



wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 11:17 pm BST

PDB ID : 7ADC / pdb_00007adc
EMDB ID : EMD-11723
Title : Transcription termination intermediate complex 3 delta NusG
Authors : Said, N.; Hilal, T.; Loll, B.; Wahl, C.M.
Deposited on : 2020-09-14
Resolution : 4.00 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

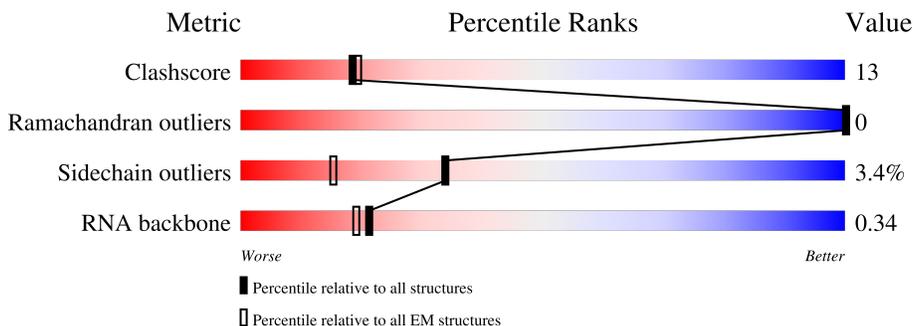
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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.



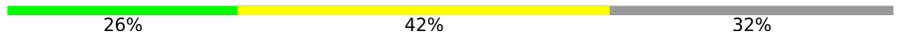
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 ≥ 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	419	
1	b	419	
1	c	419	
1	d	419	
1	e	419	
1	f	419	
2	A	497	

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Mol	Chain	Length	Quality of chain
3	U	329	
3	V	329	
4	W	91	
5	X	1342	
6	Y	1416	
7	K	50	
8	L	50	
9	R	99	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 51565 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 Transcription termination factor Rho.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	f	417	3280	2065	581	617	17	0	0
1	a	417	3280	2065	581	617	17	0	0
1	b	417	3280	2065	581	617	17	0	0
1	c	417	3280	2065	581	617	17	0	0
1	d	417	3280	2065	581	617	17	0	0
1	e	417	3280	2065	581	617	17	0	0

- Molecule 2 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	495	3852	2396	669	774	13	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP C3SSN7
A	0	ALA	-	expression tag	UNP C3SSN7

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	U	235	1825	1135	325	359	6	0	0
3	V	321	2504	1566	441	489	8	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	W	79	627	382	118	126	1	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	X	1340	10567	6631	1841	2052	43	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	Y	1358	10545	6620	1883	1992	50	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	1408	LEU	-	expression tag	UNP C3SIA2
Y	1409	GLU	-	expression tag	UNP C3SIA2
Y	1410	VAL	-	expression tag	UNP C3SIA2
Y	1411	HIS	-	expression tag	UNP C3SIA2
Y	1412	HIS	-	expression tag	UNP C3SIA2
Y	1413	HIS	-	expression tag	UNP C3SIA2
Y	1414	HIS	-	expression tag	UNP C3SIA2
Y	1415	HIS	-	expression tag	UNP C3SIA2
Y	1416	HIS	-	expression tag	UNP C3SIA2

- Molecule 7 is a DNA chain called ntDNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	K	25	515	244	98	148	25	0	0

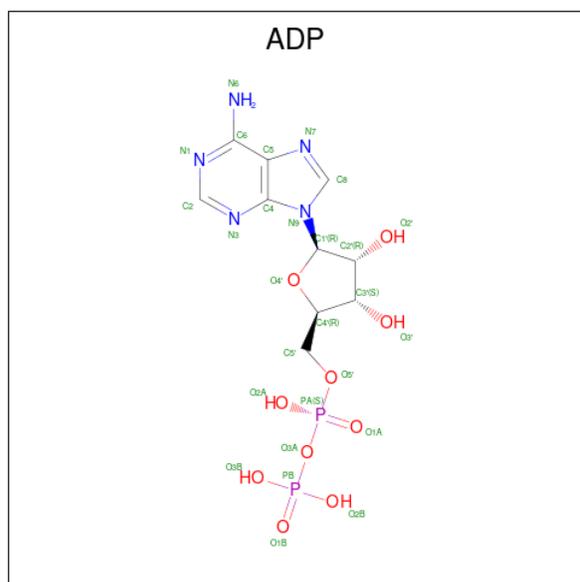
- Molecule 8 is a DNA chain called tDNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	L	34	682	325	122	202	33	0	0

- Molecule 9 is a RNA chain called rut RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	R	28	590	264	103	195	28	0	0

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



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
10	a	1	27	10	5	10	2	0
10	b	1	27	10	5	10	2	0
10	c	1	27	10	5	10	2	0
10	d	1	27	10	5	10	2	0
10	e	1	27	10	5	10	2	0

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

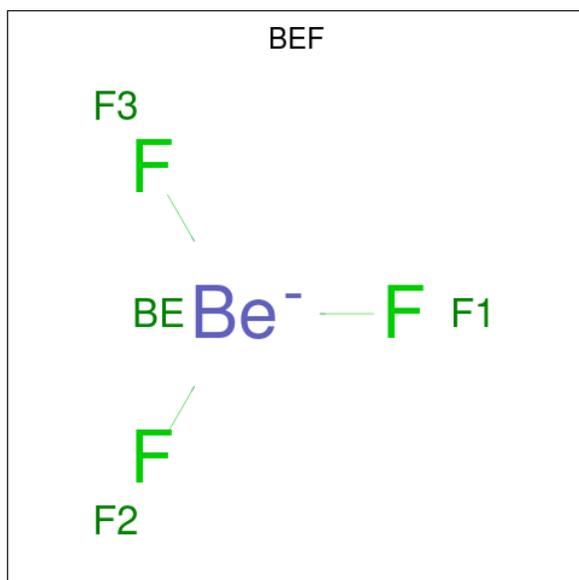
Mol	Chain	Residues	Atoms		AltConf
11	a	1	Total	Mg	0
			1	1	
11	b	1	Total	Mg	0
			1	1	
11	c	1	Total	Mg	0
			1	1	
11	d	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
11	e	1	Total	Mg	0
			1	1	
11	Y	1	Total	Mg	0
			1	1	

- Molecule 12 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF₃).



Mol	Chain	Residues	Atoms			AltConf
12	a	1	Total	Be	F	0
			4	1	3	
12	b	1	Total	Be	F	0
			4	1	3	
12	c	1	Total	Be	F	0
			4	1	3	
12	c	1	Total	Be	F	0
			4	1	3	
12	e	1	Total	Be	F	0
			4	1	3	

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	Y	2	Total	Zn	0
			2	2	

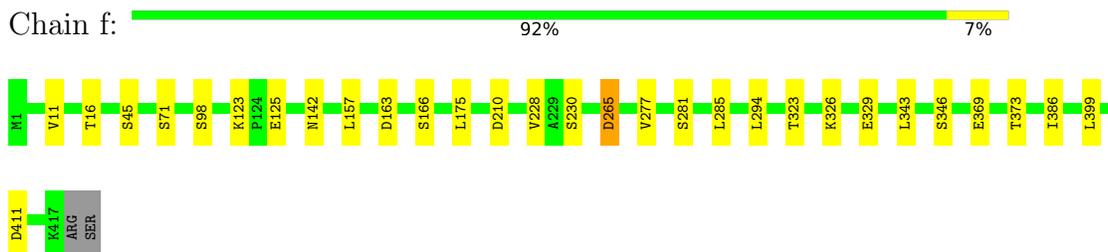
- Molecule 14 is water.

Mol	Chain	Residues	Atoms	AltConf
14	a	3	Total O 3 3	0
14	b	3	Total O 3 3	0
14	c	3	Total O 3 3	0
14	d	3	Total O 3 3	0
14	e	3	Total O 3 3	0

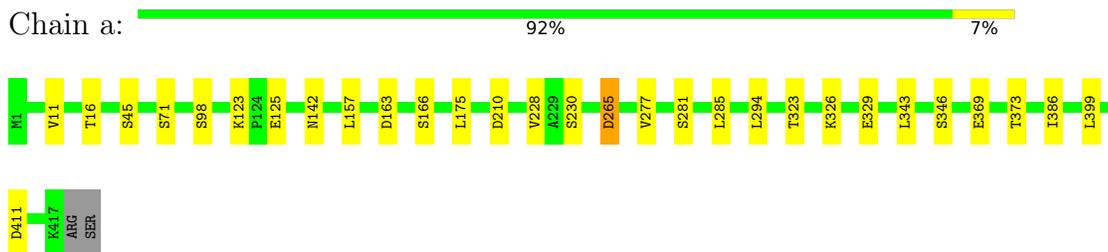
3 Residue-property plots [i](#)

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

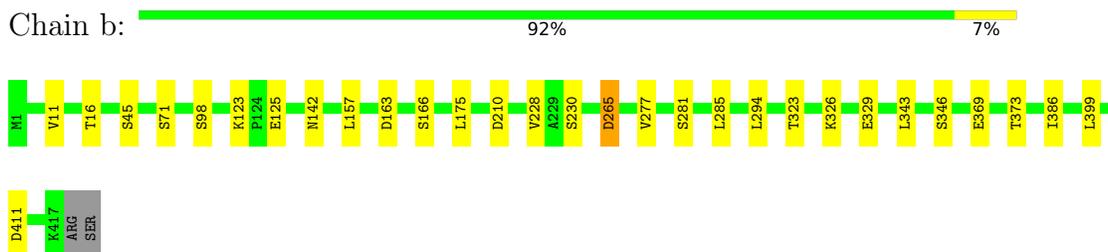
- Molecule 1: Transcription termination factor Rho



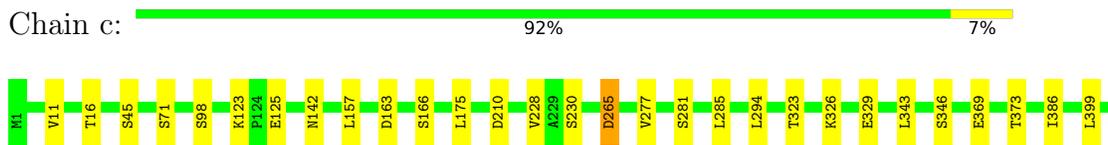
- Molecule 1: Transcription termination factor Rho



- Molecule 1: Transcription termination factor Rho



- Molecule 1: Transcription termination factor Rho





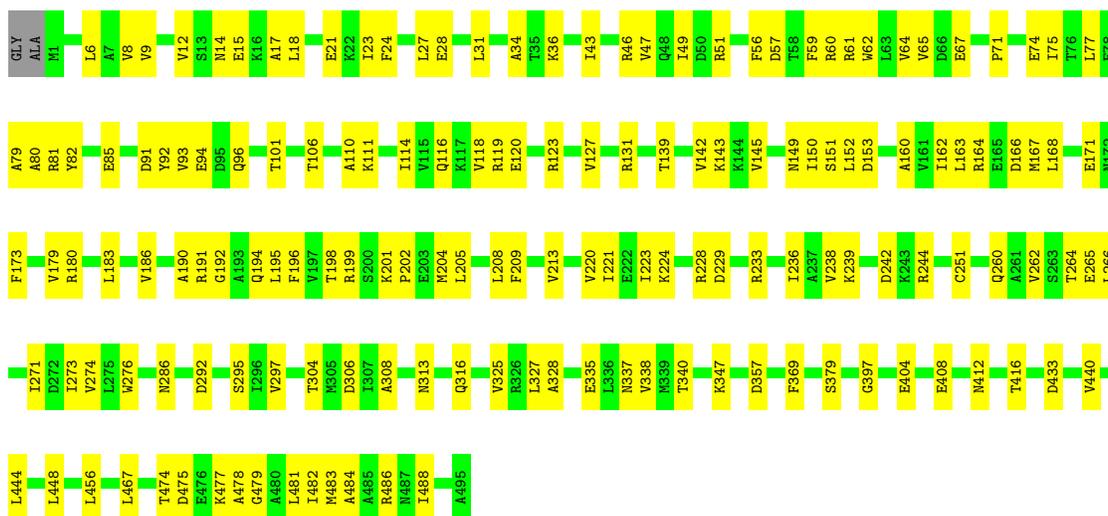
• Molecule 1: Transcription termination factor Rho



• Molecule 1: Transcription termination factor Rho

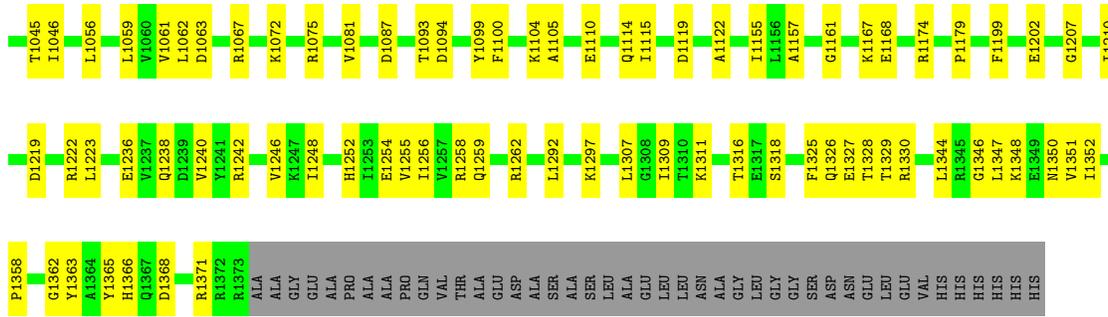


• Molecule 2: Transcription termination/antitermination protein NusA



• Molecule 3: DNA-directed RNA polymerase subunit alpha





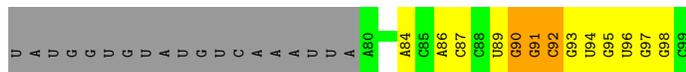
• Molecule 7: ntDNA



• Molecule 8: tDNA



• Molecule 9: rut RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	64696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	8000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k 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: ZN, 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	0/3329	0.47	1/4483 (0.0%)
1	b	0.26	0/3329	0.47	1/4483 (0.0%)
1	c	0.26	0/3329	0.47	1/4483 (0.0%)
1	d	0.26	0/3329	0.47	1/4483 (0.0%)
1	e	0.26	0/3329	0.47	1/4483 (0.0%)
1	f	0.26	0/3329	0.47	1/4483 (0.0%)
2	A	0.23	0/3897	0.43	0/5273
3	U	0.23	0/1847	0.43	0/2503
3	V	0.23	0/2538	0.44	0/3441
4	W	0.22	0/629	0.38	0/847
5	X	0.25	0/10736	0.42	0/14487
6	Y	0.24	0/10706	0.42	0/14456
7	K	0.54	0/577	0.93	0/886
8	L	0.53	0/762	0.91	0/1171
9	R	1.12	1/656 (0.2%)	1.11	2/1016 (0.2%)
All	All	0.29	1/52322 (0.0%)	0.48	8/70978 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	R	24	U	C4'-O4'	27.96	1.81	1.45

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	R	24	U	C1'-O4'-C4'	-22.31	92.05	109.90
9	R	24	U	C5'-C4'-O4'	-10.08	97.00	109.10
1	d	265	ASP	CB-CG-OD1	7.73	125.25	118.30
1	e	265	ASP	CB-CG-OD1	7.71	125.23	118.30
1	a	265	ASP	CB-CG-OD1	7.68	125.21	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	3280	0	3358	0	0
1	b	3280	0	3358	0	0
1	c	3280	0	3357	0	0
1	d	3280	0	3358	0	0
1	e	3280	0	3358	0	0
1	f	3280	0	3359	0	0
2	A	3852	0	3835	110	0
3	U	1825	0	1853	53	0
3	V	2504	0	2558	59	0
4	W	627	0	634	12	0
5	X	10567	0	10585	260	0
6	Y	10545	0	10762	245	0
7	K	515	0	282	11	0
8	L	682	0	382	19	0
9	R	590	0	304	23	0
10	a	27	0	12	0	0
10	b	27	0	12	0	0
10	c	27	0	12	0	0
10	d	27	0	12	0	0
10	e	27	0	12	0	0
11	Y	1	0	0	0	0
11	a	1	0	0	0	0
11	b	1	0	0	0	0
11	c	1	0	0	0	0
11	d	1	0	0	0	0
11	e	1	0	0	0	0
12	a	4	0	0	0	0
12	b	4	0	0	0	0
12	c	8	0	0	0	0
12	e	4	0	0	0	0
13	Y	2	0	0	0	0
14	a	3	0	0	0	0
14	b	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	c	3	0	0	0	0
14	d	3	0	0	0	0
14	e	3	0	0	0	0
All	All	51565	0	51403	743	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 13.

The worst 5 of 743 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)
9:R:24:U:C4'	9:R:24:U:O4'	1.81	1.24
6:Y:346:ARG:HE	9:R:90:G:H22	1.21	0.84
5:X:618:GLN:HB3	5:X:621:SER:HB3	1.64	0.79
6:Y:362:ARG:H	6:Y:365:GLN:HE21	1.29	0.78
2:A:14:ASN:HB3	2:A:17:ALA:HB3	1.65	0.77

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 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	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	b	415/419 (99%)	403 (97%)	12 (3%)	0	100	100
1	c	415/419 (99%)	403 (97%)	12 (3%)	0	100	100
1	d	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	e	415/419 (99%)	403 (97%)	12 (3%)	0	100	100
1	f	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
2	A	493/497 (99%)	459 (93%)	34 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	U	233/329 (71%)	217 (93%)	16 (7%)	0	100	100
3	V	319/329 (97%)	294 (92%)	25 (8%)	0	100	100
4	W	77/91 (85%)	76 (99%)	1 (1%)	0	100	100
5	X	1338/1342 (100%)	1256 (94%)	82 (6%)	0	100	100
6	Y	1356/1416 (96%)	1297 (96%)	59 (4%)	0	100	100
All	All	6306/6518 (97%)	6014 (95%)	292 (5%)	0	100	100

There are no Ramachandran outliers to report.

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 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	357/359 (99%)	327 (92%)	30 (8%)	9	31
1	b	357/359 (99%)	327 (92%)	30 (8%)	9	31
1	c	357/359 (99%)	327 (92%)	30 (8%)	9	31
1	d	357/359 (99%)	327 (92%)	30 (8%)	9	31
1	e	357/359 (99%)	327 (92%)	30 (8%)	9	31
1	f	357/359 (99%)	327 (92%)	30 (8%)	9	31
2	A	409/409 (100%)	408 (100%)	1 (0%)	92	93
3	U	203/286 (71%)	203 (100%)	0	100	100
3	V	280/286 (98%)	280 (100%)	0	100	100
4	W	67/75 (89%)	67 (100%)	0	100	100
5	X	1155/1157 (100%)	1154 (100%)	1 (0%)	92	94
6	Y	1134/1177 (96%)	1133 (100%)	1 (0%)	92	94
All	All	5390/5544 (97%)	5207 (97%)	183 (3%)	34	54

5 of 183 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	c	369	GLU
1	d	343	LEU
1	c	411	ASP
1	d	166	SER
1	e	11	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	321	ASN
5	X	808	ASN
6	Y	1367	GLN
6	Y	792	ASN
3	V	37	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	R	26/99 (26%)	9 (34%)	0

5 of 9 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	R	24	U
9	R	25	C
9	R	26	C
9	R	84	A
9	R	86	A

There are no RNA pucker outliers to report.

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 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 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
10	ADP	d	1000	11	24,29,29	0.96	1 (4%)	29,45,45	1.48	4 (13%)
12	BEF	c	504	-	0,3,3	-	-	-	-	-
12	BEF	e	1002	-	0,3,3	-	-	-	-	-
12	BEF	a	1002	-	0,3,3	-	-	-	-	-
12	BEF	b	1002	-	0,3,3	-	-	-	-	-
10	ADP	e	1000	1,11	24,29,29	0.96	1 (4%)	29,45,45	1.47	5 (17%)
12	BEF	c	503	-	0,3,3	-	-	-	-	-
10	ADP	b	1000	11	24,29,29	0.96	1 (4%)	29,45,45	1.49	4 (13%)
10	ADP	a	1000	11	24,29,29	0.96	1 (4%)	29,45,45	1.44	4 (13%)
10	ADP	c	501	1,11	24,29,29	0.95	1 (4%)	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
10	ADP	d	1000	11	-	1/12/32/32	0/3/3/3
10	ADP	e	1000	1,11	-	2/12/32/32	0/3/3/3
10	ADP	b	1000	11	-	3/12/32/32	0/3/3/3
10	ADP	a	1000	11	-	5/12/32/32	0/3/3/3
10	ADP	c	501	1,11	-	4/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	d	1000	ADP	C5-C4	2.51	1.47	1.40
10	b	1000	ADP	C5-C4	2.49	1.47	1.40
10	c	501	ADP	C5-C4	2.47	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	a	1000	ADP	C5-C4	2.43	1.47	1.40
10	e	1000	ADP	C5-C4	2.41	1.47	1.40

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	d	1000	ADP	PA-O3A-PB	-3.70	120.15	132.83
10	b	1000	ADP	PA-O3A-PB	-3.68	120.19	132.83
10	a	1000	ADP	PA-O3A-PB	-3.57	120.58	132.83
10	c	501	ADP	PA-O3A-PB	-3.45	120.97	132.83
10	b	1000	ADP	C3'-C2'-C1'	3.40	106.09	100.98

There are no chirality outliers.

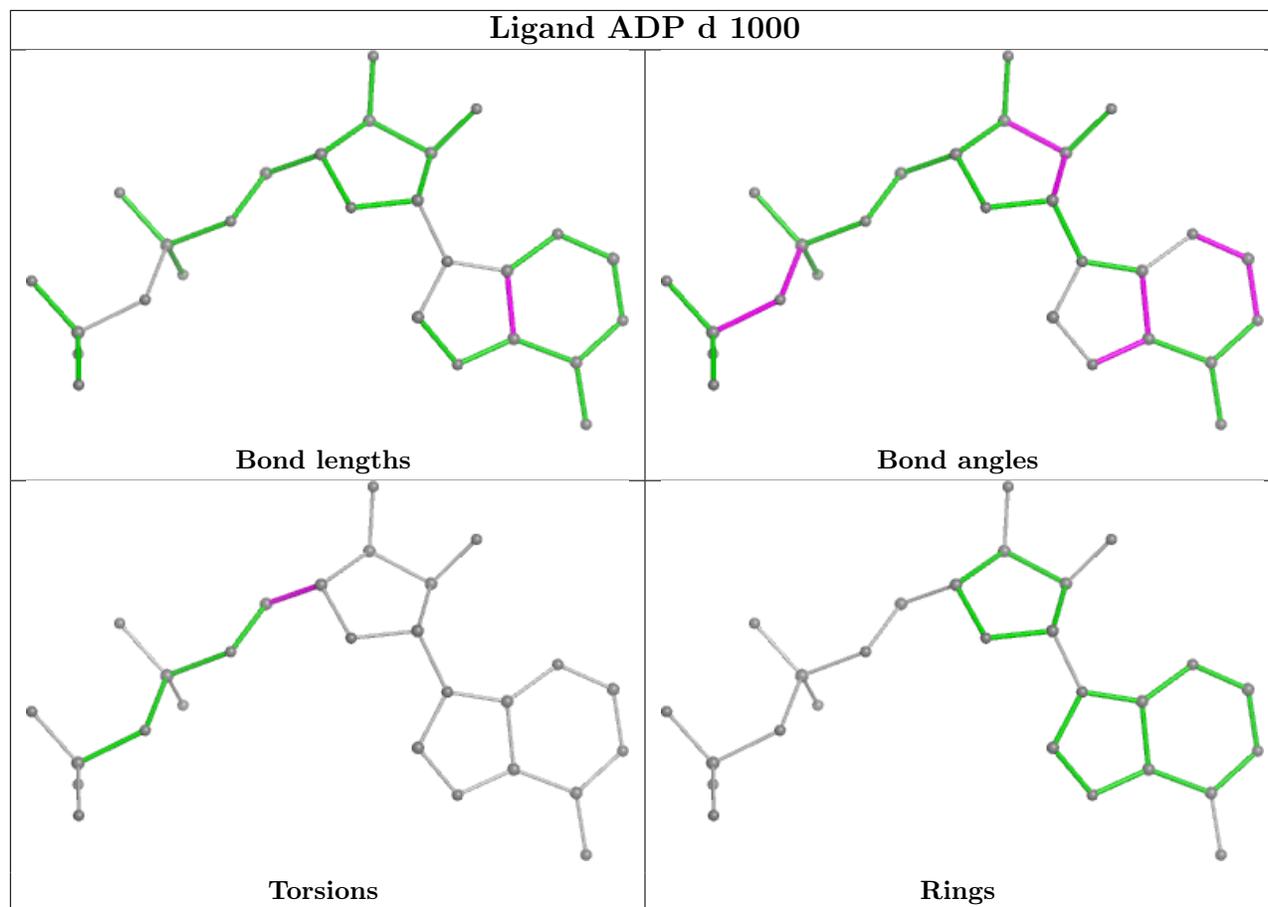
5 of 15 torsion outliers are listed below:

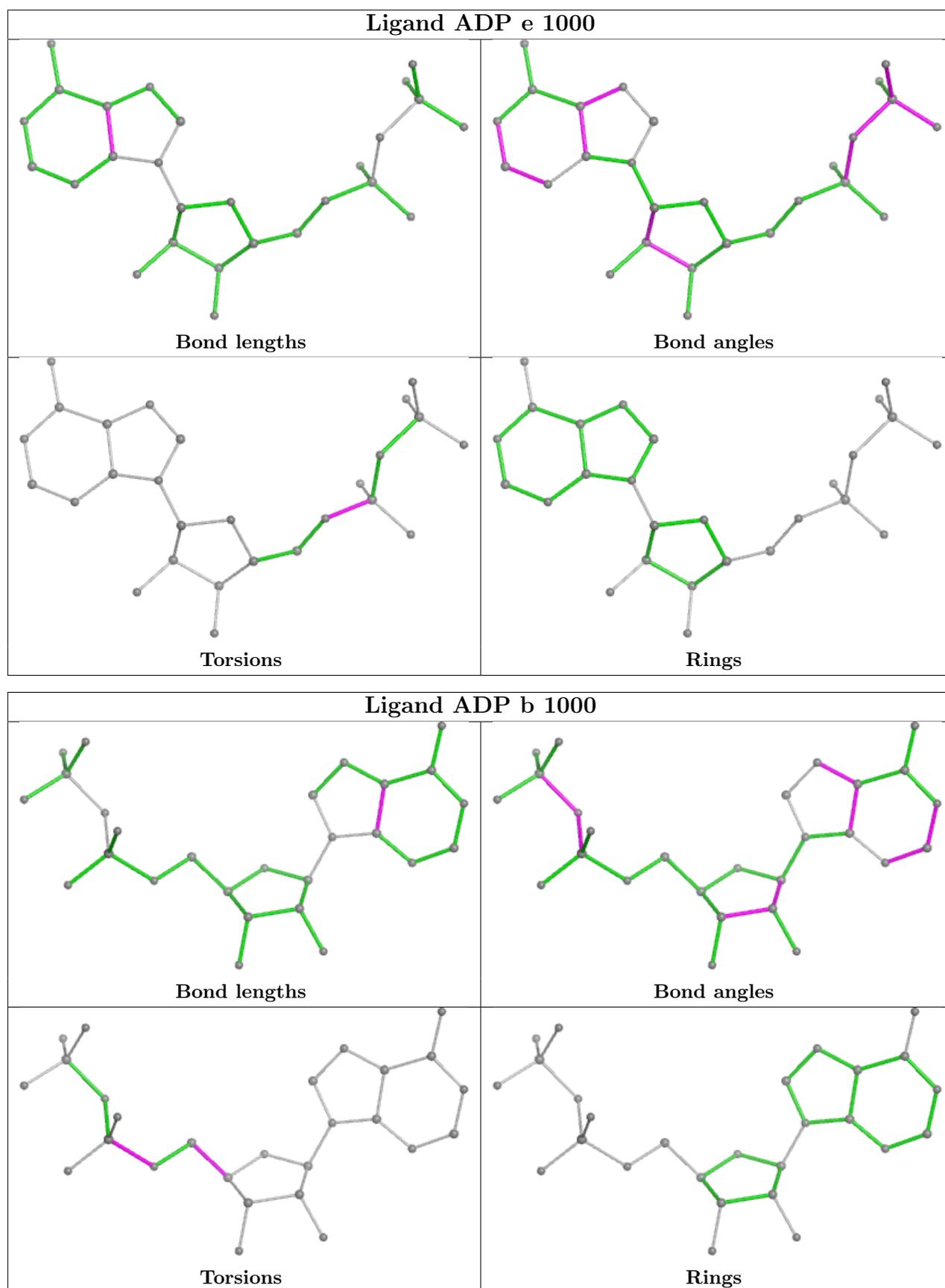
Mol	Chain	Res	Type	Atoms
10	a	1000	ADP	PA-O3A-PB-O3B
10	b	1000	ADP	C5'-O5'-PA-O3A
10	c	501	ADP	O4'-C4'-C5'-O5'
10	c	501	ADP	C3'-C4'-C5'-O5'
10	a	1000	ADP	O4'-C4'-C5'-O5'

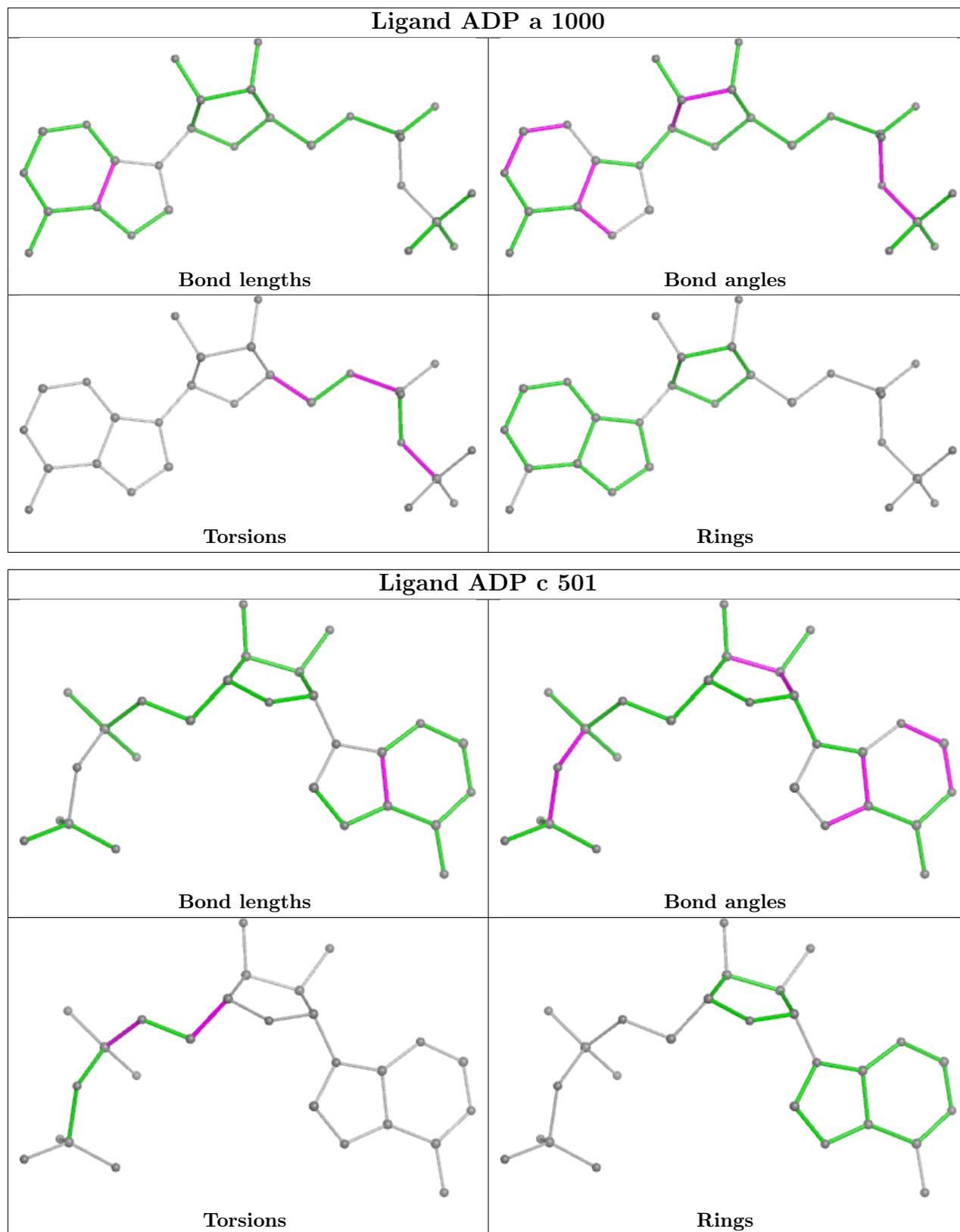
There are no ring outliers.

No monomer is involved in short contacts.

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

This section contains visualisations of the EMDB entry EMD-11723. 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 standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 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.