



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 5, 2023 – 09:35 AM EDT

PDB ID : 3V11  
Title : Structure of the ternary initiation complex AIF2:GDPNP:methionylated initiator TRNA  
Authors : Mechulam, Y.; Schmitt, E.  
Deposited on : 2011-12-09  
Resolution : 5.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 2.35  
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) : 2.35

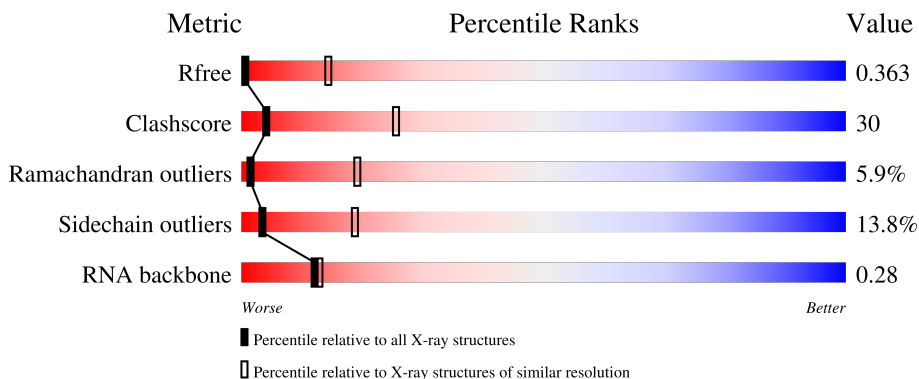
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 5.00 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1140 (6.20-3.80)
Clashscore	141614	1000 (6.16-3.82)
Ramachandran outliers	138981	1146 (6.20-3.80)
Sidechain outliers	138945	1122 (6.20-3.80)
RNA backbone	3102	1068 (7.00-3.00)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	414	 42% 46% 9% ..
2	B	266	 36% 48% 11% • 5%
3	C	138	 6% 5% • 88%
4	D	77	 10% 35% 38% 16% •

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6975 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 Translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	404	3131	2004	533	582	12	0	0	0

- Molecule 2 is a protein called Translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	254	2033	1301	346	384	2	0	0	0

- Molecule 3 is a protein called Translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	17	146	94	22	29	1	0	0	0

- Molecule 4 is a RNA chain called Initiator tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
4	D	76	1624	725	294	528	76	1	0	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

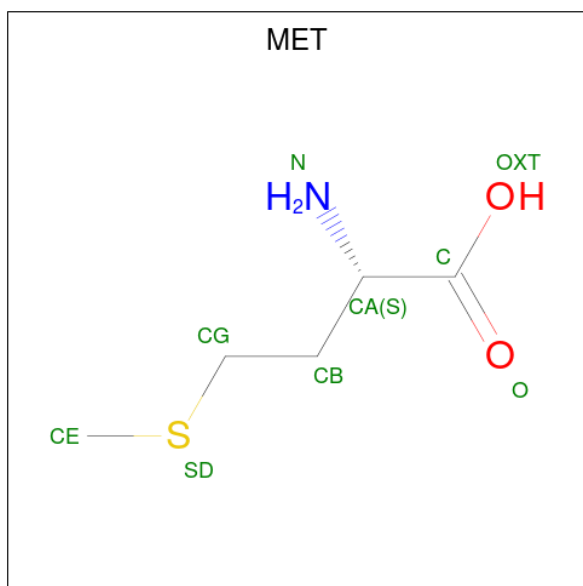
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
5	A	1	1	1	0	0

- Molecule 6 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	A	1	32	10	6	13	3	0	0

- Molecule 7 is METHIONINE (three-letter code: MET) (formula: C<sub>5</sub>H<sub>11</sub>NO<sub>2</sub>S).

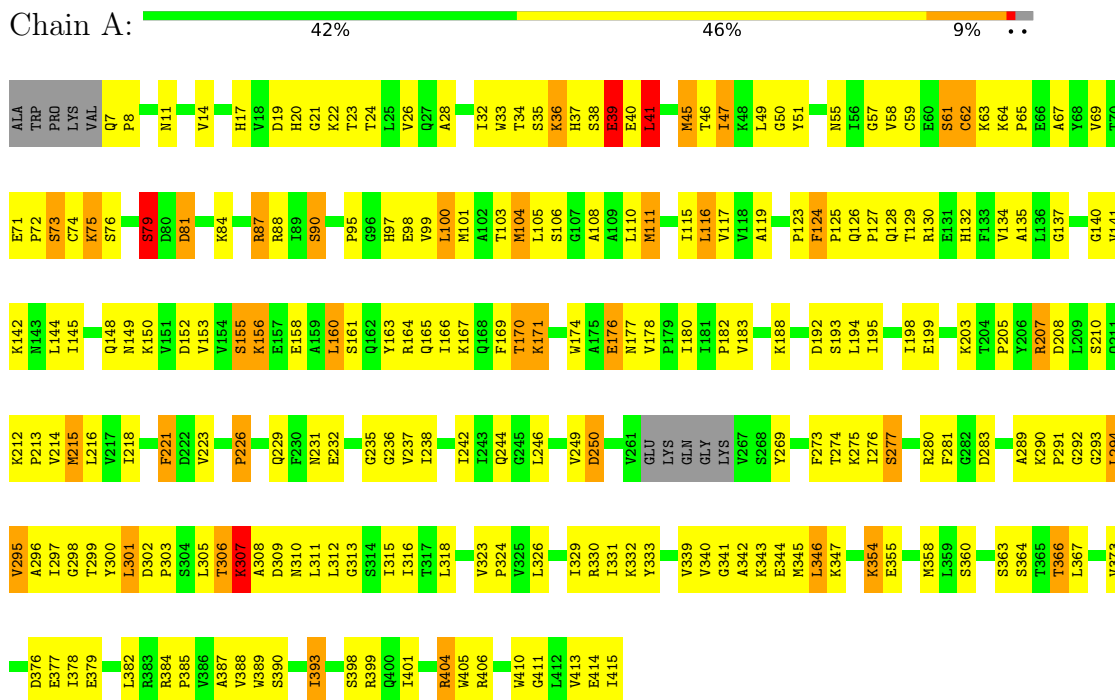


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
7	D	1	8	5	1	1	1	0	0

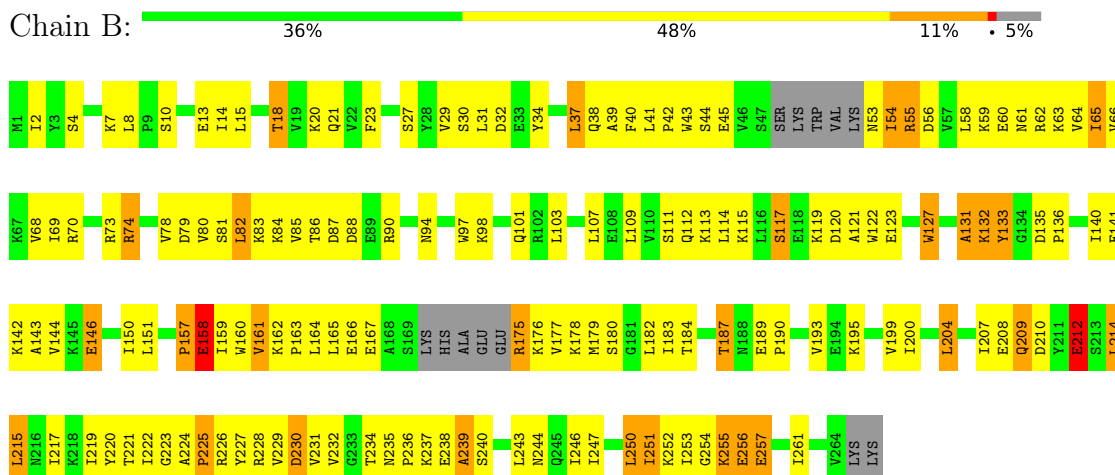
### 3 Residue-property plots

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: Translation initiation factor 2 subunit gamma

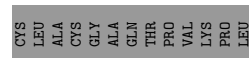
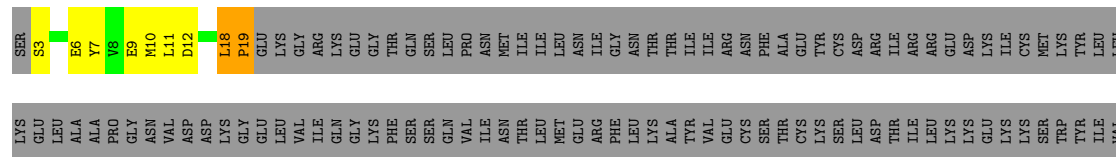


- Molecule 2: Translation initiation factor 2 subunit alpha



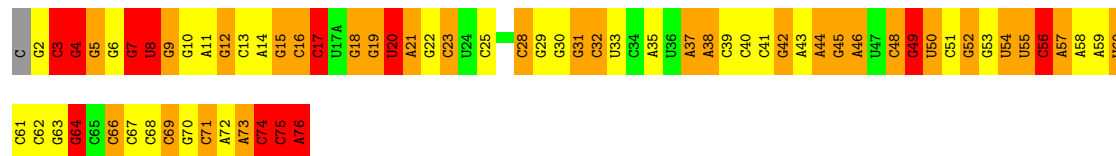
• Molecule 3: Translation initiation factor 2 subunit beta

Chain C:  6% 5% 88%



• Molecule 4: Initiator tRNA

Chain D:  10% 35% 38% 16%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.00Å 133.00Å 167.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.43 – 5.00 47.43 – 5.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (47.43-5.00) 98.8 (47.43-5.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 5.10Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, $R_{free}$	0.262 , 0.344 0.289 , 0.363	Depositor DCC
$R_{free}$ test set	360 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	341.3	Xtrriage
Anisotropy	0.509	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 390.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.071 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6975	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	300.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, H2U, 4SU, MG, GNP, 5MU, PSU

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	0.51	0/3186	0.79	1/4313 (0.0%)
2	B	0.52	0/2058	0.76	1/2770 (0.0%)
3	C	0.65	0/148	1.10	2/197 (1.0%)
4	D	0.99	4/1702 (0.2%)	1.76	46/2653 (1.7%)
All	All	0.66	4/7094 (0.1%)	1.13	50/9933 (0.5%)

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
2	B	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	76	A	N3-C4	16.59	1.44	1.34
4	D	76	A	C8-N7	12.46	1.40	1.31
4	D	76	A	C5-C4	6.94	1.43	1.38
4	D	76	A	C6-N1	5.21	1.39	1.35

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	76	A	C2-N3-C4	18.67	119.94	110.60
4	D	76	A	C8-N9-C4	18.01	113.00	105.80
4	D	76	A	N7-C8-N9	-15.89	105.85	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	76	A	N1-C2-N3	-15.02	121.79	129.30
4	D	56	C	C6-N1-C2	-13.76	114.80	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	79	SER	Peptide
2	B	212	GLU	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	3131	0	3248	194	0
2	B	2033	0	2145	119	0
3	C	146	0	146	6	0
4	D	1624	0	830	97	0
5	A	1	0	0	0	0
6	A	32	0	13	2	0
7	D	8	0	8	5	0
All	All	6975	0	6390	393	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 30.

The worst 5 of 393 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:294:LEU:HB3	7:D:101:MET:HG2	1.48	0.94
2:B:18:THR:HB	2:B:63:LYS:HG2	1.52	0.91
1:A:37:HIS:HB2	4:D:74:C:C4	2.08	0.88
2:B:240:SER:HA	2:B:243:LEU:HB3	1.55	0.88
1:A:62:CYS:SG	1:A:63:LYS:N	2.45	0.87

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	400/414 (97%)	314 (78%)	64 (16%)	22 (6%)	2	21
2	B	248/266 (93%)	183 (74%)	48 (19%)	17 (7%)	1	16
3	C	15/138 (11%)	9 (60%)	6 (40%)	0	100	100
All	All	663/818 (81%)	506 (76%)	118 (18%)	39 (6%)	1	19

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	39	GLU
1	A	75	LYS
1	A	124	PHE
1	A	176	GLU
1	A	307	LYS

### 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	348/356 (98%)	296 (85%)	52 (15%)	3	16
2	B	227/239 (95%)	199 (88%)	28 (12%)	4	21
3	C	17/125 (14%)	16 (94%)	1 (6%)	19	46
All	All	592/720 (82%)	511 (86%)	81 (14%)	3	19

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	59	LYS
2	B	208	GLU
2	B	70	ARG
2	B	135	ASP
2	B	222	ILE

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	37	HIS
1	A	177	ASN
1	A	400	GLN
2	B	61	ASN
2	B	245	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	75/77 (97%)	34 (45%)	2 (2%)

5 of 34 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	3	C
4	D	4	G
4	D	5	G
4	D	7	G
4	D	8	4SU

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	D	73	A
4	D	74	C

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

5 non-standard protein/DNA/RNA residues 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
4	H2U	D	20	4	18,21,22	1.28	2 (11%)	21,30,33	2.95	6 (28%)
4	OMC	D	32	4	19,22,23	1.91	3 (15%)	26,31,34	1.03	1 (3%)
4	4SU	D	8	4	18,21,22	2.18	5 (27%)	26,30,33	1.76	4 (15%)
4	PSU	D	55	4	18,21,22	1.18	1 (5%)	22,30,33	1.32	3 (13%)
4	5MU	D	54	4	19,22,23	2.30	6 (31%)	28,32,35	1.47	4 (14%)

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	H2U	D	20	4	-	3/7/38/39	0/2/2/2
4	OMC	D	32	4	-	2/9/27/28	0/2/2/2
4	4SU	D	8	4	-	2/7/25/26	0/2/2/2
4	PSU	D	55	4	-	0/7/25/26	0/2/2/2
4	5MU	D	54	4	-	0/7/25/26	0/2/2/2

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	54	5MU	C6-N1	6.84	1.49	1.38
4	D	8	4SU	C4-N3	5.21	1.43	1.37
4	D	8	4SU	C5-C4	4.72	1.48	1.42
4	D	32	OMC	C4-N4	4.67	1.44	1.33
4	D	32	OMC	C2-N3	4.47	1.45	1.36

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	20	H2U	O2-C2-N1	8.03	133.19	123.11
4	D	20	H2U	O2-C2-N3	-6.56	109.28	121.50
4	D	20	H2U	C4-N3-C2	6.48	131.17	125.79
4	D	8	4SU	C5-C4-S4	-5.45	117.45	124.47
4	D	54	5MU	O4-C4-C5	-4.52	119.66	124.90

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	20	H2U	C4'-C5'-O5'-P
4	D	20	H2U	O4'-C1'-N1-C2
4	D	20	H2U	O4'-C1'-N1-C6
4	D	8	4SU	O4'-C4'-C5'-O5'
4	D	32	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	20	H2U	1	0
4	D	8	4SU	5	0
4	D	55	PSU	2	0
4	D	54	5MU	3	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is 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	GNP	A	502	5	29,34,34	2.05	8 (27%)	33,54,54	2.40	9 (27%)
7	MET	D	101	4	6,7,8	1.30	1 (16%)	2,7,9	1.76	1 (50%)

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	GNP	A	502	5	-	6/14/38/38	0/3/3/3
7	MET	D	101	4	-	1/5/6/8	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	502	GNP	PB-O3A	-7.41	1.49	1.59
6	A	502	GNP	C6-N1	3.85	1.39	1.33
6	A	502	GNP	PB-O2B	-3.61	1.47	1.56
7	D	101	MET	CB-CA	-2.93	1.49	1.53
6	A	502	GNP	PG-O3G	-2.39	1.50	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	502	GNP	C5-C6-N1	-8.62	111.64	123.43
6	A	502	GNP	C2-N1-C6	5.56	124.76	115.93
6	A	502	GNP	O3G-PG-O1G	-3.60	104.41	113.45
6	A	502	GNP	C3'-C2'-C1'	3.42	106.13	100.98
6	A	502	GNP	PB-O3A-PA	-3.42	120.56	132.62

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	502	GNP	PG-N3B-PB-O1B
6	A	502	GNP	PG-N3B-PB-O3A
6	A	502	GNP	C5'-O5'-PA-O3A
7	D	101	MET	N-CA-CB-CG
6	A	502	GNP	O4'-C4'-C5'-O5'

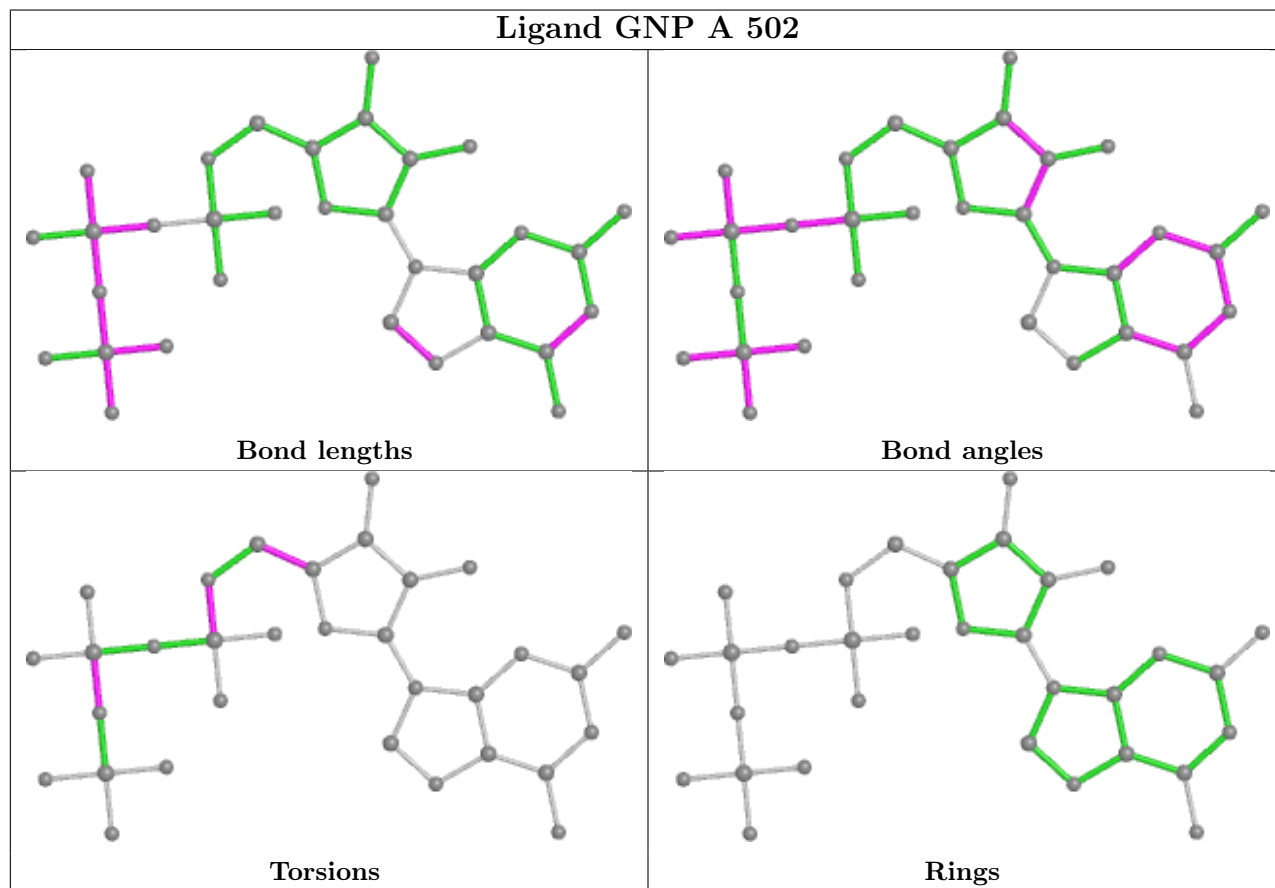
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	502	GNP	2	0
7	D	101	MET	5	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 Fit of model and data [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

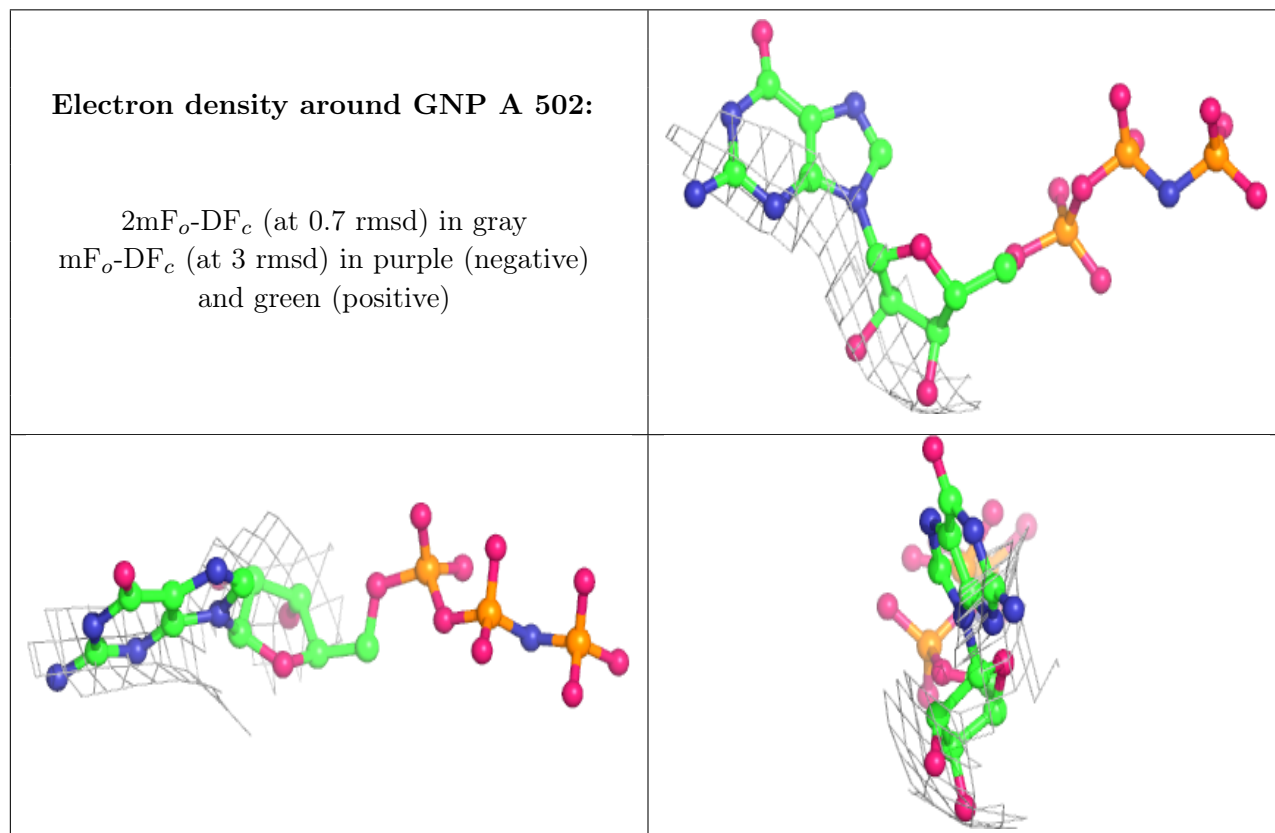
### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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.





## 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.