



## wwPDB EM Validation Summary Report ⓘ

Apr 11, 2022 – 01:12 pm BST

PDB ID : 7Q2Y  
EMDB ID : EMD-13784  
Title : Cryo-EM structure of clamped S.cerevisiae condensin-DNA complex (form II)  
Authors : Lee, B.-G.; Rhodes, J.; Lowe, J.  
Deposited on : 2021-10-26  
Resolution : Not provided  
Based on initial models : 6YVU, 6ZZ6

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.0.dev97  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.27

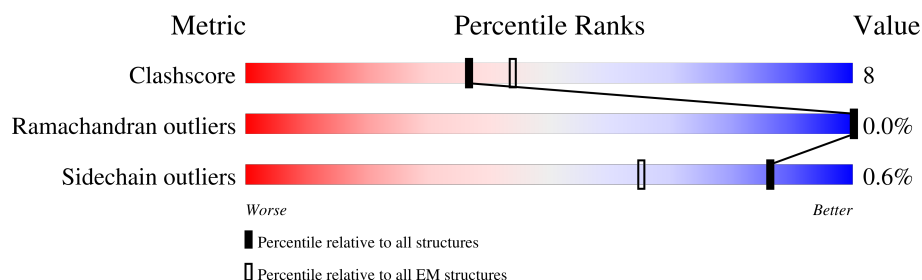
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is unknown.

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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	1170	28% 9% 63%
2	B	1418	23% 73%
3	C	754	31% 6% 63%
4	D	1176	63% 19% 17%
5	F	28	29% 71%
6	G	28	75% 25%

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 17754 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Structural maintenance of chromosomes protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	431	Total	C	N	O	S	0	0
			3413	2163	587	646	17		

- Molecule 2 is a protein called Structural maintenance of chromosomes protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	388	Total	C	N	O	S	0	0
			3102	1970	529	590	13		

- Molecule 3 is a protein called Condensin complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	281	Total	C	N	O	S	0	0
			2251	1418	374	448	11		

- Molecule 4 is a protein called Condensin complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	976	Total	C	N	O	S	0	0
			7776	4984	1279	1463	50		

- Molecule 5 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	28	Total	C	N	O	P	0	0
			588	280	140	140	28		

- Molecule 6 is a DNA chain called DNA (28-MER).

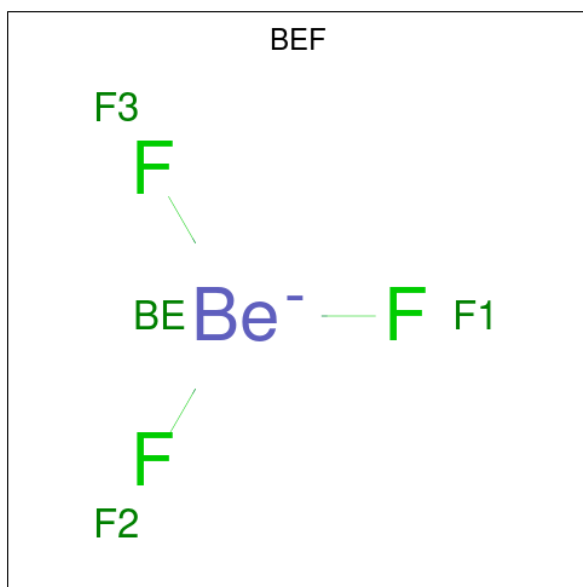
Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	28	Total	C	N	O	P	0	0
			560	280	56	196	28		

- Molecule 7 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

- Molecule 8 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula:  $BeF_3$ ).



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

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

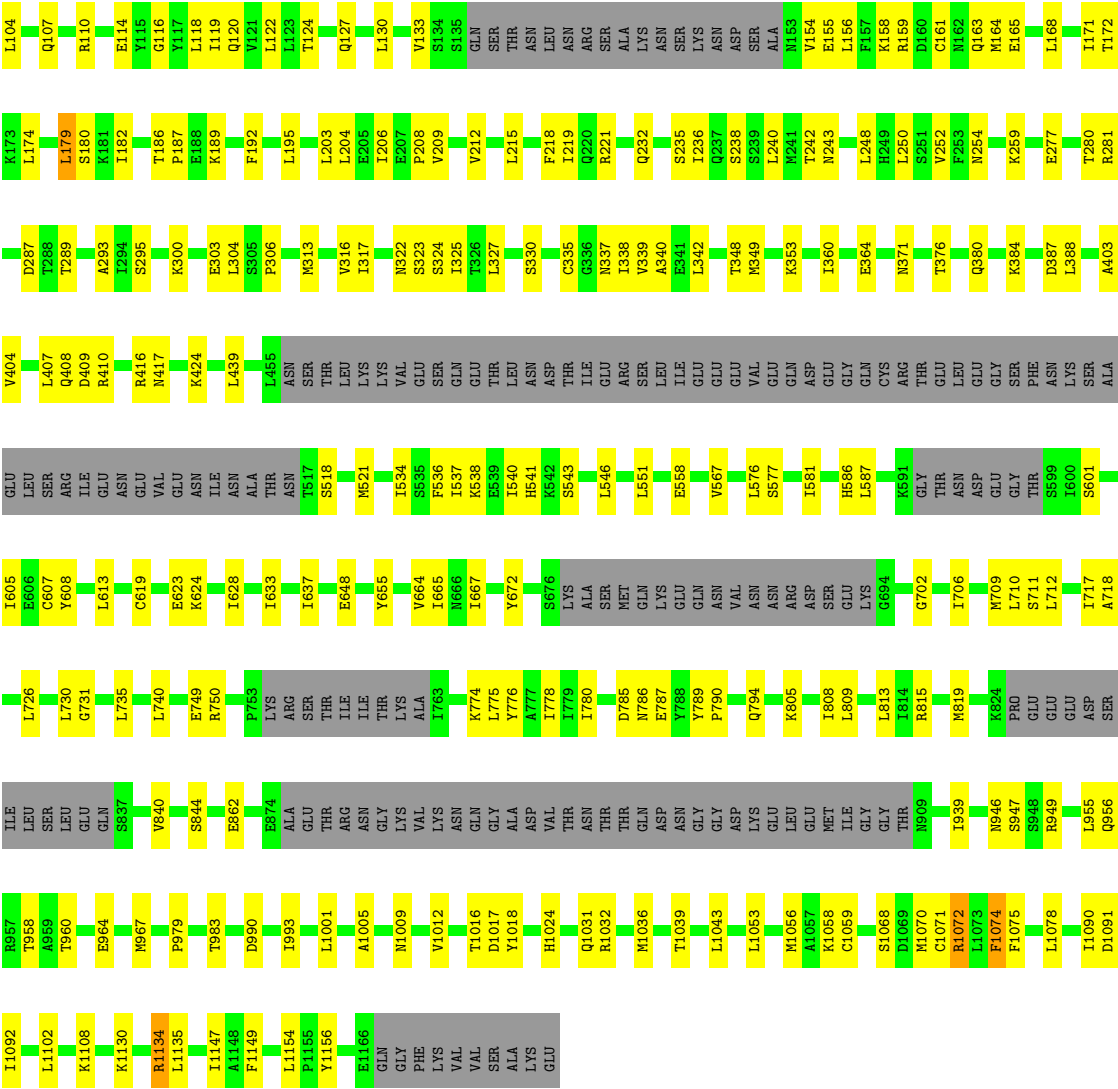
Mol	Chain	Residues	Atoms		AltConf
9	A	1	Total 1	Mg 1	0
9	B	1	Total 1	Mg 1	0







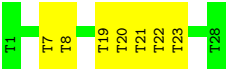




● Molecule 5: DNA (28-MER)



● Molecule 6: DNA (28-MER)



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	251999	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

## 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: MG, BEF, ADP

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	0.26	0/3457	0.49	0/4646
2	B	0.25	0/3152	0.47	0/4236
3	C	0.24	0/2277	0.46	0/3064
4	D	0.25	0/7885	0.46	0/10617
5	F	0.47	0/671	0.68	0/1032
6	G	0.54	0/615	1.28	0/948
All	All	0.28	0/18057	0.53	0/24543

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
1	A	0	1
4	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	215	ARG	Sidechain
4	D	1072	ARG	Sidechain

## 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	3413	0	3547	72	0
2	B	3102	0	3133	38	0
3	C	2251	0	2226	36	0
4	D	7776	0	8026	149	0
5	F	588	0	309	16	0
6	G	560	0	337	4	0
7	A	27	0	12	2	0
7	B	27	0	12	0	0
8	A	4	0	0	0	0
8	B	4	0	0	1	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
All	All	17754	0	17602	293	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 8.

The worst 5 of 293 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:A:224:GLN:HG3	1:A:228:GLU:OE2	1.77	0.83
4:D:340:ALA:HA	4:D:388:LEU:HD11	1.66	0.78
4:D:259:LYS:HD2	4:D:304:LEU:HB3	1.66	0.76
4:D:10:LEU:HD11	4:D:195:LEU:HD21	1.70	0.74
1:A:220:PHE:CZ	1:A:975:PHE:HE1	2.05	0.73

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	427/1170 (36%)	404 (95%)	23 (5%)	0	100	100
2	B	382/1418 (27%)	374 (98%)	8 (2%)	0	100	100
3	C	269/754 (36%)	254 (94%)	14 (5%)	1 (0%)	34	34
4	D	954/1176 (81%)	925 (97%)	29 (3%)	0	100	100
All	All	2032/4518 (45%)	1957 (96%)	74 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	312	ILE

### 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 PDB entries followed by that with respect to all EM entries.

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	386/1071 (36%)	383 (99%)	3 (1%)	81	81
2	B	347/1301 (27%)	345 (99%)	2 (1%)	86	86
3	C	257/688 (37%)	256 (100%)	1 (0%)	91	91
4	D	894/1072 (83%)	888 (99%)	6 (1%)	84	84
All	All	1884/4132 (46%)	1872 (99%)	12 (1%)	86	86

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	163	GLN
4	D	179	LEU
4	D	1134	ARG
4	D	1074	PHE
2	B	132	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such

sidechains are listed below:

Mol	Chain	Res	Type
4	D	408	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z  > 2$
7	ADP	A	2001	9	24,29,29	0.93	1 (4%)	29,45,45	1.48	4 (13%)
8	BEF	B	2002	-	0,3,3	-	-	-		
8	BEF	A	2002	-	0,3,3	-	-	-		
7	ADP	B	2001	9	24,29,29	0.99	0	29,45,45	1.47	4 (13%)

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
7	ADP	A	2001	9	-	2/12/32/32	0/3/3/3
7	ADP	B	2001	9	-	0/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	2001	ADP	C5-C4	2.48	1.47	1.40

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	2001	ADP	PA-O3A-PB	-3.51	120.77	132.83
7	B	2001	ADP	PA-O3A-PB	-3.23	121.74	132.83
7	A	2001	ADP	C3'-C2'-C1'	3.18	105.77	100.98
7	B	2001	ADP	N3-C2-N1	-3.17	123.72	128.68
7	A	2001	ADP	N3-C2-N1	-3.14	123.77	128.68

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2001	ADP	O4'-C4'-C5'-O5'
7	A	2001	ADP	C3'-C4'-C5'-O5'

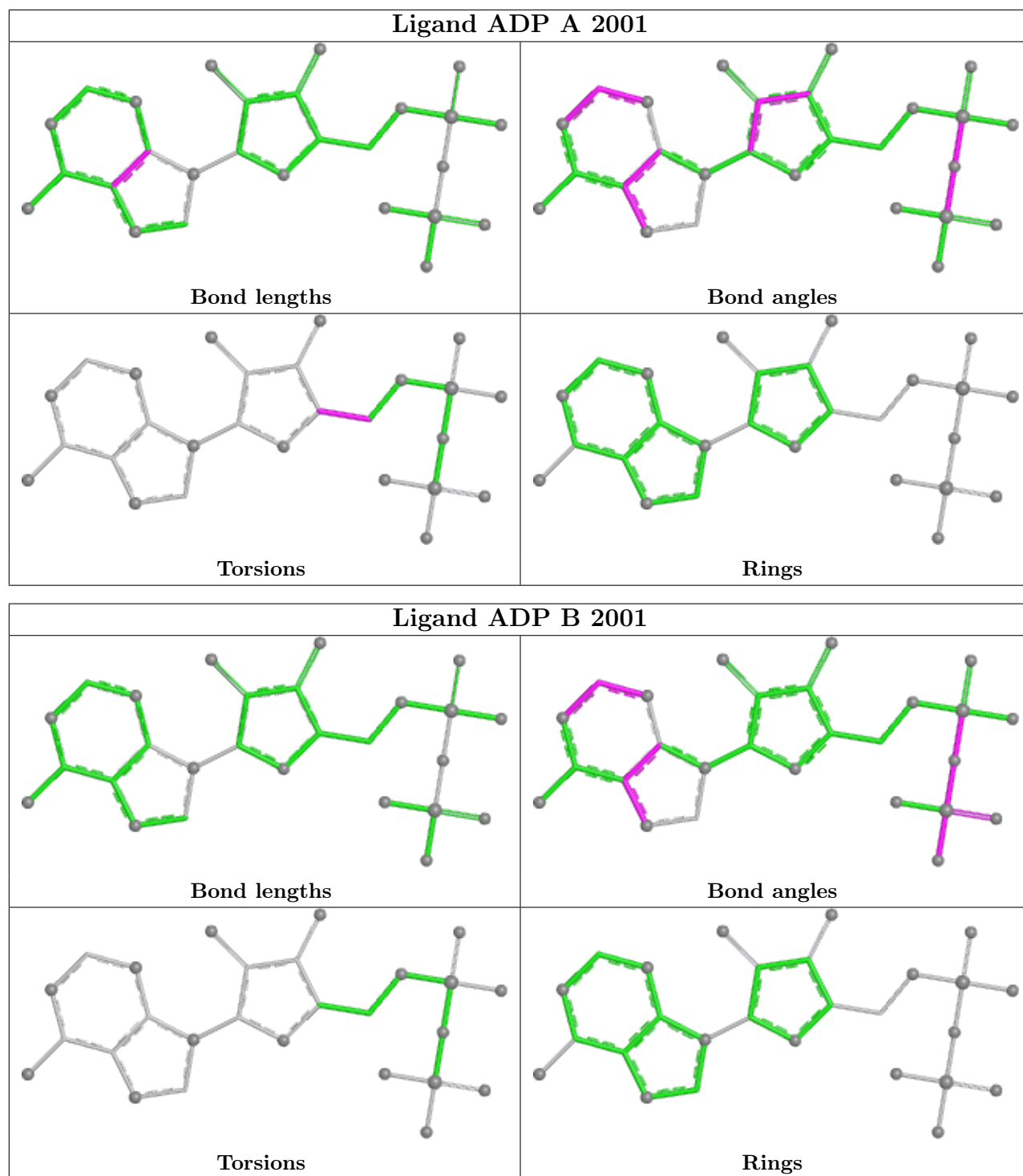
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	2001	ADP	2	0
8	B	2002	BEF	1	0

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

equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.



## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13784. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal surface views

This section was not generated.

### 6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution ⓘ

This section was not generated.

### 7.2 Volume estimate versus contour level ⓘ

This section was not generated.

### 7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit

This section was not generated.