



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 8, 2024 – 06:03 PM EST

PDB ID : 8ECC  
Title : Structure of Ternary Complex of cGAS with dsDNA and Bound 5-pppI(2,5)pA  
Authors : Wu, S.; Sohn, J.  
Deposited on : 2022-09-01  
Resolution : 2.44 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

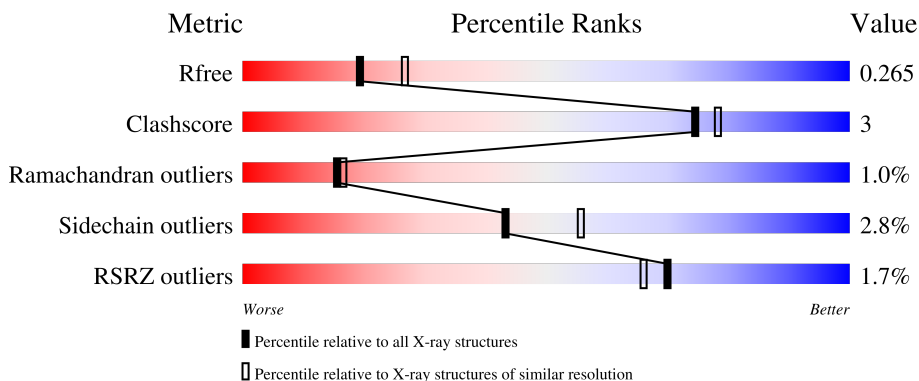
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.44 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.



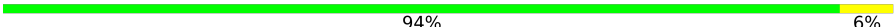
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	364	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 86%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">2%      86%      8%      • 5%</p>
1	C	364	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">%      84%      9%      • 6%</p>
2	E	18	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 83%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: yellow;"></div> </div> <p style="margin-left: 20px;">83%      17%</p>
2	F	18	<div style="display: flex; align-items: center;"> <div style="width: 6%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 78%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 22%; height: 10px; background-color: yellow;"></div> </div> <p style="margin-left: 20px;">6%      78%      22%</p>
2	I	18	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 83%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: yellow;"></div> </div> <p style="margin-left: 20px;">83%      17%</p>

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Mol	Chain	Length	Quality of chain
2	J	18	 94% 6%

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7313 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Cyclic GMP-AMP synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	346	Total 2858	C 1838	N 484	O 523	S 13	0	0	0
1	C	343	Total 2843	C 1833	N 481	O 516	S 13	0	0	0

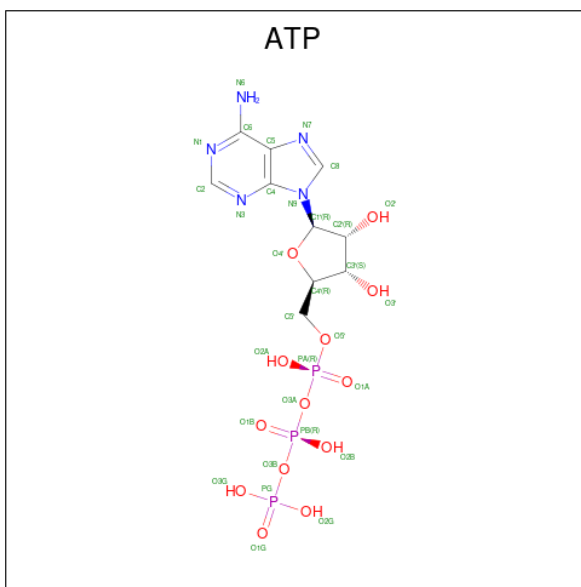
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	144	GLY	-	expression tag	UNP Q8C6L5
A	145	THR	-	expression tag	UNP Q8C6L5
A	146	GLY	-	expression tag	UNP Q8C6L5
C	144	GLY	-	expression tag	UNP Q8C6L5
C	145	THR	-	expression tag	UNP Q8C6L5
C	146	GLY	-	expression tag	UNP Q8C6L5

- Molecule 2 is a DNA chain called Palindromic DNA18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	E	18	Total 366	C 177	N 66	O 106	P 17	0	0	0
2	F	18	Total 366	C 177	N 66	O 106	P 17	0	0	0
2	I	18	Total 366	C 177	N 66	O 106	P 17	0	0	0
2	J	18	Total 366	C 177	N 66	O 106	P 17	0	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



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

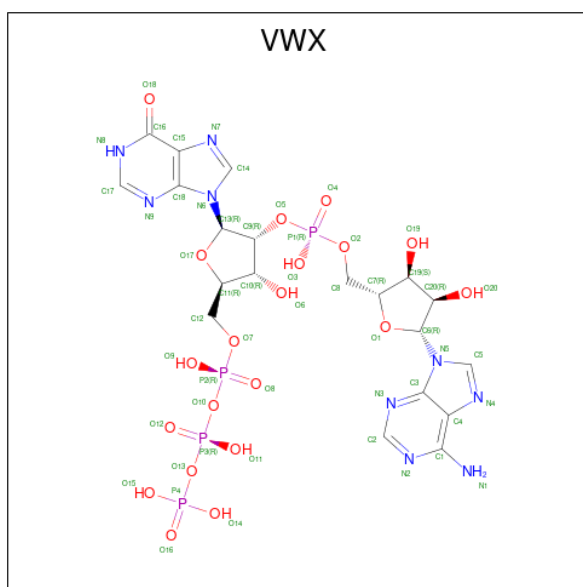
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0
4	C	1	1	1	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
5	A	1	1	1	0	0
5	C	1	1	1	0	0

- Molecule 6 is [(2 {R},3 {R},4 {R},5 {R})-4-[(2 {R},3 {S},4 {R},5 {R})-5-(6-am inopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]oxy-3-ox idanyl-5-(6-oxidanylidene-1 {H}-purin-9-yl)oxolan-2-yl]methoxy-oxidanyl-phospho ryl] phosphono hydrogen phosphate (three-letter code: VWX) (formula: C<sub>20</sub>H<sub>27</sub>N<sub>9</sub>O<sub>20</sub>P<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	C	1	53	20	9	20	4	0	0

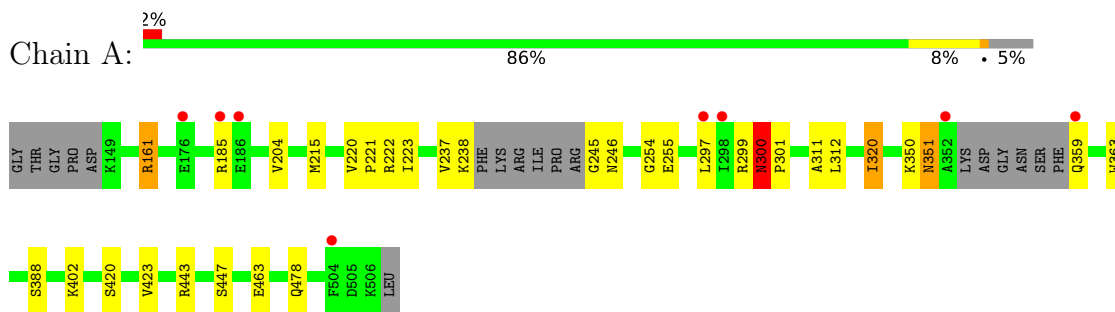
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	30	Total	O	0	0
			30	30		
7	C	26	Total	O	0	0
			26	26		
7	E	1	Total	O	0	0
			1	1		
7	F	1	Total	O	0	0
			1	1		
7	I	1	Total	O	0	0
			1	1		
7	J	1	Total	O	0	0
			1	1		

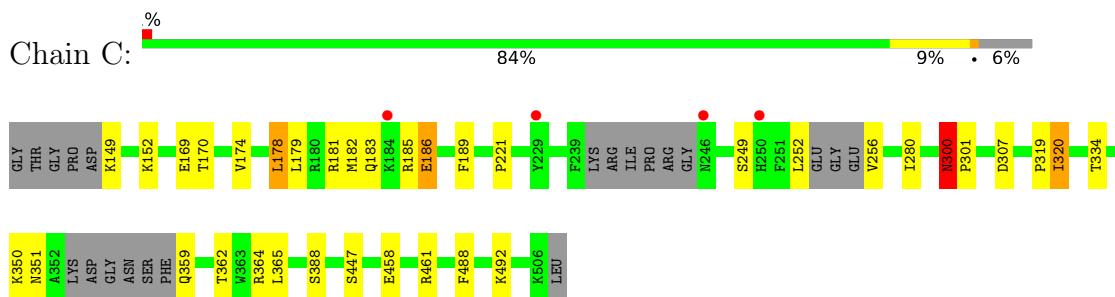
### 3 Residue-property plots i

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

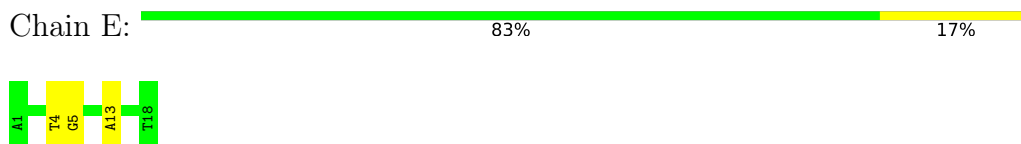
- Molecule 1: Cyclic GMP-AMP synthase



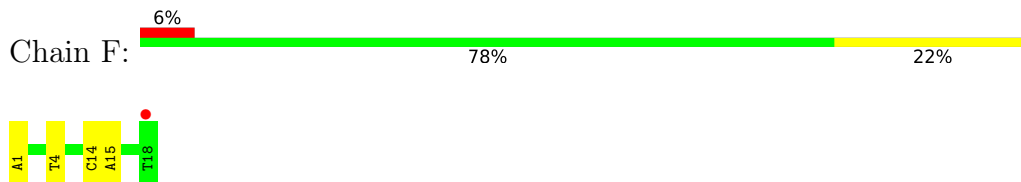
- Molecule 1: Cyclic GMP-AMP synthase



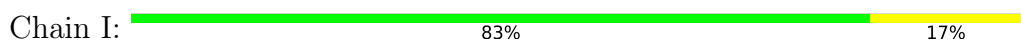
- Molecule 2: Palindromic DNA18

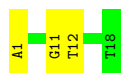


- Molecule 2: Palindromic DNA18



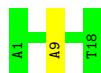
- Molecule 2: Palindromic DNA18





- Molecule 2: Palindromic DNA18

Chain J:  94% 6%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.05Å 98.53Å 141.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.90 – 2.44 80.90 – 2.44	Depositor EDS
% Data completeness (in resolution range)	83.3 (80.90-2.44) 77.3 (80.90-2.44)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	-0.17 (at 2.42Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.222 , 0.259 0.225 , 0.265	Depositor DCC
$R_{free}$ test set	1719 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.9	Xtrriage
Anisotropy	0.055	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 22.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7313	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4548e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.40	0/2917	0.63	0/3914
1	C	0.39	0/2902	0.61	0/3893
2	E	0.53	0/410	0.89	0/631
2	F	0.47	0/410	0.79	1/631 (0.2%)
2	I	0.53	0/410	0.84	1/631 (0.2%)
2	J	0.48	0/410	0.81	0/631
All	All	0.42	0/7459	0.68	2/10331 (0.0%)

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
1	C	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	DA	C1'-O4'-C4'	-6.12	103.98	110.10
2	I	1	DA	C1'-O4'-C4'	-5.27	104.83	110.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	300	ASN	Peptide
1	C	300	ASN	Peptide

## 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	2858	0	2903	18	0
1	C	2843	0	2893	22	0
2	E	366	0	206	2	0
2	F	366	0	206	2	0
2	I	366	0	206	3	0
2	J	366	0	206	1	0
3	A	31	0	12	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	C	53	0	0	3	0
7	A	30	0	0	2	0
7	C	26	0	0	1	0
7	E	1	0	0	0	0
7	F	1	0	0	0	0
7	I	1	0	0	0	0
7	J	1	0	0	0	0
All	All	7313	0	6632	45	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 (45) 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:C:364:ARG:NH2	6:C:601:VWX:N4	2.10	1.00
1:C:350:LYS:NZ	6:C:601:VWX:O4	2.03	0.90
1:A:300:ASN:HB3	1:A:301:PRO:CD	2.19	0.72
1:C:307:ASP:OD2	6:C:601:VWX:O19	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:14:DC:H2''	2:F:15:DA:N7	2.06	0.71
1:A:299:ARG:O	1:A:301:PRO:C	2.32	0.68
1:C:300:ASN:HB3	1:C:301:PRO:CD	2.31	0.61
1:A:204:VAL:O	1:A:402:LYS:HE2	2.01	0.60
1:C:179:LEU:O	1:C:183:GLN:OE1	2.20	0.60
1:C:170:THR:HG23	1:C:280:ILE:HD13	1.85	0.58
1:A:300:ASN:HB3	1:A:301:PRO:HD2	1.86	0.58
2:E:4:DT:H2''	2:E:5:DG:N7	2.21	0.56
1:A:299:ARG:O	1:A:300:ASN:C	2.45	0.55
1:A:351:ASN:N	1:A:351:ASN:HD22	2.05	0.54
1:C:334:THR:HB	2:E:13:DA:OP1	2.08	0.53
1:A:161:ARG:NH2	2:F:4:DT:O2	2.43	0.51
1:A:312:LEU:HD13	1:A:363:TRP:CZ3	2.46	0.50
1:C:300:ASN:CB	1:C:301:PRO:CD	2.89	0.50
1:A:351:ASN:N	1:A:351:ASN:ND2	2.59	0.50
1:A:215:MET:HE3	1:A:311:ALA:HB2	1.93	0.50
1:C:174:VAL:HG12	1:C:178:LEU:CD2	2.44	0.48
1:A:245:GLY:N	7:A:702:HOH:O	2.47	0.47
1:A:420:SER:O	1:A:423:VAL:HG22	2.14	0.47
1:C:320:ILE:HD12	1:C:320:ILE:H	1.80	0.47
1:C:174:VAL:O	1:C:178:LEU:HD22	2.14	0.47
1:C:182:MET:HE3	1:C:189:PHE:HB2	1.96	0.46
1:C:186:GLU:OE1	1:C:186:GLU:CA	2.63	0.46
1:C:256:VAL:N	7:C:702:HOH:O	2.48	0.46
1:C:181:ARG:HD2	1:C:185:ARG:HG3	1.98	0.45
1:C:319:PRO:HG2	1:C:365:LEU:HD21	1.98	0.45
1:A:220:VAL:CG2	1:A:223:ILE:HD12	2.48	0.44
1:C:351:ASN:HA	1:C:362:THR:OG1	2.18	0.43
2:I:11:DG:H2'	2:I:12:DT:C6	2.53	0.43
2:I:11:DG:C2	2:J:9:DA:C2	3.06	0.43
1:C:249:SER:O	1:C:252:LEU:HD23	2.18	0.43
1:A:463:GLU:OE1	1:A:478:GLN:NE2	2.52	0.43
1:C:488:PHE:O	1:C:492:LYS:HG2	2.18	0.43
1:A:238:LYS:HA	1:A:255:GLU:O	2.19	0.42
1:C:300:ASN:HB3	1:C:301:PRO:HD3	2.00	0.42
1:A:359:GLN:N	7:A:704:HOH:O	2.53	0.42
1:C:186:GLU:OE1	1:C:186:GLU:HA	2.20	0.42
1:C:458:GLU:OE2	1:C:461:ARG:NH2	2.47	0.41
1:A:320:ILE:H	1:A:320:ILE:HD13	1.86	0.41
1:A:223:ILE:HD11	1:A:237:VAL:CG1	2.51	0.41
2:I:11:DG:H2''	2:I:12:DT:H5'	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 X-ray entries followed by that with respect to entries of similar resolution.

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	340/364 (93%)	326 (96%)	9 (3%)	5 (2%)	10	9
1	C	335/364 (92%)	324 (97%)	9 (3%)	2 (1%)	25	29
All	All	675/728 (93%)	650 (96%)	18 (3%)	7 (1%)	15	16

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	ARG
1	A	300	ASN
1	C	300	ASN
1	A	222	ARG
1	A	254	GLY
1	C	221	PRO
1	A	221	PRO

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	320/335 (96%)	311 (97%)	9 (3%)	43	56
1	C	319/335 (95%)	310 (97%)	9 (3%)	43	56
All	All	639/670 (95%)	621 (97%)	18 (3%)	43	56

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	161	ARG
1	A	246	ASN
1	A	297	LEU
1	A	320	ILE
1	A	350	LYS
1	A	351	ASN
1	A	388	SER
1	A	443	ARG
1	A	447	SER
1	C	149	LYS
1	C	152	LYS
1	C	169	GLU
1	C	178	LEU
1	C	186	GLU
1	C	320	ILE
1	C	359	GLN
1	C	388	SER
1	C	447	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	351	ASN
1	A	444	ASN
1	A	478	GLN
1	C	422	HIS
1	C	478	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

Of 6 ligands modelled in this entry, 4 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
6	VWX	C	601	4	46,58,58	0.77	0	55,91,91	0.76	1 (1%)
3	ATP	A	601	4	26,33,33	0.63	0	31,52,52	0.77	1 (3%)

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
6	VWX	C	601	4	-	8/29/69/69	0/6/6/6
3	ATP	A	601	4	-	6/18/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	ATP	C5-C6-N6	2.13	123.59	120.35
6	C	601	VWX	C4-C1-N1	2.00	123.40	120.35

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	ATP	PB-O3B-PG-O2G
6	C	601	VWX	C9-O5-P1-O2
6	C	601	VWX	P3-O13-P4-O16
3	A	601	ATP	PA-O3A-PB-O1B
6	C	601	VWX	O1-C7-C8-O2
6	C	601	VWX	P3-O13-P4-O15

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Mol	Chain	Res	Type	Atoms
3	A	601	ATP	PA-O3A-PB-O2B
3	A	601	ATP	PB-O3A-PA-O1A
6	C	601	VWX	C19-C7-C8-O2
3	A	601	ATP	PB-O3B-PG-O1G
3	A	601	ATP	PB-O3A-PA-O2A
6	C	601	VWX	P2-O10-P3-O12
6	C	601	VWX	C8-O2-P1-O4
6	C	601	VWX	C12-O7-P2-O8

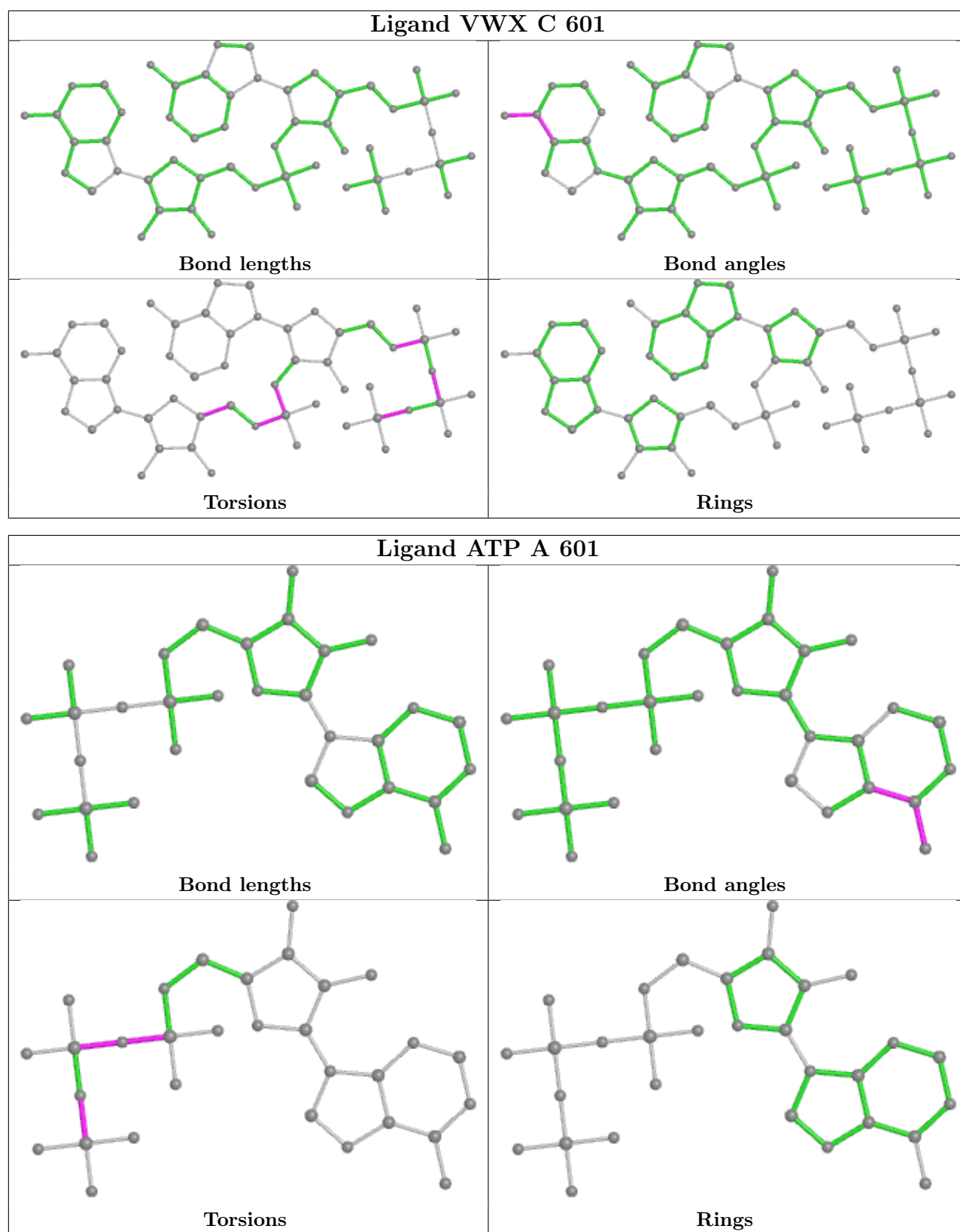
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	601	VWX	3	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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	346/364 (95%)	0.03	8 (2%) 60 56	26, 47, 76, 105	0
1	C	343/364 (94%)	-0.08	4 (1%) 79 77	27, 53, 83, 108	0
2	E	18/18 (100%)	-0.05	0 100 100	34, 56, 116, 123	0
2	F	18/18 (100%)	-0.02	1 (5%) 24 20	34, 66, 111, 129	0
2	I	18/18 (100%)	-0.22	0 100 100	37, 59, 116, 119	0
2	J	18/18 (100%)	-0.27	0 100 100	37, 69, 118, 128	0
All	All	761/800 (95%)	-0.03	13 (1%) 70 66	26, 51, 87, 129	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	246	ASN	2.8
1	C	229	TYR	2.8
1	A	359	GLN	2.6
1	C	250	HIS	2.5
1	A	186	GLU	2.4
1	A	185	ARG	2.3
1	A	297	LEU	2.3
1	A	352	ALA	2.3
1	A	298	ILE	2.3
2	F	18	DT	2.3
1	A	504	PHE	2.2
1	A	176	GLU	2.0
1	C	184	LYS	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

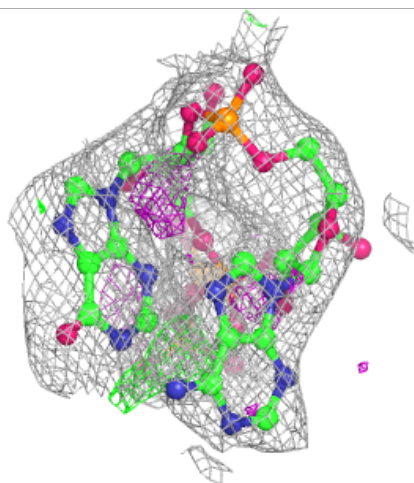
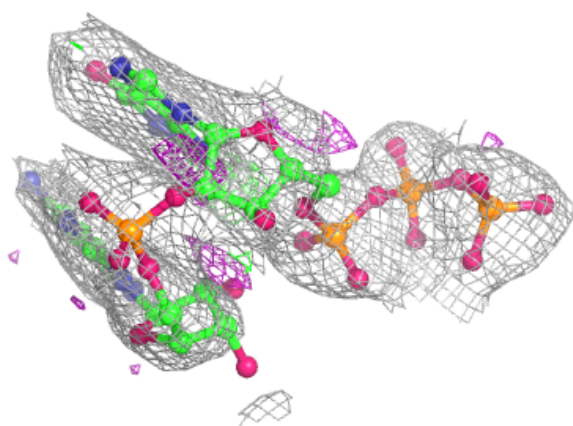
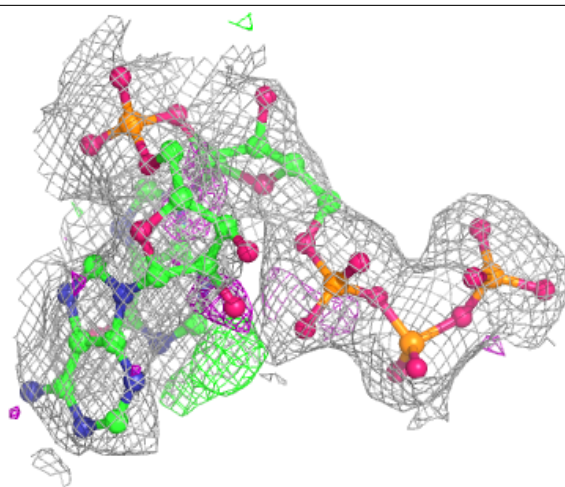
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

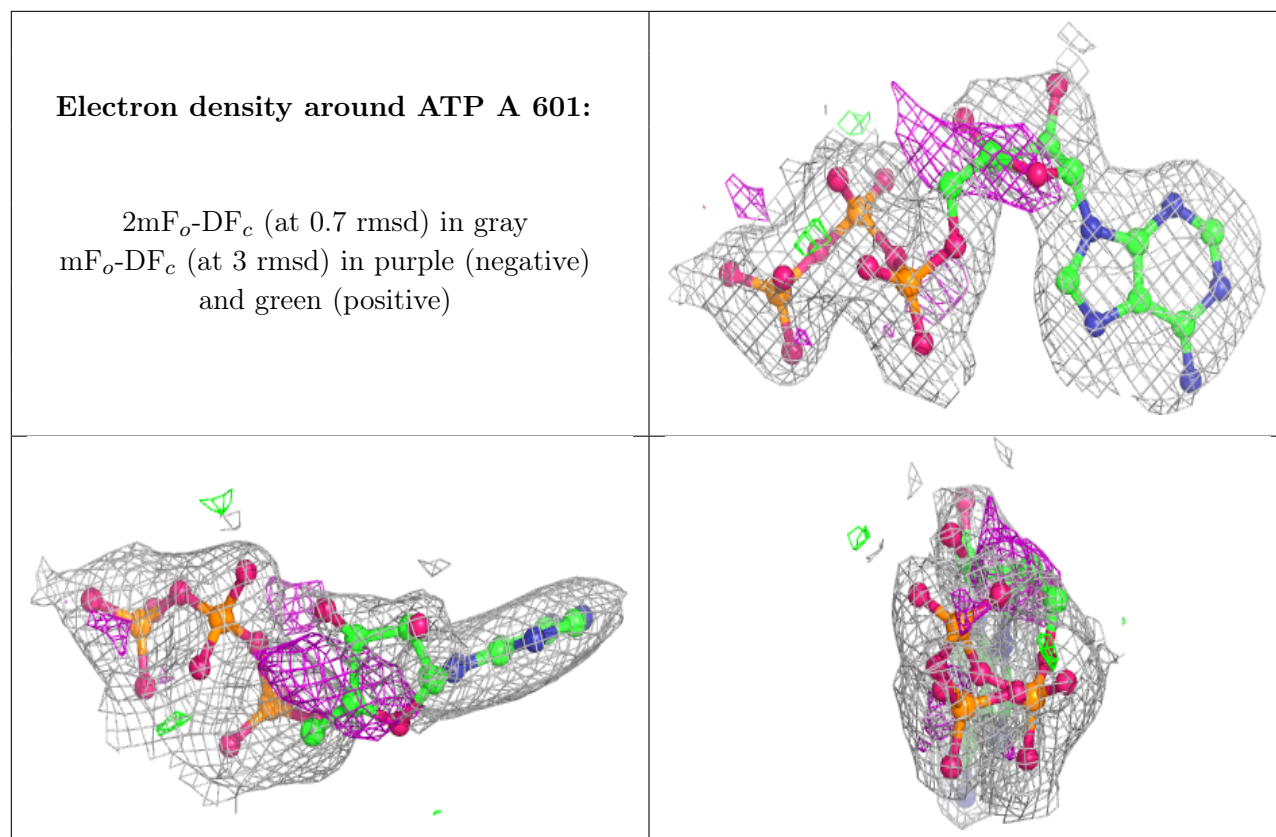
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	MG	A	602	1/1	0.92	0.08	34,34,34,34	0
6	VWX	C	601	53/53	0.92	0.19	51,68,87,93	0
3	ATP	A	601	31/31	0.94	0.17	42,50,61,64	0
5	ZN	A	603	1/1	0.99	0.10	30,30,30,30	0
5	ZN	C	603	1/1	0.99	0.11	31,31,31,31	0
4	MG	C	602	1/1	0.99	0.07	54,54,54,54	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around VWX C 601:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.