



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 11:54 PM UTC

PDB ID : 6IFR / pdb_00006ifr
EMDB ID : EMD-9656
Title : Type III-A Csm complex, Cryo-EM structure of Csm-NTR, ATP bound
Authors : You, L.; Ma, J.; Wang, J.; Zhang, X.; Wang, Y.
Deposited on : 2018-09-21
Resolution : 3.40 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

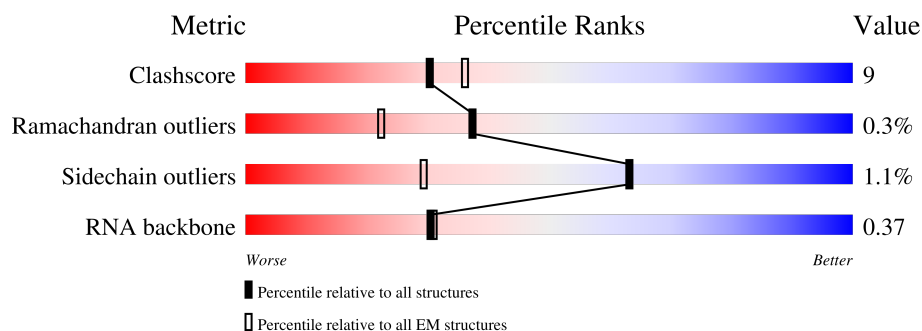
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	758	73% 18% 8%
2	C	126	79% 17% .
2	D	126	79% 17% .
3	E	220	68% 24% . 7%
3	F	220	73% 25% ..
3	G	220	67% 28% ..
4	B	299	76% 20% .

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Mol	Chain	Length	Quality of chain
5	H	357	80% 19%
6	N	36	42% 50% 6%
7	J	43	40% 37% 5% 19%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 19219 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 Type III-A CRISPR-associated protein Csm1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	694	Total	C	N	O	S	0	0
			5549	3569	930	1036	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ASN	ASP	engineered mutation	UNP A0A2U2M0F3

- Molecule 2 is a protein called Type III-A CRISPR-associated protein Csm2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	121	Total	C	N	O	S	0	0
			995	642	166	185	2		
2	C	121	Total	C	N	O	S	0	0
			995	642	166	185	2		

- Molecule 3 is a protein called Type III-A CRISPR-associated RAMP protein Csm3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	217	Total	C	N	O	S	0	0
			1703	1079	291	331	2		
3	F	217	Total	C	N	O	S	0	0
			1695	1075	291	327	2		
3	E	205	Total	C	N	O	S	0	0
			1610	1024	277	307	2		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	33	ASN	ASP	engineered mutation	UNP A0A2U2M035
F	33	ASN	ASP	engineered mutation	UNP A0A2U2M035
E	33	ASN	ASP	engineered mutation	UNP A0A2U2M035

- Molecule 4 is a protein called Type III-A CRISPR-associated RAMP protein Csm4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	288	Total	C	N	O	S	0	0
			2289	1465	375	444	5		

- Molecule 5 is a protein called Type III-A CRISPR-associated RAMP protein Csm5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	353	Total	C	N	O	S	0	0
			2832	1824	487	514	7		

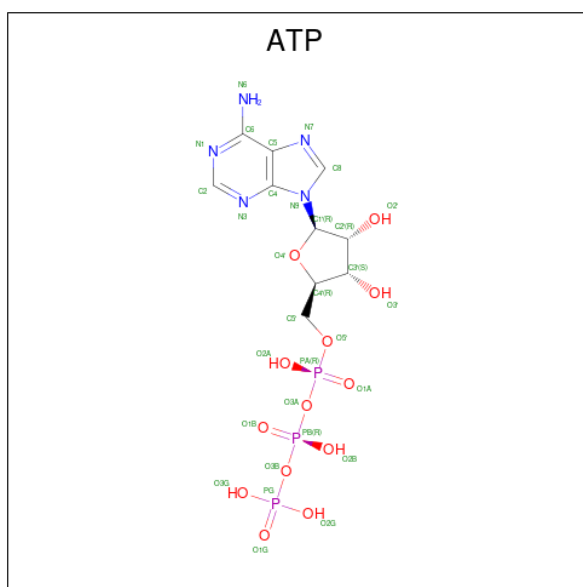
- Molecule 6 is a RNA chain called type III-A CRISPR-Cas interference complex, crRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	35	Total	C	N	O	P	0	0
			735	330	125	245	35		

- Molecule 7 is a RNA chain called type III-A CRISPR-Cas interference complex, NTR.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	35	Total	C	N	O	P	0	0
			752	336	138	243	35		

- Molecule 8 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
8	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

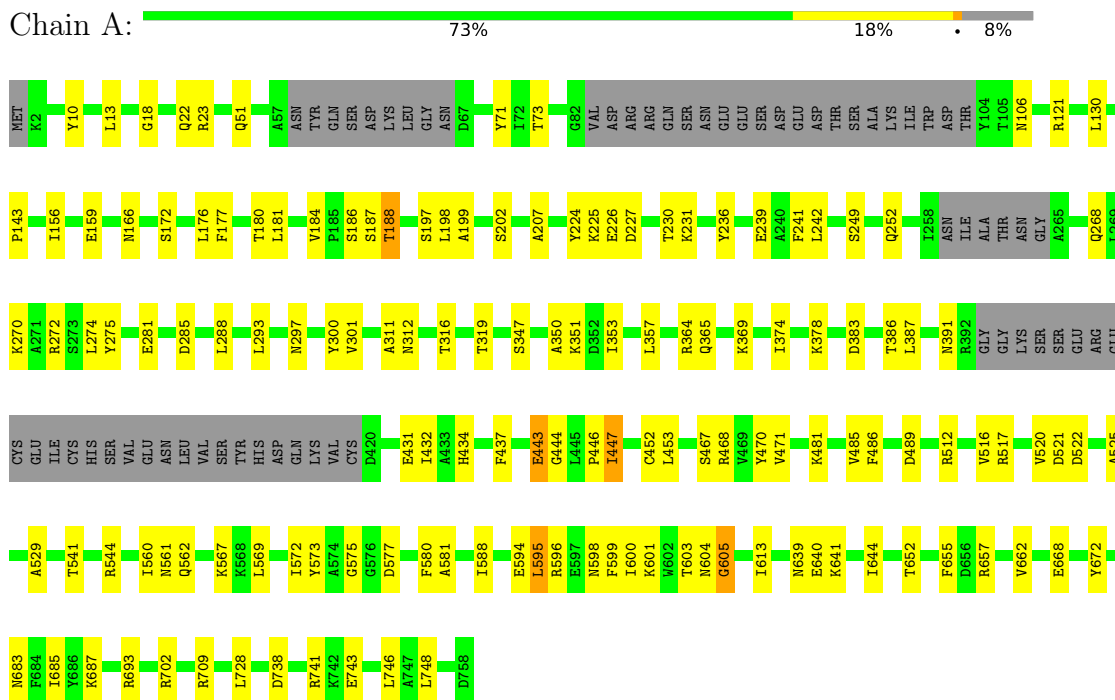
- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
9	A	2	Total	Mg	0
			2	2	

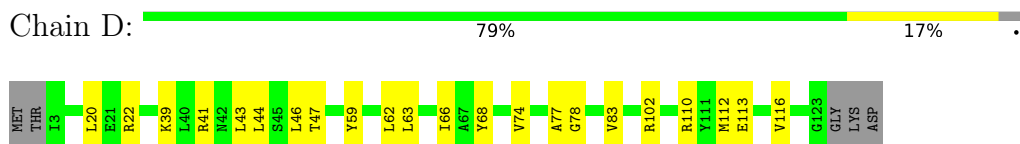
3 Residue-property plots

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.

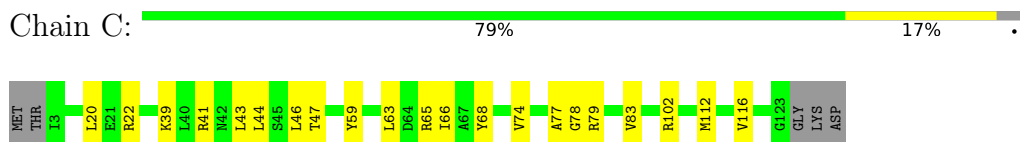
- Molecule 1: Type III-A CRISPR-associated protein Csm1



- Molecule 2: Type III-A CRISPR-associated protein Csm2

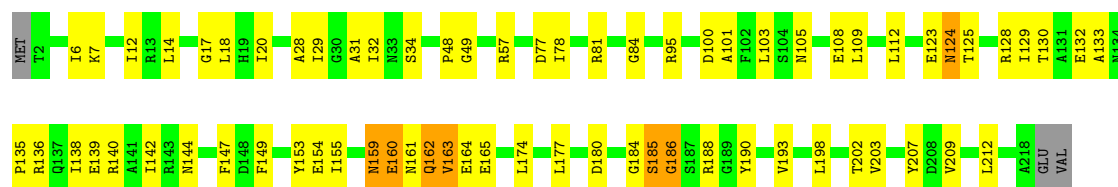


- Molecule 2: Type III-A CRISPR-associated protein Csm2



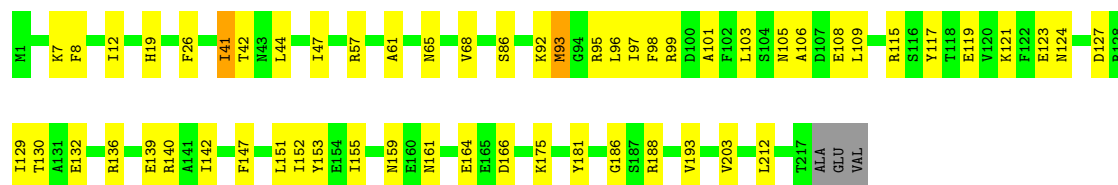
- Molecule 3: Type III-A CRISPR-associated RAMP protein Csm3

Chain G:  67% 28% ..



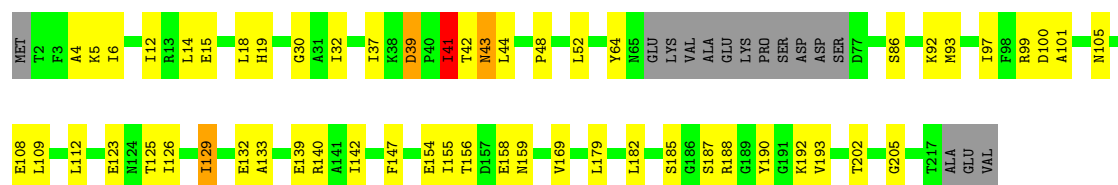
- Molecule 3: Type III-A CRISPR-associated RAMP protein Csm3

Chain F:  73% 25% ..



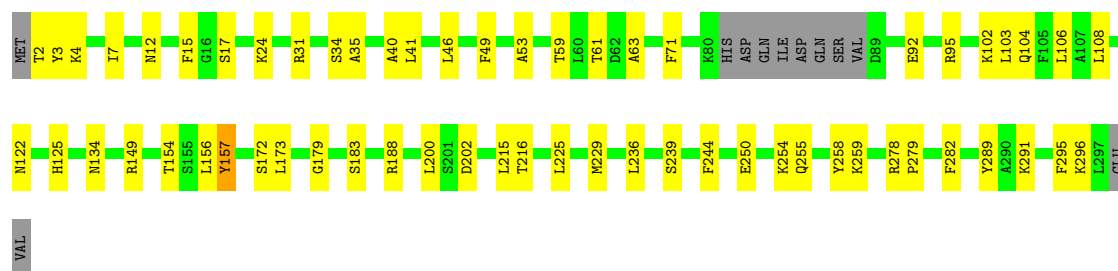
- Molecule 3: Type III-A CRISPR-associated RAMP protein Csm3

Chain E:  68% 24% 7%



- Molecule 4: Type III-A CRISPR-associated RAMP protein Csm4

Chain B:  76% 20%



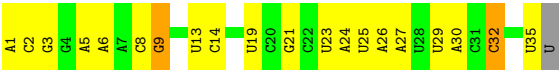
- Molecule 5: Type III-A CRISPR-associated RAMP protein Csm5

Chain H:  80% 19%

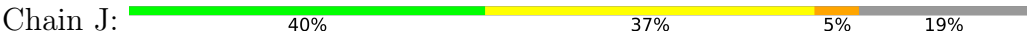




- Molecule 6: type III-A CRISPR-Cas interference complex, crRNA



- Molecule 7: type III-A CRISPR-Cas interference complex, NTR



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54012	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, MG

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	0.28	0/5662	0.65	5/7635 (0.1%)
2	C	0.27	0/1009	0.54	0/1358
2	D	0.27	0/1009	0.53	0/1358
3	E	0.34	0/1633	0.69	1/2197 (0.0%)
3	F	0.33	0/1720	0.67	2/2316 (0.1%)
3	G	0.35	0/1728	0.80	5/2326 (0.2%)
4	B	0.29	0/2339	0.61	1/3161 (0.0%)
5	H	0.28	0/2899	0.71	5/3904 (0.1%)
6	N	0.35	0/819	0.40	0/1271
7	J	0.29	0/842	0.39	0/1311
All	All	0.30	0/19660	0.64	19/26837 (0.1%)

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
3	E	0	1
5	H	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	186	GLY	N-CA-C	11.63	126.68	112.73
3	G	185	SER	N-CA-C	-10.94	89.52	108.56
5	H	104	ASN	CA-C-N	7.83	127.73	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	104	ASN	C-N-CA	7.83	127.73	119.05
1	A	143	PRO	N-CA-CB	6.54	110.12	103.25

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	604	ASN	Peptide
3	E	112	LEU	Peptide
5	H	20	ILE	Peptide
5	H	87	ARG	Peptide

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	5549	0	5385	87	0
2	C	995	0	1012	13	0
2	D	995	0	1012	13	0
3	E	1610	0	1628	61	0
3	F	1695	0	1709	47	0
3	G	1703	0	1716	51	0
4	B	2289	0	2227	46	0
5	H	2832	0	2824	51	0
6	N	735	0	376	23	0
7	J	752	0	377	9	0
8	A	62	0	24	2	0
9	A	2	0	0	0	0
All	All	19219	0	18290	337	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 9.

The worst 5 of 337 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)
3:G:81:ARG:NH1	3:G:162:GLN:OE1	1.60	1.32
3:E:39:ASP:HB3	4:B:149:ARG:NH1	1.45	1.28
3:G:185:SER:O	3:G:190:TYR:HD2	1.27	1.14
3:E:39:ASP:HB3	4:B:149:ARG:HH12	0.92	1.05
3:E:41:ILE:HD11	4:B:149:ARG:HG3	1.36	1.05

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	684/758 (90%)	585 (86%)	98 (14%)	1 (0%)	48	78
2	C	119/126 (94%)	109 (92%)	10 (8%)	0	100	100
2	D	119/126 (94%)	110 (92%)	9 (8%)	0	100	100
3	E	201/220 (91%)	176 (88%)	23 (11%)	2 (1%)	12	40
3	F	215/220 (98%)	196 (91%)	19 (9%)	0	100	100
3	G	215/220 (98%)	191 (89%)	21 (10%)	3 (1%)	9	31
4	B	284/299 (95%)	250 (88%)	34 (12%)	0	100	100
5	H	351/357 (98%)	301 (86%)	49 (14%)	1 (0%)	36	65
All	All	2188/2326 (94%)	1918 (88%)	263 (12%)	7 (0%)	37	65

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	160	GLU
3	G	163	VAL
3	E	129	ILE
3	G	77	ASP
3	E	43	ASN

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	568/651 (87%)	560 (99%)	8 (1%)	59	70
2	C	105/112 (94%)	105 (100%)	0	100	100
2	D	105/112 (94%)	104 (99%)	1 (1%)	68	75
3	E	173/188 (92%)	169 (98%)	4 (2%)	44	63
3	F	182/188 (97%)	180 (99%)	2 (1%)	65	74
3	G	184/188 (98%)	180 (98%)	4 (2%)	45	63
4	B	250/263 (95%)	249 (100%)	1 (0%)	84	83
5	H	297/312 (95%)	296 (100%)	1 (0%)	86	84
All	All	1864/2014 (93%)	1843 (99%)	21 (1%)	63	74

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	212	LEU
3	E	41	ILE
5	H	298	ILE
3	E	179	LEU
3	E	39	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	246	HIS
4	B	249	ASN
5	H	80	ASN
2	D	23	ASN
1	A	604	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	N	34/36 (94%)	6 (17%)	0
7	J	34/43 (79%)	10 (29%)	1 (2%)
All	All	68/79 (86%)	16 (23%)	1 (1%)

5 of 16 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	N	2	C
6	N	8	C
6	N	9	G
6	N	23	U
6	N	24	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	J	20	A

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
8	ATP	A	802	9	32,33,33	1.37	5 (15%)	48,52,52	1.98	12 (25%)
8	ATP	A	801	-	32,33,33	1.30	5 (15%)	48,52,52	1.77	11 (22%)

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
8	ATP	A	802	9	-	5/22/38/38	0/3/3/3
8	ATP	A	801	-	-	4/22/38/38	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	802	ATP	C5-C4	4.44	1.47	1.39
8	A	801	ATP	C5-C4	4.28	1.46	1.39
8	A	802	ATP	C5-C6	2.56	1.48	1.41
8	A	801	ATP	C5-C6	2.53	1.48	1.41
8	A	801	ATP	C5-N7	-2.43	1.34	1.39

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	801	ATP	C5-C4-N3	-5.67	118.91	126.72
8	A	802	ATP	C5-C4-N3	-5.42	119.26	126.72
8	A	802	ATP	N3-C4-N9	4.58	134.96	127.17
8	A	801	ATP	N3-C4-N9	4.34	134.55	127.17
8	A	802	ATP	C4-C5-N7	-4.00	106.00	110.58

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

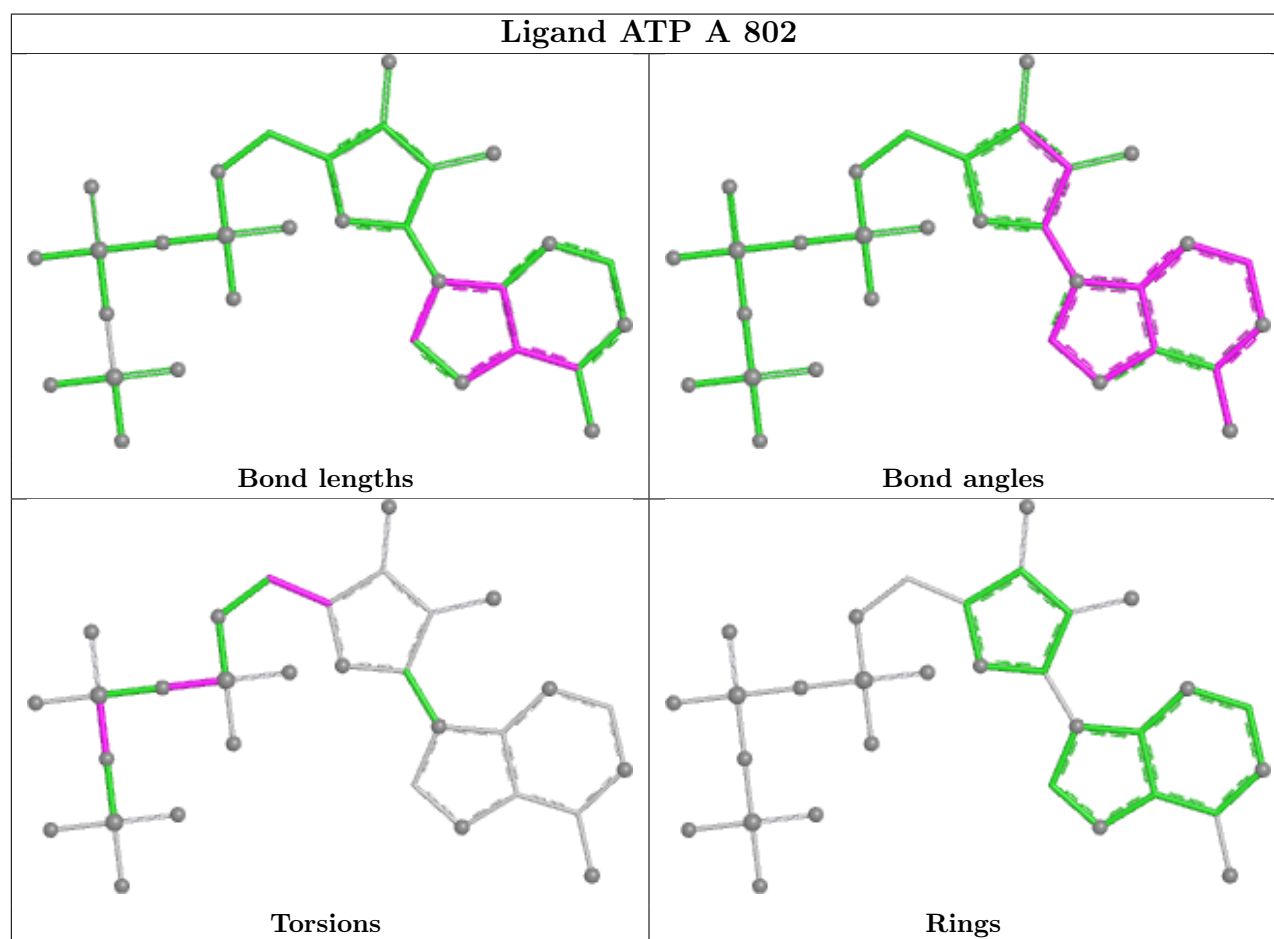
Mol	Chain	Res	Type	Atoms
8	A	801	ATP	C5'-O5'-PA-O1A
8	A	802	ATP	O4'-C4'-C5'-O5'
8	A	802	ATP	C3'-C4'-C5'-O5'
8	A	802	ATP	PG-O3B-PB-O3A
8	A	802	ATP	PB-O3A-PA-O5'

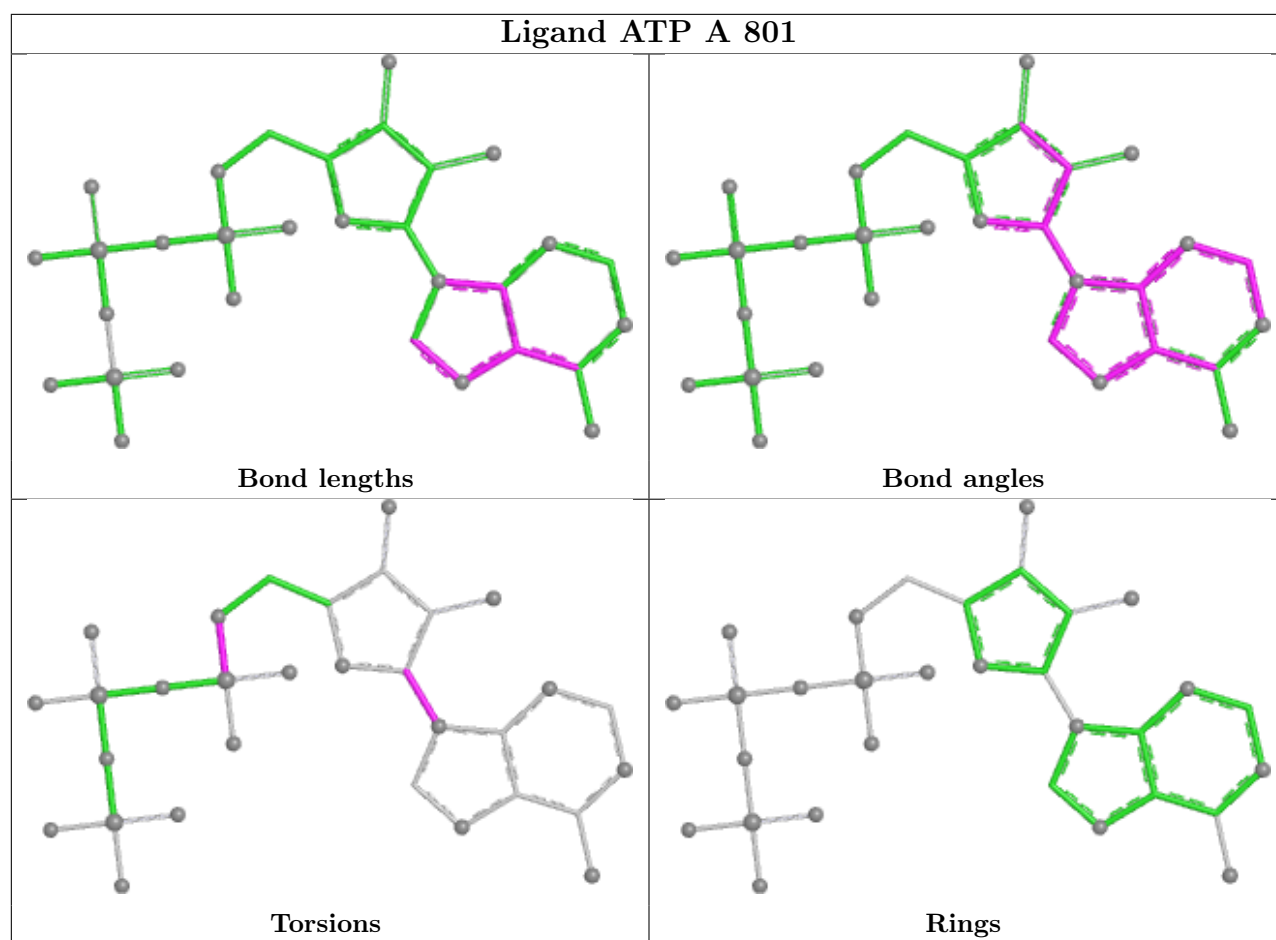
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	802	ATP	1	0
8	A	801	ATP	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.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9656. 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 [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 ⓘ

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.