



Full wwPDB EM Validation Report ⓘ

Mar 3, 2025 – 12:16 pm GMT

PDB ID : 9FZQ
EMDB ID : EMD-50894
Title : Proton conductance by human uncoupling protein 1 is inhibited by both purine and pyrimidine nucleotides
Authors : Jones, S.A.; Sowton, A.P.; Lacabanne, D.; King, M.S.; Palmer, S.M.; Zogg, T.; Pardon, E.; Steyaert, J.; Ruprecht, J.J.; Kunji, E.R.S.
Deposited on : 2024-07-05
Resolution : 3.03 Å(reported)

This is a Full wwPDB EM Validation 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 : **FAILED**
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) : 2.41

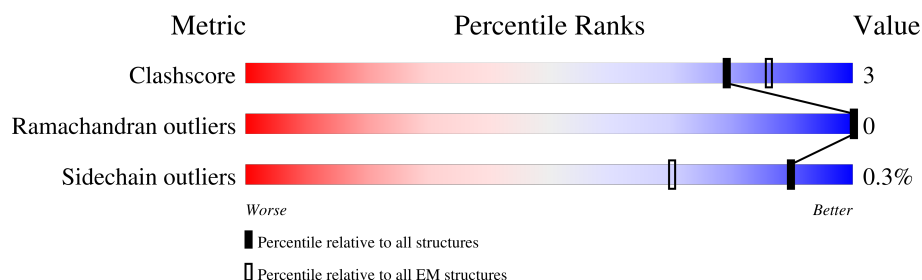
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.03 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

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	310	 87% 6% 7%
2	B	124	 95% 5%
3	C	128	 95% 5% •

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4088 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 Mitochondrial brown fat uncoupling protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	289	Total	C	N	O	S	0	0
			2164	1391	368	392	13		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	THR	-	expression tag	UNP P25874
A	-1	SER	-	expression tag	UNP P25874
A	0	GLU	-	expression tag	UNP P25874
A	1	ASP	-	expression tag	UNP P25874

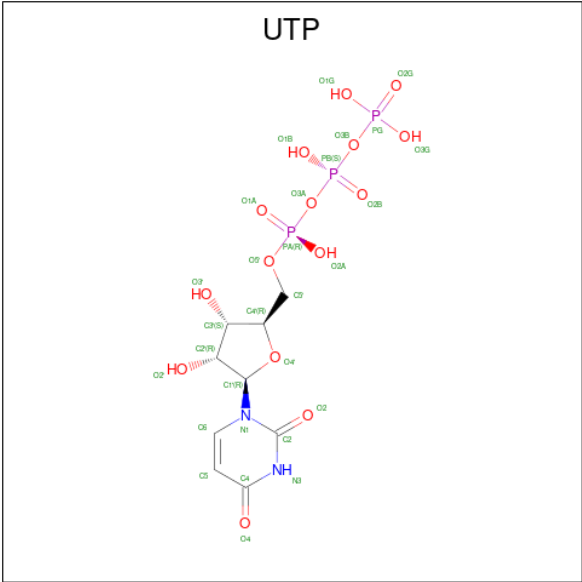
- Molecule 2 is a protein called CA9871.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	124	Total	C	N	O	S	0	0
			934	587	160	183	4		

- Molecule 3 is a protein called CA9865.

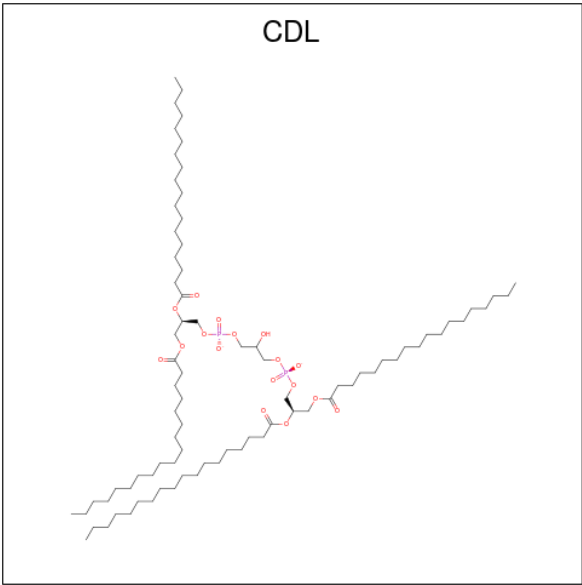
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	127	Total	C	N	O	S	0	0
			868	562	147	155	4		

- Molecule 4 is URIDINE 5'-TRIPHOSPHATE (three-letter code: UTP) (formula: C₉H₁₅N₂O₁₅P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			29	9	2	15	3	

- Molecule 5 is CARDIOLIPIN (three-letter code: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).

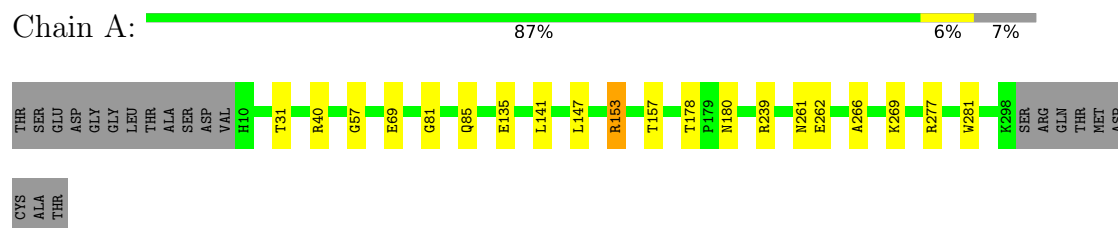


Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	O	P	0
			26	17	8	1	
5	A	1	Total	C	O	P	0
			26	13	11	2	
5	A	1	Total	C	O	P	0
			41	23	16	2	

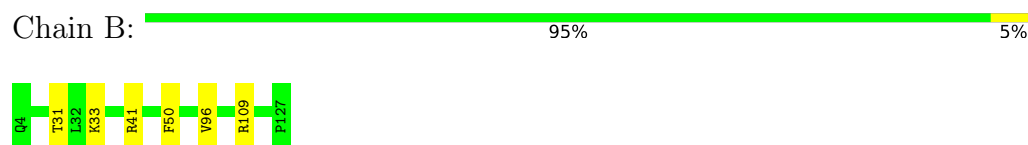
3 Residue-property plots [i](#)

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.

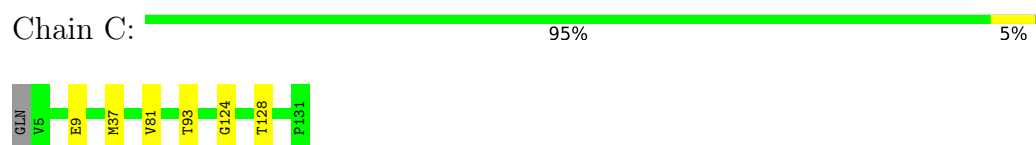
- Molecule 1: Mitochondrial brown fat uncoupling protein 1



- Molecule 2: CA9871



- Molecule 3: CA9865



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	705820	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
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: UTP, CDL

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	0.38	0/2206	0.56	0/2999
2	B	0.40	0/958	0.58	0/1303
3	C	0.31	0/894	0.49	0/1230
All	All	0.37	0/4058	0.55	0/5532

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	153	ARG	Sidechain

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	2164	0	2216	14	0
2	B	934	0	868	4	0
3	C	868	0	732	3	0
4	A	29	0	11	1	0
5	A	93	0	75	4	0
All	All	4088	0	3902	21	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 3.

All (21) 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:135:GLU:OE1	1:A:180:ASN:ND2	2.24	0.70
3:C:37:MET:HG3	3:C:81:VAL:HG21	1.80	0.62
1:A:262:GLU:OE1	1:A:269:LYS:NZ	2.26	0.61
2:B:31:THR:HG22	2:B:33:LYS:HG2	1.83	0.61
1:A:31:THR:OG1	1:A:277:ARG:NH1	2.38	0.57
1:A:40:ARG:NH1	1:A:69:GLU:OE1	2.39	0.55
1:A:178:THR:HG23	5:A:404:CDL:H512	1.93	0.50
1:A:239:ARG:NH1	1:A:262:GLU:OE2	2.39	0.49
1:A:141:LEU:HD11	1:A:157:THR:HA	1.95	0.49
3:C:9:GLU:CD	3:C:124:GLY:H	2.19	0.46
1:A:261:ASN:OD1	1:A:262:GLU:N	2.49	0.46
1:A:262:GLU:HB3	1:A:266:ALA:HB2	2.00	0.44
1:A:147:LEU:HA	2:B:109:ARG:HG3	2.01	0.43
1:A:57:GLY:H	5:A:403:CDL:HB21	1.84	0.43
1:A:281:TRP:CE2	4:A:401:UTP:H5'1	2.54	0.43
5:A:402:CDL:H111	5:A:402:CDL:H141	1.91	0.42
2:B:50:PHE:CE2	2:B:109:ARG:HG2	2.55	0.42
3:C:93:THR:HG23	3:C:128:THR:HA	2.03	0.41
1:A:81:GLY:O	1:A:85:GLN:HG2	2.20	0.41
1:A:57:GLY:HA2	5:A:403:CDL:CA2	2.51	0.40
2:B:41:ARG:HA	2:B:96:VAL:O	2.20	0.40

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	287/310 (93%)	284 (99%)	3 (1%)	0	100	100
2	B	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
3	C	125/128 (98%)	125 (100%)	0	0	100	100
All	All	534/562 (95%)	530 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	232/258 (90%)	231 (100%)	1 (0%)	89	94
2	B	94/97 (97%)	94 (100%)	0	100	100
3	C	66/102 (65%)	66 (100%)	0	100	100
All	All	392/457 (86%)	391 (100%)	1 (0%)	90	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ARG

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

Mol	Chain	Res	Type
1	A	148	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	CDL	A	403	-	25,25,99	0.58	0	28,32,111	0.46	0
5	CDL	A	402	-	25,25,99	0.52	0	29,30,111	0.73	2 (6%)
4	UTP	A	401	-	22,30,30	1.00	1 (4%)	27,47,47	1.01	1 (3%)
5	CDL	A	404	-	40,40,99	0.58	1 (2%)	45,51,111	0.39	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
5	CDL	A	403	-	-	18/29/29/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	CDL	A	402	-	-	13/27/27/110	-
4	UTP	A	401	-	-	8/20/38/38	0/2/2/2
5	CDL	A	404	-	-	23/49/49/110	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	UTP	C4-N3	2.95	1.38	1.33
5	A	404	CDL	PB2-OB4	-2.36	1.44	1.55

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	UTP	C5-C4-N3	-3.87	114.79	123.31
5	A	402	CDL	OA2-PA1-OA5	-2.31	100.59	106.73
5	A	402	CDL	OA4-PA1-OA5	2.00	112.07	106.73

There are no chirality outliers.

All (62) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	401	UTP	C5'-O5'-PA-O2A
4	A	401	UTP	O4'-C1'-N1-C6
4	A	401	UTP	C2'-C1'-N1-C6
5	A	403	CDL	O1-C1-CA2-OA2
5	A	403	CDL	CA2-OA2-PA1-OA3
5	A	403	CDL	CA2-OA2-PA1-OA4
5	A	403	CDL	CA2-OA2-PA1-OA5
5	A	403	CDL	CA3-OA5-PA1-OA4
5	A	403	CDL	CB2-OB2-PB2-OB3
5	A	403	CDL	CB3-OB5-PB2-OB2
5	A	403	CDL	CB3-OB5-PB2-OB3
5	A	403	CDL	CB3-OB5-PB2-OB4
5	A	403	CDL	OB5-CB3-CB4-OB6
5	A	404	CDL	CA2-C1-CB2-OB2
5	A	404	CDL	CA3-OA5-PA1-OA4
5	A	404	CDL	CB2-OB2-PB2-OB3
5	A	404	CDL	CB3-OB5-PB2-OB4
5	A	404	CDL	O1-C1-CA2-OA2
5	A	404	CDL	OA5-CA3-CA4-OA6

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Mol	Chain	Res	Type	Atoms
5	A	402	CDL	C11-CA5-OA6-CA4
5	A	402	CDL	C11-C12-C13-C14
5	A	403	CDL	CB2-C1-CA2-OA2
5	A	404	CDL	OA5-CA3-CA4-CA6
5	A	402	CDL	OA7-CA5-OA6-CA4
5	A	402	CDL	CA7-C31-C32-C33
5	A	403	CDL	CB5-C51-C52-C53
5	A	404	CDL	CA7-C31-C32-C33
5	A	404	CDL	O1-C1-CB2-OB2
5	A	404	CDL	CA3-OA5-PA1-OA2
5	A	404	CDL	CB3-OB5-PB2-OB2
5	A	404	CDL	C71-CB7-OB8-CB6
5	A	403	CDL	C1-CB2-OB2-PB2
5	A	404	CDL	OB9-CB7-OB8-CB6
5	A	404	CDL	C71-C72-C73-C74
5	A	404	CDL	C51-CB5-OB6-CB4
5	A	404	CDL	OB5-CB3-CB4-OB6
4	A	401	UTP	C3'-C4'-C5'-O5'
5	A	404	CDL	OB7-CB5-OB6-CB4
5	A	403	CDL	CB2-OB2-PB2-OB5
5	A	404	CDL	CB2-C1-CA2-OA2
5	A	402	CDL	C31-CA7-OA8-CA6
4	A	401	UTP	O4'-C4'-C5'-O5'
5	A	404	CDL	OB5-CB3-CB4-CB6
5	A	402	CDL	OA5-CA3-CA4-OA6
5	A	402	CDL	OA9-CA7-OA8-CA6
5	A	403	CDL	CB4-CB3-OB5-PB2
5	A	404	CDL	C1-CA2-OA2-PA1
5	A	404	CDL	C32-C33-C34-C35
5	A	402	CDL	C12-C13-C14-C15
4	A	401	UTP	C5'-O5'-PA-O3A
5	A	403	CDL	CB2-OB2-PB2-OB4
5	A	402	CDL	OA5-CA3-CA4-CA6
5	A	402	CDL	C34-C35-C36-C37
5	A	402	CDL	CA6-CA4-OA6-CA5
5	A	404	CDL	CB2-OB2-PB2-OB5
5	A	403	CDL	C52-C51-CB5-OB6
4	A	401	UTP	PA-O3A-PB-O1B
5	A	402	CDL	C12-C11-CA5-OA6
5	A	403	CDL	C51-C52-C53-C54
5	A	402	CDL	C12-C11-CA5-OA7
5	A	404	CDL	C31-C32-C33-C34

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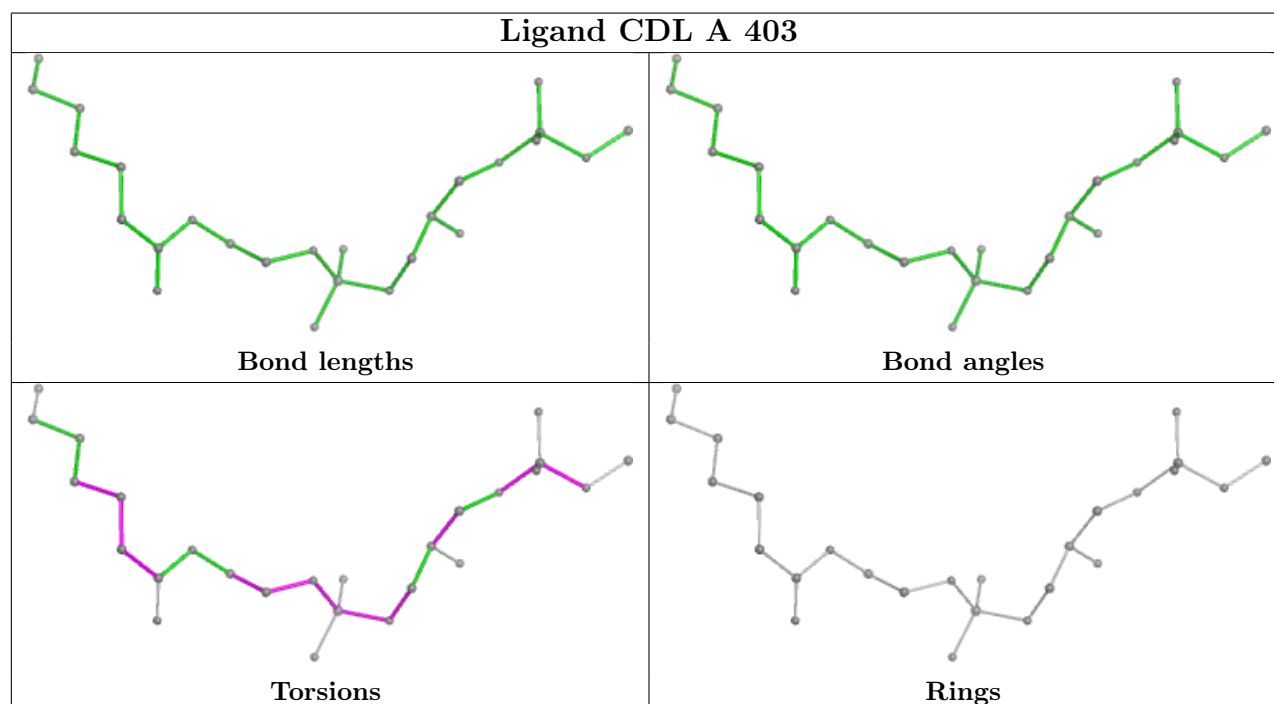
Mol	Chain	Res	Type	Atoms
4	A	401	UTP	C5'-O5'-PA-O1A

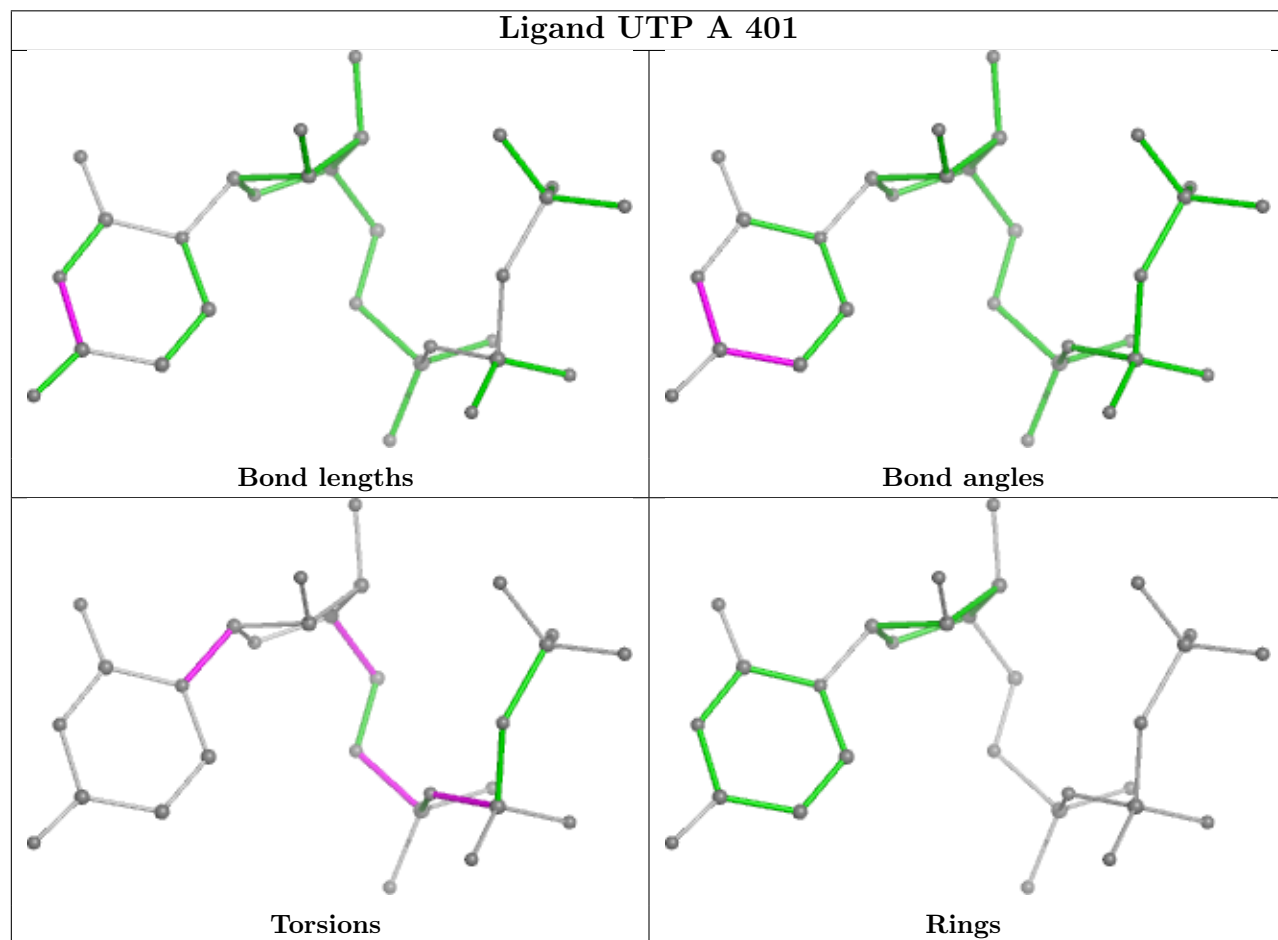
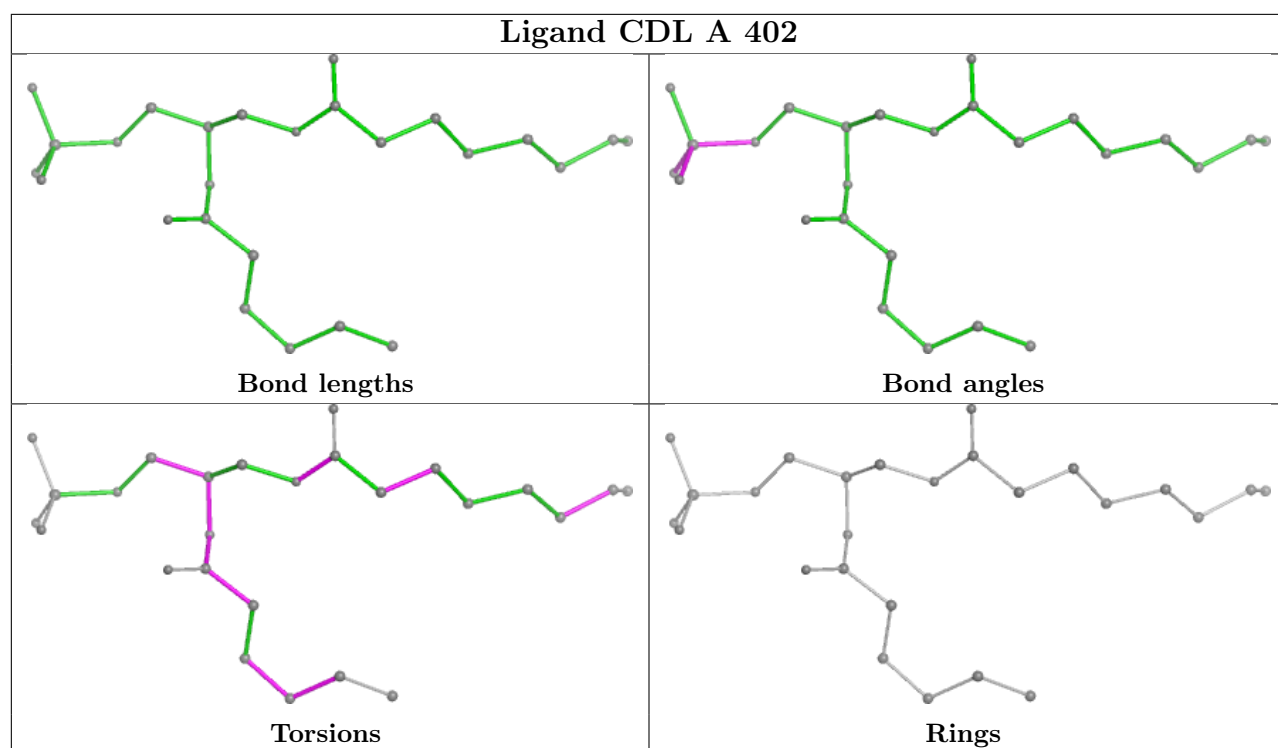
There are no ring outliers.

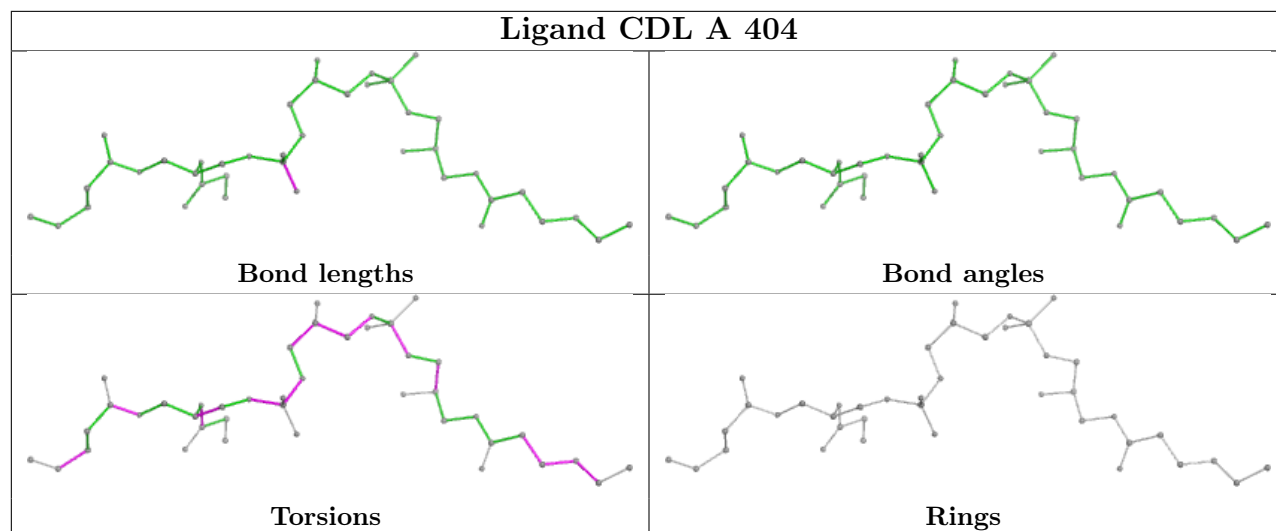
4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	403	CDL	2	0
5	A	402	CDL	1	0
4	A	401	UTP	1	0
5	A	404	CDL	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 [i](#)

There are no chain breaks in this entry.