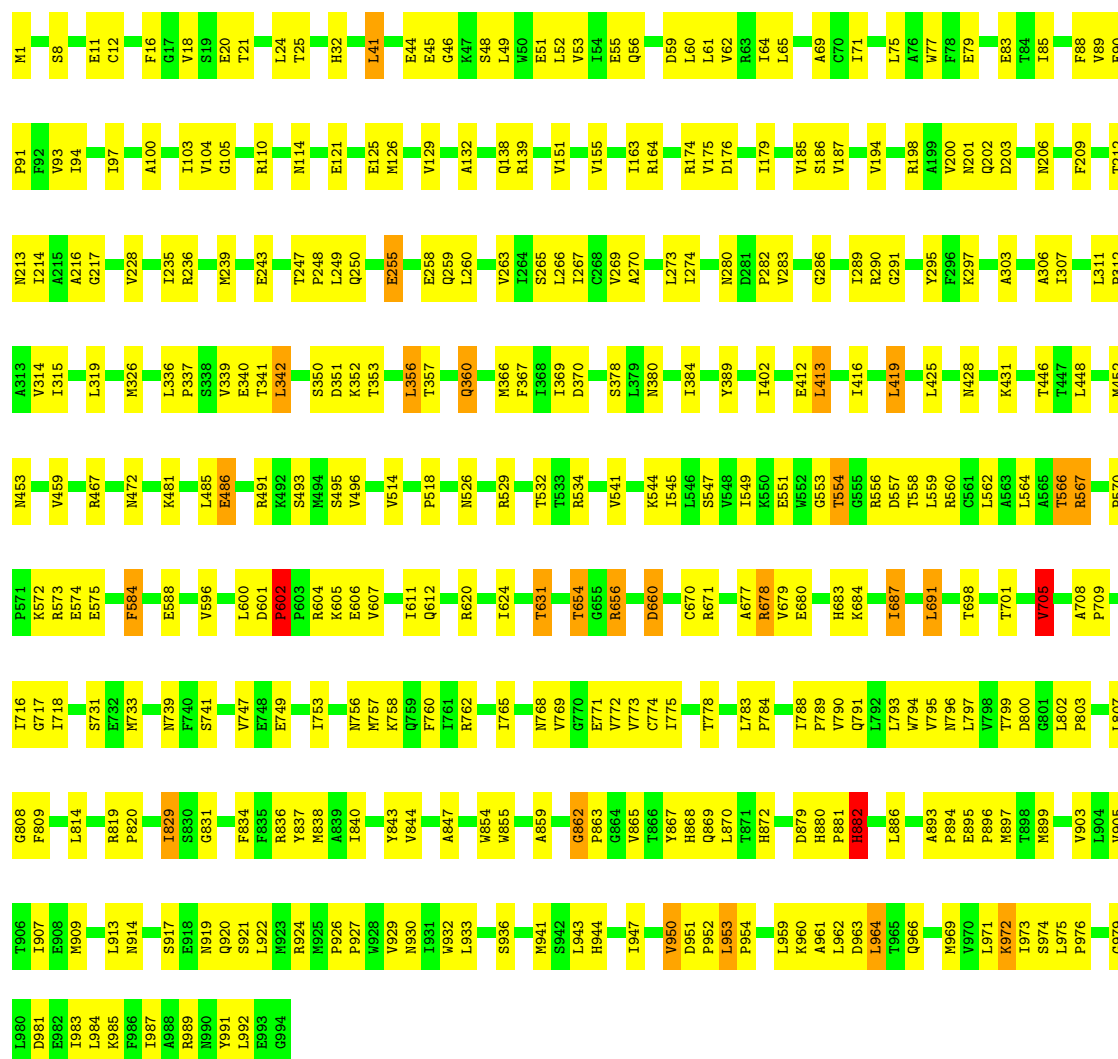
Chain C: 66% 31%





● Molecule 1: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1

Chain D: 65% 32% .



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.21Å 275.39Å 109.94Å 90.00° 90.01° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30	Depositor
% Data completeness (in resolution range)	93.4 (15.00-2.30)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.223 , 0.245	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	31698	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

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: ADP, MG, TG1, NA, MF4

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	0.46	9/7812 (0.1%)	0.89	19/10592 (0.2%)
1	B	0.51	7/7812 (0.1%)	0.90	15/10592 (0.1%)
1	C	0.51	8/7812 (0.1%)	0.91	18/10592 (0.2%)
1	D	0.47	9/7812 (0.1%)	0.89	22/10592 (0.2%)
All	All	0.49	33/31248 (0.1%)	0.90	74/42368 (0.2%)

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	526	ASN	CG-OD1	5.54	1.34	1.23
1	C	32	HIS	ND1-CE1	5.41	1.38	1.32
1	C	526	ASN	CG-OD1	5.41	1.33	1.23
1	A	202	GLN	CD-OE1	5.40	1.33	1.23
1	B	32	HIS	ND1-CE1	5.34	1.37	1.32

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	556	ARG	N-CA-C	-8.97	102.35	113.20
1	C	556	ARG	N-CA-C	-8.85	102.49	113.20
1	D	602	PRO	N-CA-C	8.39	120.94	110.70
1	C	602	PRO	N-CA-C	8.37	119.54	110.58
1	A	602	PRO	N-CA-C	8.00	120.47	110.70

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	7671	0	7764	256	0
1	B	7671	0	7764	281	0
1	C	7671	0	7764	278	0
1	D	7671	0	7764	254	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
5	A	27	0	12	0	0
5	B	27	0	12	2	0
5	C	27	0	12	2	0
5	D	27	0	12	0	0
6	A	46	0	50	0	0
6	B	46	0	50	2	0
6	C	46	0	50	2	0
6	D	46	0	50	0	0
7	A	165	0	0	5	0
7	B	180	0	0	8	0
7	C	180	0	0	7	0
7	D	165	0	0	6	0
All	All	31698	0	31304	1065	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 17.

The worst 5 of 1065 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:460:ARG:H	1:C:460:ARG:HD3	1.09	1.15
1:B:460:ARG:HD3	1:B:460:ARG:H	1.10	1.13
1:B:1:MET:HE1	1:B:12:CYS:HA	1.38	1.03
1:C:1:MET:HE1	1:C:12:CYS:HA	1.37	1.02
1:D:679:VAL:HG13	1:D:683:HIS:HB2	1.47	0.96

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	992/994 (100%)	932 (94%)	51 (5%)	9 (1%)	14	17
1	B	992/994 (100%)	934 (94%)	52 (5%)	6 (1%)	21	27
1	C	992/994 (100%)	933 (94%)	53 (5%)	6 (1%)	21	27
1	D	992/994 (100%)	931 (94%)	52 (5%)	9 (1%)	14	17
All	All	3968/3976 (100%)	3730 (94%)	208 (5%)	30 (1%)	16	20

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	882	HIS
1	B	882	HIS
1	C	882	HIS
1	D	882	HIS
1	A	961	ALA

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	840/840 (100%)	808 (96%)	32 (4%)	29	44
1	B	840/840 (100%)	804 (96%)	36 (4%)	26	39
1	C	840/840 (100%)	803 (96%)	37 (4%)	25	38
1	D	840/840 (100%)	807 (96%)	33 (4%)	28	43
All	All	3360/3360 (100%)	3222 (96%)	138 (4%)	27	41

5 of 138 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	413	LEU
1	D	554	THR
1	D	678	ARG
1	B	449	VAL
1	B	445	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	177	GLN
1	C	510	ASN
1	C	244	GLN
1	C	359	ASN
1	C	919	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 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
6	TG1	C	1203	-	44,48,48	1.77	11 (25%)	47,72,72	1.74	9 (19%)
6	TG1	D	1303	-	44,48,48	1.74	11 (25%)	47,72,72	1.71	11 (23%)
4	MF4	C	1198	1	0,4,4	-	-	-	-	-
4	MF4	A	998	1	0,4,4	-	-	-	-	-
5	ADP	B	1102	2	28,29,29	1.61	8 (28%)	43,45,45	2.17	13 (30%)
5	ADP	D	1302	2	28,29,29	1.58	7 (25%)	43,45,45	2.21	14 (32%)
6	TG1	B	1103	-	44,48,48	1.76	11 (25%)	47,72,72	1.75	9 (19%)
6	TG1	A	1003	-	44,48,48	1.75	11 (25%)	47,72,72	1.70	10 (21%)
5	ADP	C	1202	2	28,29,29	1.57	8 (28%)	43,45,45	2.15	13 (30%)
4	MF4	B	1098	1	0,4,4	-	-	-	-	-
5	ADP	A	1002	2	28,29,29	1.58	7 (25%)	43,45,45	2.20	14 (32%)
4	MF4	D	1298	1	0,4,4	-	-	-	-	-

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
6	TG1	C	1203	-	-	12/33/99/99	0/3/3/3
6	TG1	D	1303	-	-	9/33/99/99	0/3/3/3
5	ADP	D	1302	2	-	4/16/32/32	0/3/3/3
5	ADP	B	1102	2	-	6/16/32/32	0/3/3/3
6	TG1	B	1103	-	-	11/33/99/99	0/3/3/3
6	TG1	A	1003	-	-	9/33/99/99	0/3/3/3
5	ADP	A	1002	2	-	4/16/32/32	0/3/3/3
5	ADP	C	1202	2	-	6/16/32/32	0/3/3/3

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1203	TG1	O4-C21	6.12	1.33	1.21
6	B	1103	TG1	O4-C21	5.98	1.33	1.21
6	A	1003	TG1	O4-C21	5.70	1.33	1.21
6	D	1303	TG1	O4-C21	5.56	1.32	1.21
5	B	1102	ADP	C5-N7	-3.66	1.32	1.39

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1302	ADP	N3-C2-N1	-7.01	117.97	128.58
5	B	1102	ADP	N3-C2-N1	-6.99	118.01	128.58
5	A	1002	ADP	N3-C2-N1	-6.97	118.02	128.58
5	C	1202	ADP	N3-C2-N1	-6.95	118.06	128.58
6	D	1303	TG1	C10-O9-C32	5.65	134.59	121.36

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1102	ADP	O4'-C4'-C5'-O5'
5	C	1202	ADP	O4'-C4'-C5'-O5'
6	A	1003	TG1	O3-C21-C22-C23
6	A	1003	TG1	O3-C21-C22-C24
6	B	1103	TG1	O3-C21-C22-C23

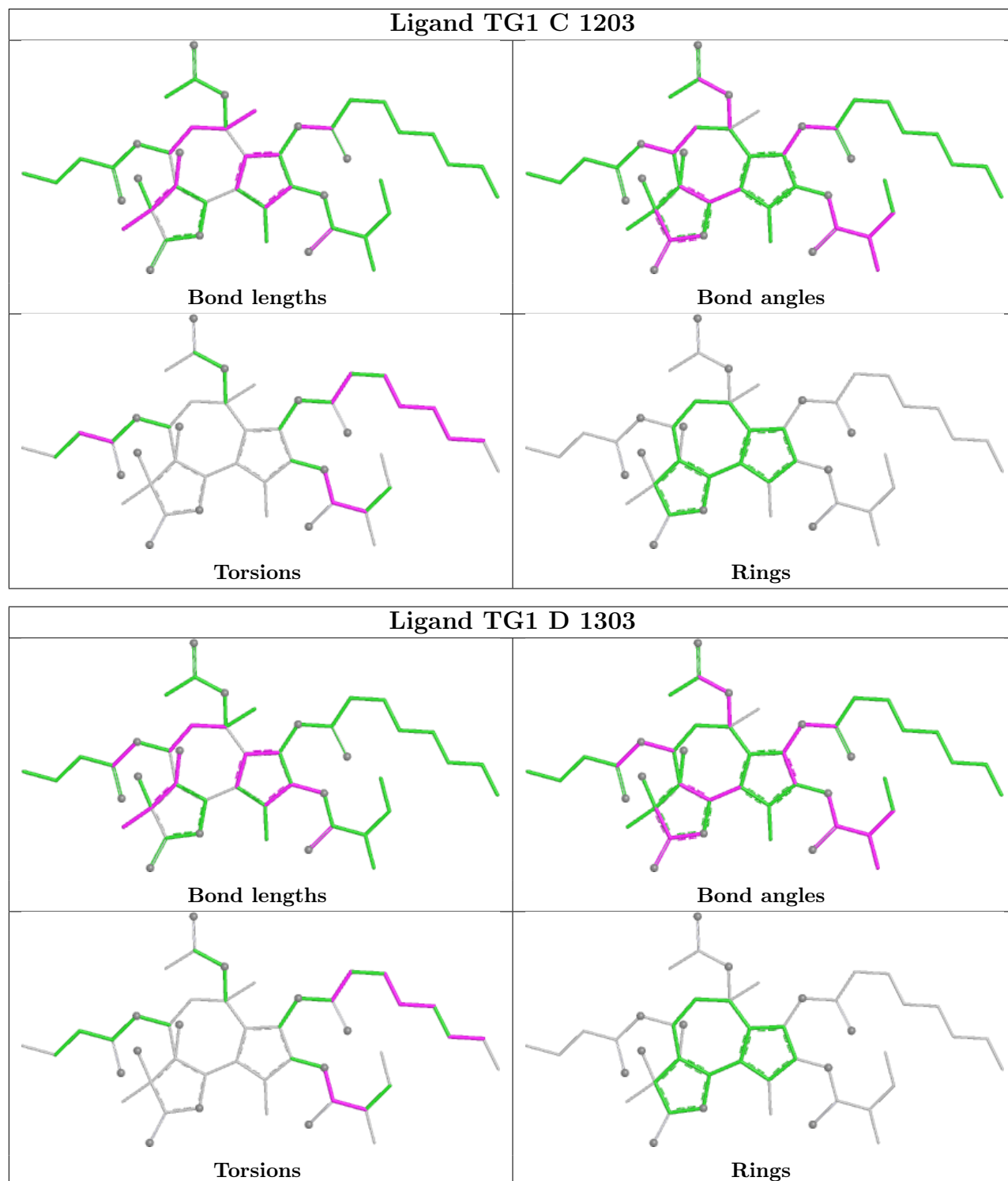
There are no ring outliers.

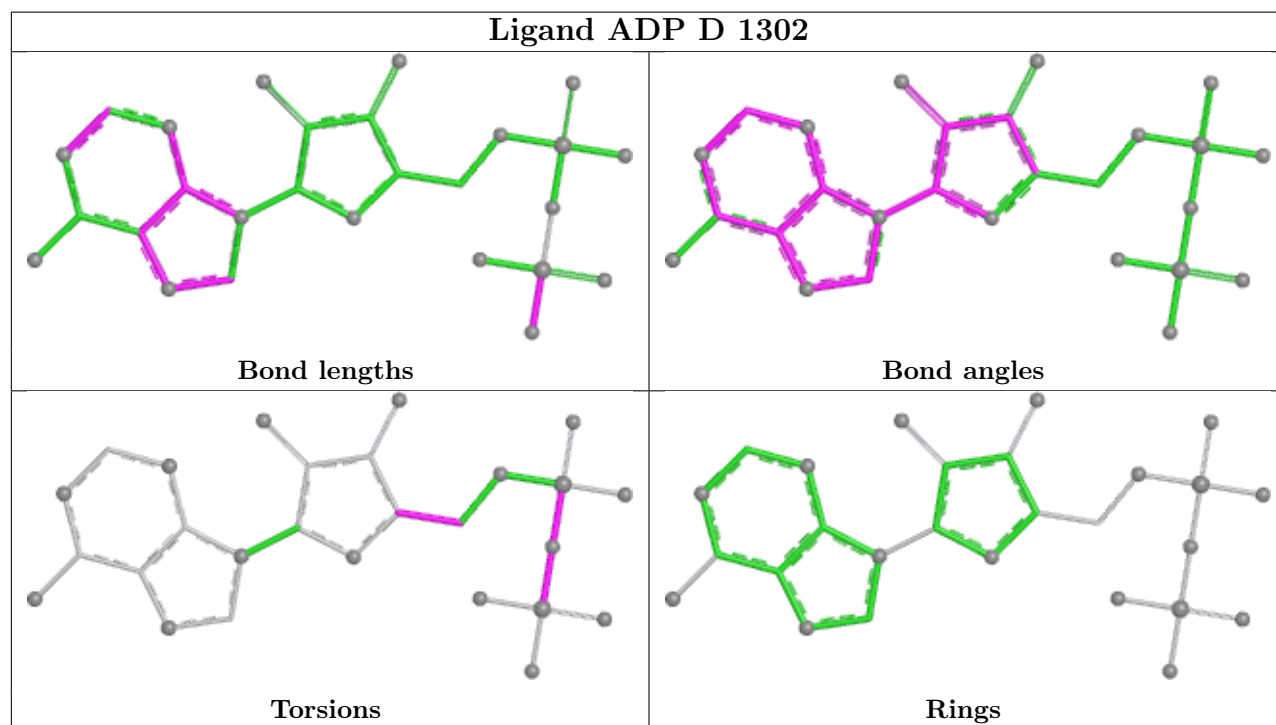
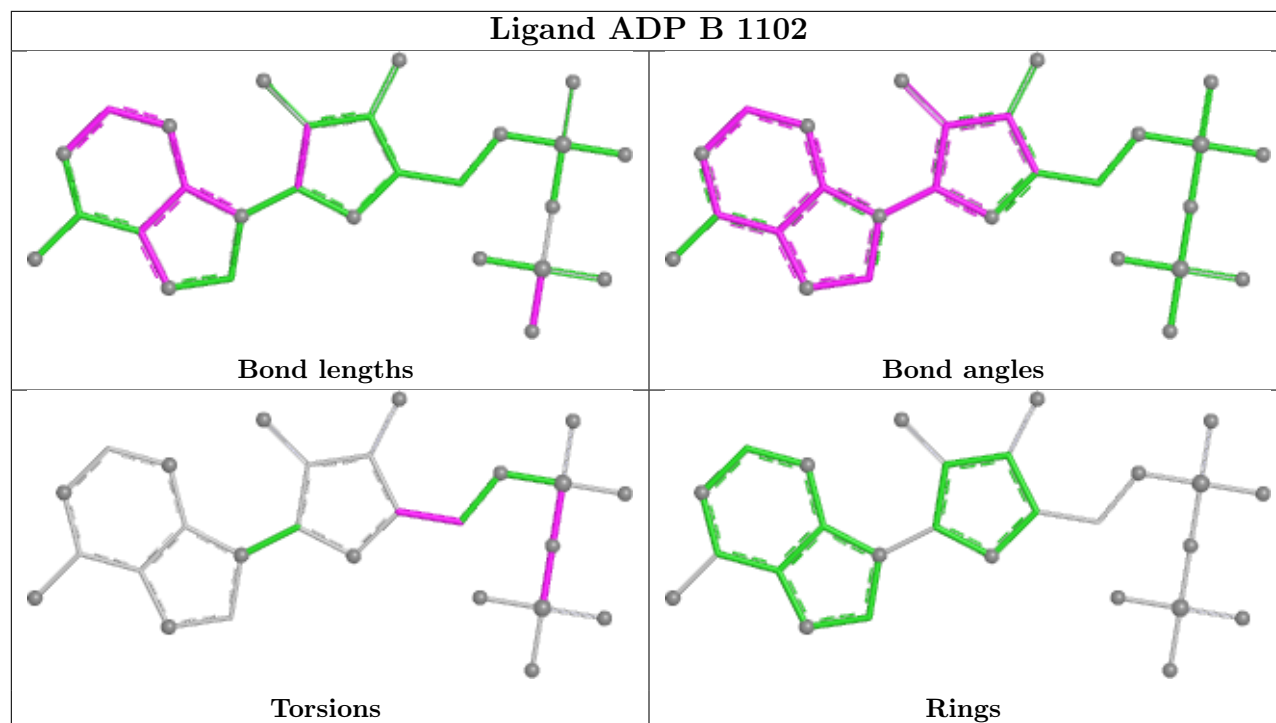
4 monomers are involved in 8 short contacts:

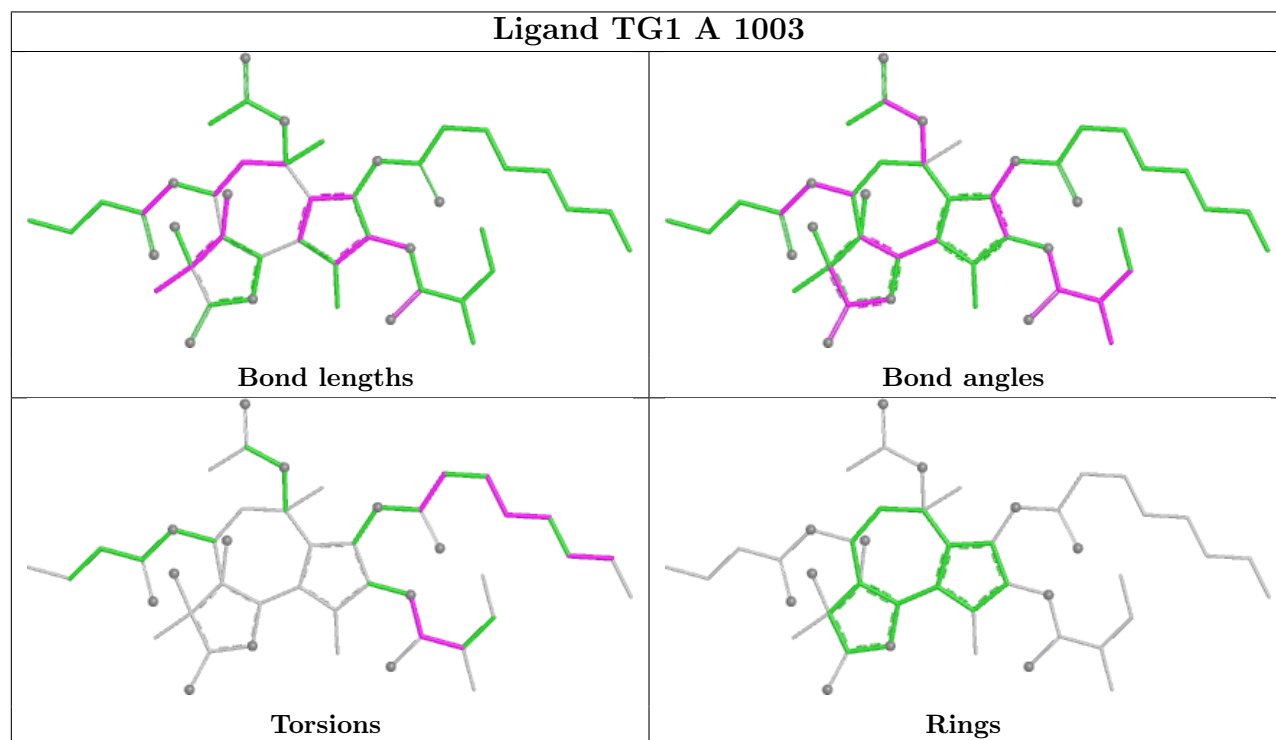
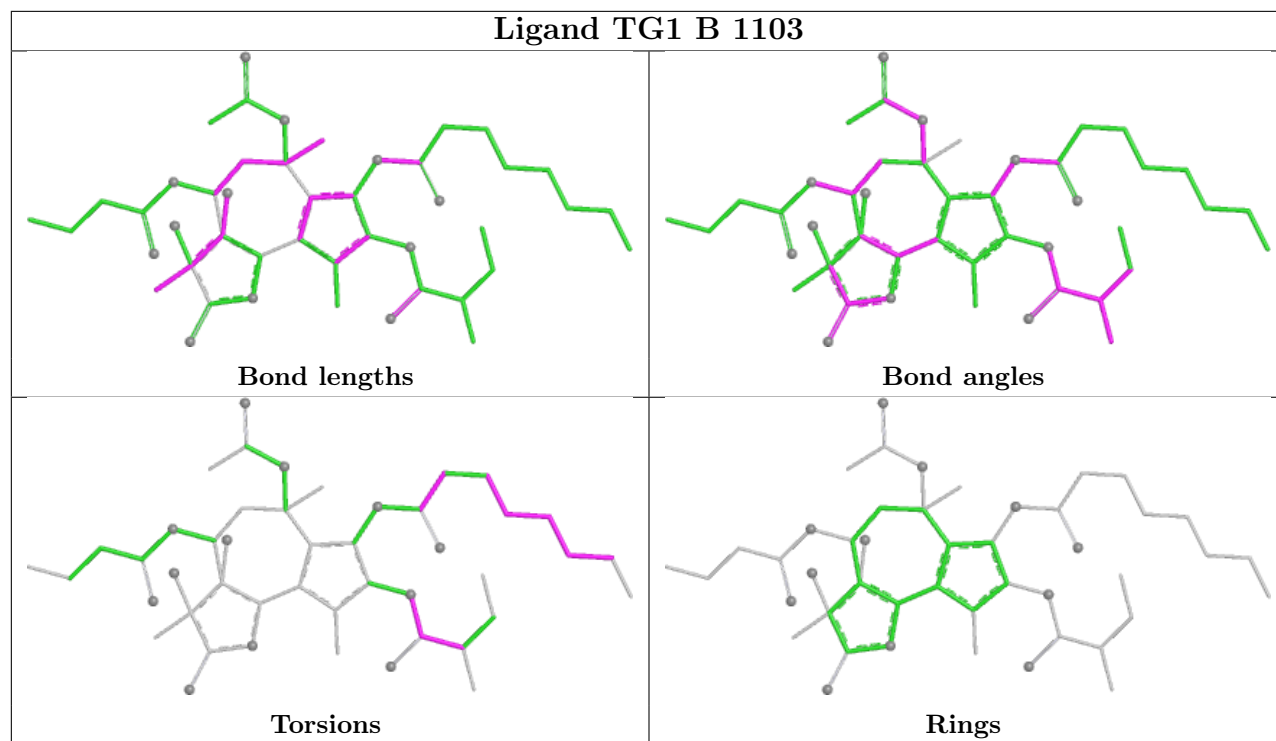
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1203	TG1	2	0
5	B	1102	ADP	2	0
6	B	1103	TG1	2	0
5	C	1202	ADP	2	0

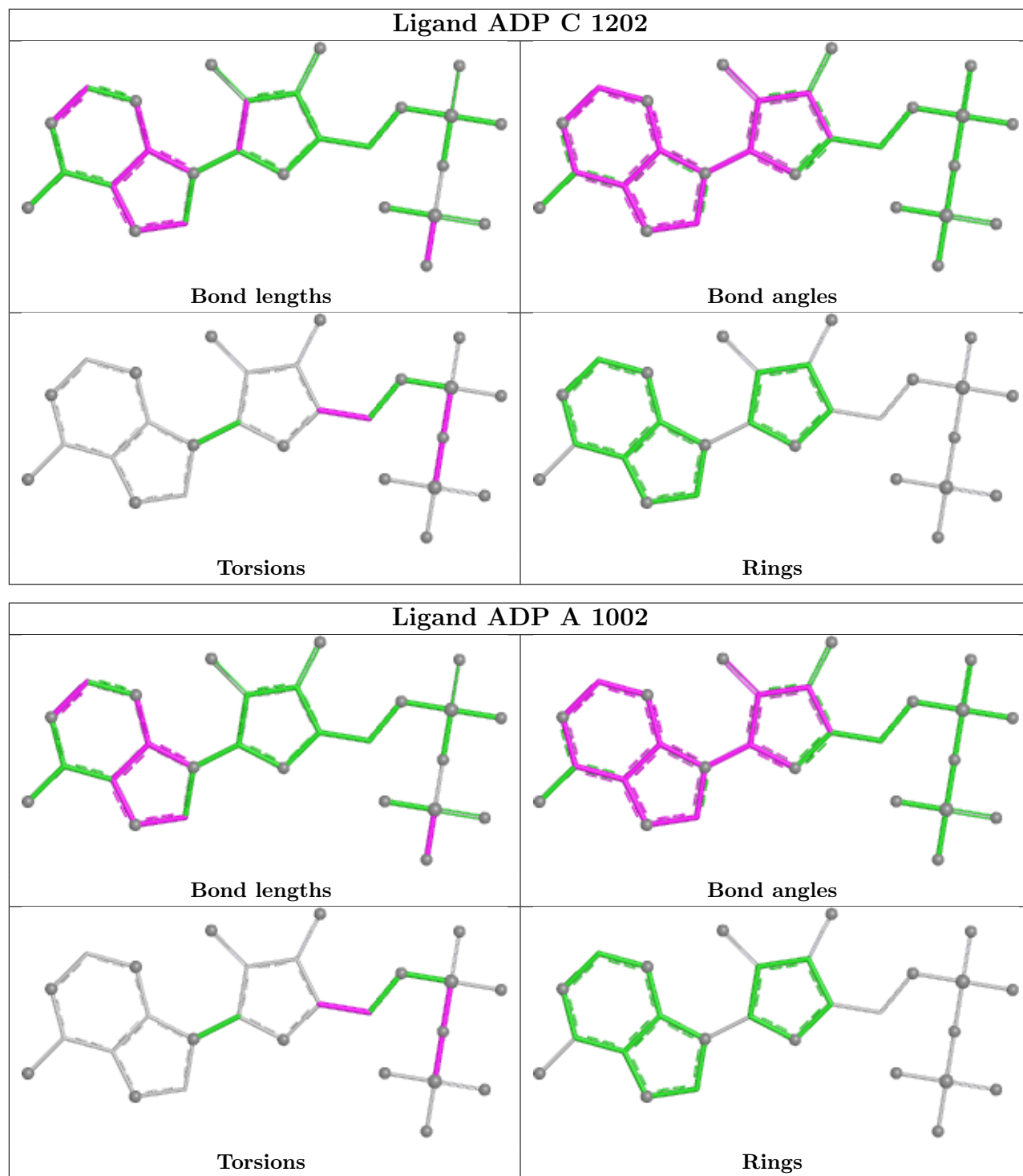
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.