Full wwPDB EM Validation Report (i)

May 14, 2024 – 05:04 pm BST

PDB ID	:	8ROX
EMDB ID	:	EMD-19406
Title	:	Structure of the human DDB1-DDA1-DCAF15 E3 ubiquitin ligase bound to compound furan 12
Authors	:	Shilliday, F.; Lucas, S.C.C.; Richter, M.; Michaelides, I.N.; Fusani, L.
Deposited on	:	2024-01-12
Resolution	:	3.30 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 (i) 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 (1)) were used in the production of this report:

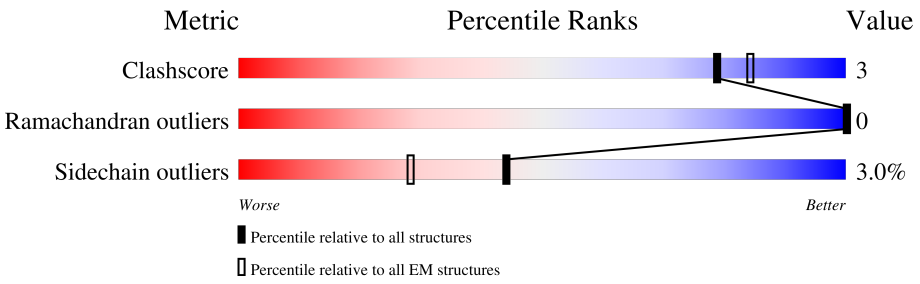
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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)	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 >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	603	50% · 47%
2	B	836	84% 6% 9%
3	D	102	49% · 49%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7249 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 DDB1- and CUL4-associated factor 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	322	2101	1355	350	386	10	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q66K64
A	-1	SER	-	expression tag	UNP Q66K64
A	0	HIS	-	expression tag	UNP Q66K64

- Molecule 2 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	760	4783	3056	837	879	11	0	0

There are 6 discrepancies between the modelled and reference sequences:

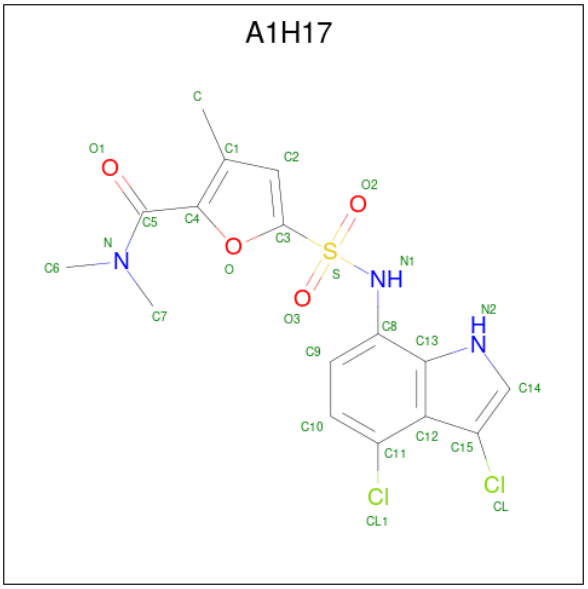
Chain	Residue	Modelled	Actual	Comment	Reference
B	700	GLY	-	linker	UNP Q16531
B	701	ASN	-	linker	UNP Q16531
B	702	GLY	-	linker	UNP Q16531
B	703	ASN	-	linker	UNP Q16531
B	704	SER	-	linker	UNP Q16531
B	705	GLY	-	linker	UNP Q16531

- Molecule 3 is a protein called DET1- and DDB1-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	D	52	339	224	54	61	0	0

- Molecule 4 is 5-[[3,4-bis(chloranyl)-1 {H}-indol-7-yl]sulfamoyl]- {N}, {N},3-trimethyl-fura

n-2-carboxamide;ethane (three-letter code: A1H17) (formula: $C_{16}H_{15}Cl_2N_3O_4S$) (labeled as "Ligand of Interest" by depositor).



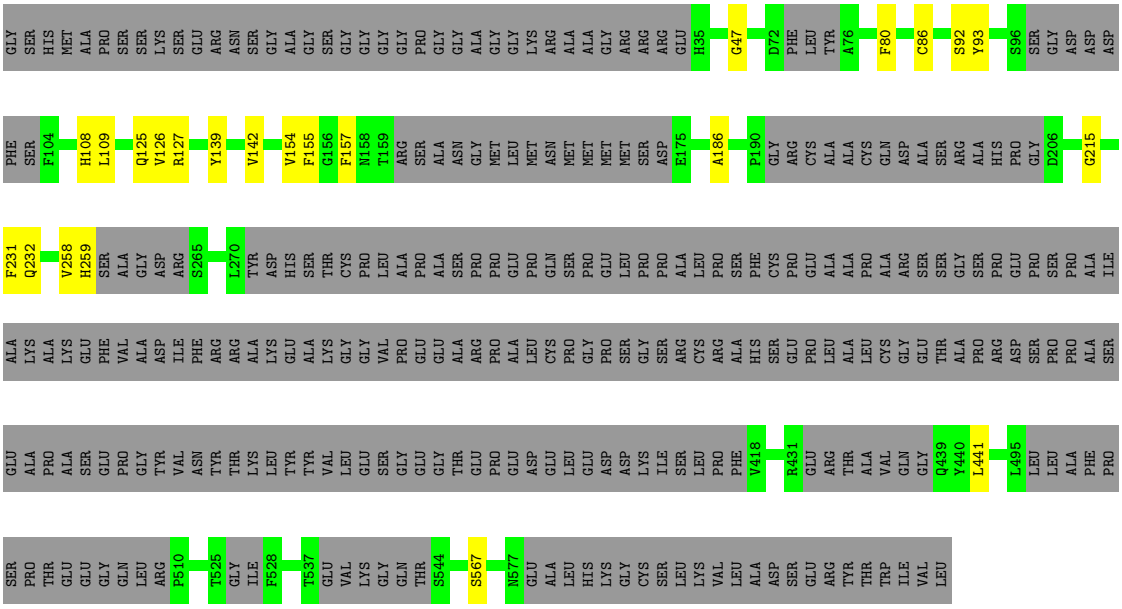
Mol	Chain	Residues	Atoms						AltConf
			Total	C	Cl	N	O	S	
4	A	1	26	16	2	3	4	1	0

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.

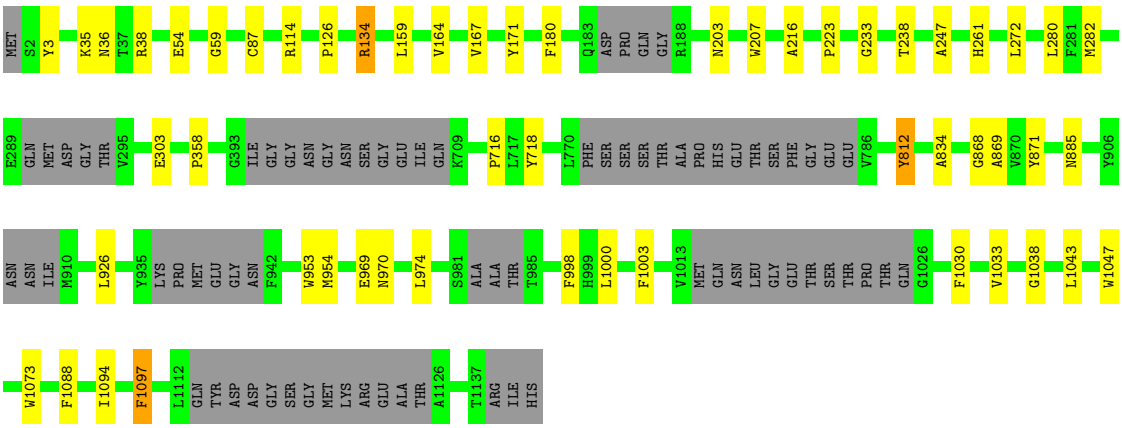
- Molecule 1: DDB1- and CUL4-associated factor 15

Chain A: 50% • 47%



- Molecule 2: DNA damage-binding protein 1

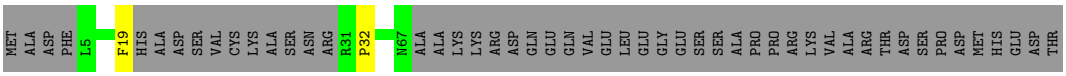
Chain B: 84% 6% 9%



- Molecule 3: DET1- and DDB1-associated protein 1

Chain D:

49%
49%


MET
ALA
ASP
PHE
L5
F19
HIS
ALA
ASP
SER
VAL
CYS
LYS
ALA
SER
ASN
ARG
R31
P32
N67
ALA
ALA
LYS
LYS
ARG
ASP
GLN
GLU
GLN
VAL
GLU
LEU
GLU
GLY
GLU
SER
SER
ALA
PRO
PRO
ARG
LYS
VAL
ALA
ARG
THR
ASP
SER
PRO
ASP
MET
HIS
GLU
ASP
THR

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	259210	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (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: A1H17

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	0/2150	0.53	0/2967
2	B	0.45	0/4876	0.53	0/6723
3	D	0.39	0/348	0.56	0/483
All	All	0.45	0/7374	0.53	0/10173

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
2	B	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
2	B	134	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	2101	0	1602	11	0
2	B	4783	0	3674	27	0
3	D	339	0	253	1	0
4	A	26	0	0	0	0
All	All	7249	0	5529	36	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 (36) 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)
2:B:868:GLY:HA3	2:B:885:ASN:HD21	1.45	0.81
1:A:258:VAL:HA	1:A:441:LEU:HA	1.80	0.62
2:B:868:GLY:HA3	2:B:885:ASN:ND2	2.17	0.57
2:B:954:MET:HA	2:B:969:GLU:HA	1.87	0.55
1:A:109:LEU:N	1:A:126:VAL:O	2.41	0.54
1:A:108:HIS:HA	1:A:127:ARG:HA	1.90	0.53
2:B:998:PHE:HB2	2:B:1088:PHE:CD1	2.44	0.52
1:A:142:VAL:HA	1:A:154:VAL:HA	1.92	0.52
2:B:216:ALA:HA	2:B:233:GLY:HA3	1.92	0.51
2:B:238:THR:HA	2:B:247:ALA:HA	1.93	0.51
2:B:358:PRO:HA	2:B:1033:VAL:HA	1.92	0.51
2:B:59:GLY:HA2	2:B:1073:TRP:CZ3	2.47	0.49
2:B:970:ASN:HA	2:B:1003:PHE:HE1	1.77	0.49
2:B:869:ALA:HB3	2:B:871:TYR:CE1	2.50	0.47
2:B:1094:ILE:O	2:B:1097:PHE:HB3	2.15	0.47
2:B:35:LYS:O	2:B:36:ASN:C	2.53	0.46
2:B:3:TYR:O	2:B:1043:LEU:N	2.47	0.46
1:A:80:PHE:HA	1:A:92:SER:HA	1.98	0.45
2:B:1030:PHE:CZ	2:B:1038:GLY:HA3	2.51	0.45
2:B:926:LEU:O	2:B:953:TRP:HA	2.17	0.45
2:B:126:PRO:HB3	2:B:171:TYR:CE1	2.53	0.44
1:A:186:ALA:HB3	1:A:215:GLY:HA2	2.00	0.43
2:B:35:LYS:O	2:B:38:ARG:N	2.51	0.43
2:B:261:HIS:HA	2:B:272:LEU:O	2.18	0.42
1:A:47:GLY:HA2	2:B:1003:PHE:CD2	2.54	0.42
2:B:974:LEU:HG	2:B:1000:LEU:HB2	2.01	0.42
2:B:716:PRO:HB2	2:B:718:TYR:CE1	2.54	0.42
2:B:812:TYR:O	2:B:834:ALA:N	2.50	0.42
2:B:282:MET:O	2:B:303:GLU:N	2.52	0.41
1:A:231:PHE:O	1:A:232:GLN:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:SER:HA	2:B:114:ARG:HA	2.03	0.41
2:B:171:TYR:CG	2:B:223:PRO:HA	2.56	0.41
1:A:109:LEU:O	1:A:125:GLN:HA	2.21	0.40
1:A:139:TYR:N	1:A:157:PHE:O	2.47	0.40
2:B:54:GLU:CB	3:D:32:PRO:HG2	2.51	0.40
2:B:167:VAL:HG12	2:B:180:PHE:HB3	2.02	0.40

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	300/603 (50%)	280 (93%)	20 (7%)	0	100	100
2	B	740/836 (88%)	706 (95%)	34 (5%)	0	100	100
3	D	48/102 (47%)	47 (98%)	1 (2%)	0	100	100
All	All	1088/1541 (71%)	1033 (95%)	55 (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	161/516 (31%)	157 (98%)	4 (2%)	47	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	318/727 (44%)	308 (97%)	10 (3%)	40	67
3	D	24/93 (26%)	23 (96%)	1 (4%)	30	60
All	All	503/1336 (38%)	488 (97%)	15 (3%)	44	68

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	CYS
1	A	93	TYR
1	A	155	PHE
1	A	259	HIS
2	B	87	CYS
2	B	134	ARG
2	B	159	LEU
2	B	164	VAL
2	B	203	ASN
2	B	207	TRP
2	B	280	LEU
2	B	812	TYR
2	B	1047	TRP
2	B	1097	PHE
3	D	19	PHE

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

Mol	Chain	Res	Type
2	B	885	ASN

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)

1 ligand is 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	$\#\|Z\| > 2$
4	A1H17	A	701	-	22,28,28	1.75	2 (9%)	24,43,43	2.07	3 (12%)

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
4	A1H17	A	701	-	-	1/9/19/19	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	701	A1H17	C3-S	-7.56	1.64	1.76
4	A	701	A1H17	C11-C12	-2.23	1.39	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	701	A1H17	C3-S-N1	-8.35	97.52	107.27
4	A	701	A1H17	O3-S-C3	4.10	114.41	107.66
4	A	701	A1H17	C13-C8-N1	3.10	119.90	115.50

There are no chirality outliers.

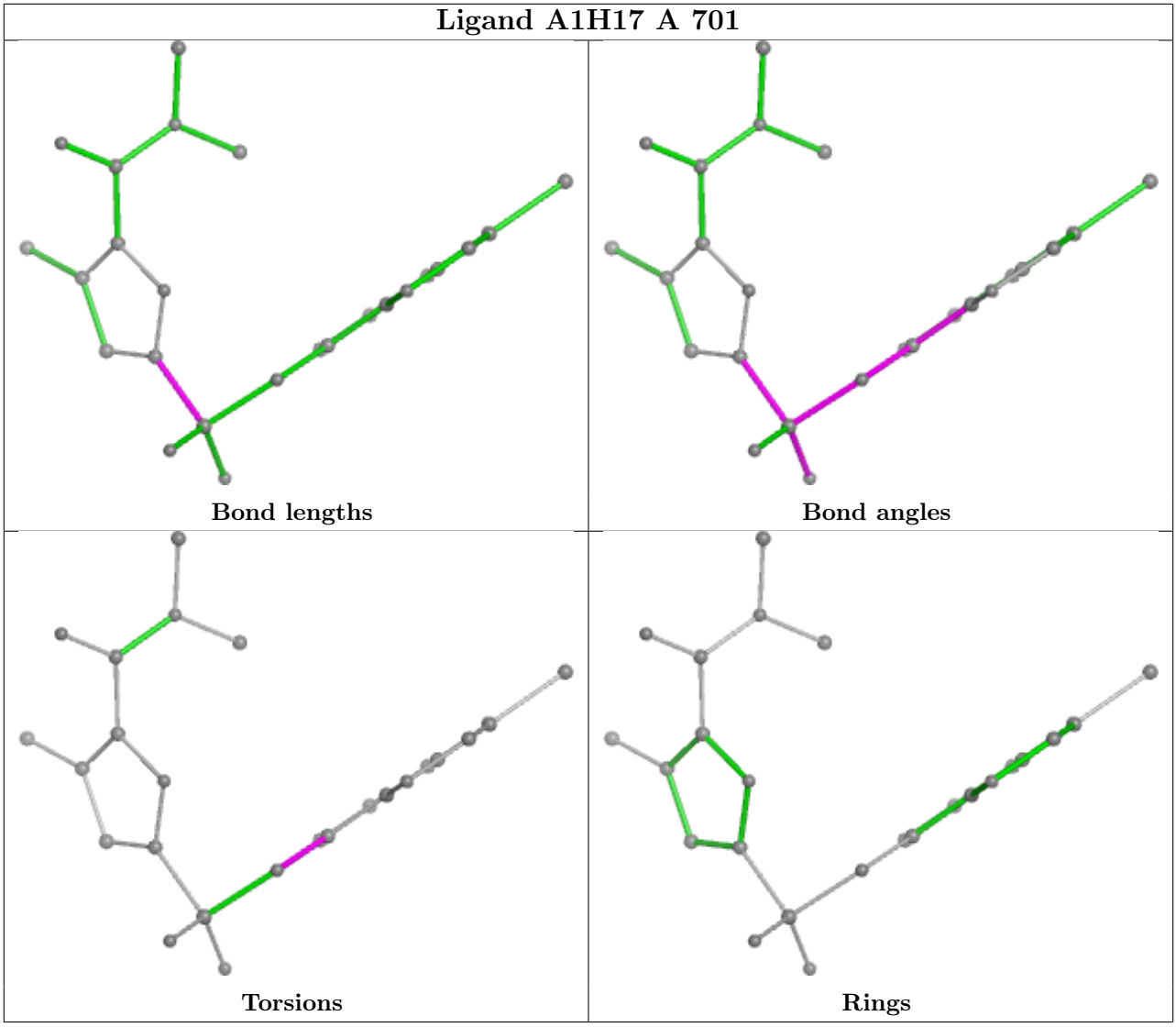
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	701	A1H17	C9-C8-N1-S

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 then 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 (i)

This section contains visualisations of the EMDB entry EMD-19406. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

This section was not generated.

6.2 Central slices (i)

This section was not generated.

6.3 Largest variance slices (i)

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color) (i)

This section was not generated.

6.5 Orthogonal surface views (i)

This section was not generated.

6.6 Mask visualisation (i)

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

7 Map analysis (i)

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

7.1 Map-value distribution (i)

This section was not generated.

7.2 Volume estimate versus contour level (i)

This section was not generated.

7.3 Rotationally averaged power spectrum (i)

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

8 Fourier-Shell correlation (i)

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

9 Map-model fit (i)

This section was not generated.