



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 12:27 PM UTC

PDB ID : 1TTT / pdb_00001ttt
Title : Phe-tRNA, elongation factor EF-TU:GDPNP ternary complex
Authors : Nissen, P.; Kjeldgaard, M.; Thirup, S.; Polekhina, G.; Reshetnikova, L.; Clark, B.F.C.; Nyborg, J.
Deposited on : 1995-11-16
Resolution : 2.70 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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

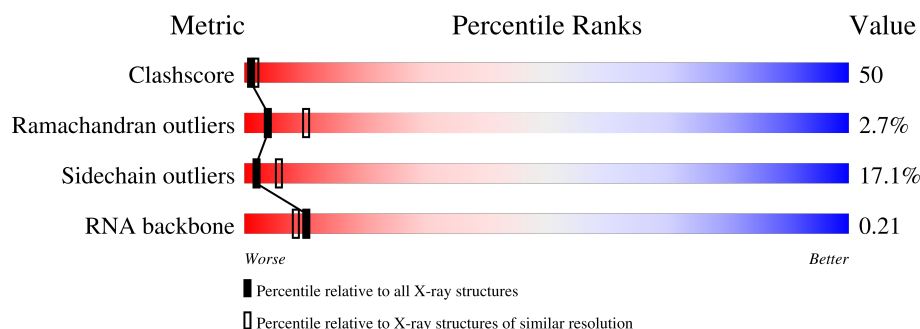
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

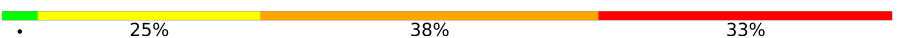
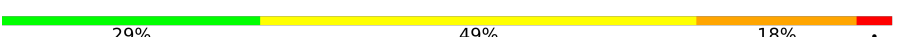
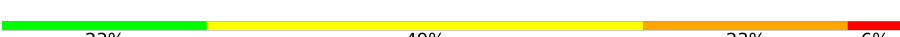
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

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 ≥ 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	D	76	
1	E	76	
1	F	76	
2	A	405	
2	B	405	
2	C	405	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	M2G	D	26	-	-	X	-
1	2MG	E	10	-	-	X	-
1	M2G	E	26	-	-	X	-
1	2MG	F	10	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14573 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 RNA chain called TRANSFER RIBONUCLEIC ACID (YEAST, PHE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	76	Total	C	N	O	P	0	0	0
			1652	746	294	536	76			
1	E	76	Total	C	N	O	P	0	0	0
			1652	746	294	536	76			
1	F	76	Total	C	N	O	P	0	0	0
			1652	746	294	536	76			

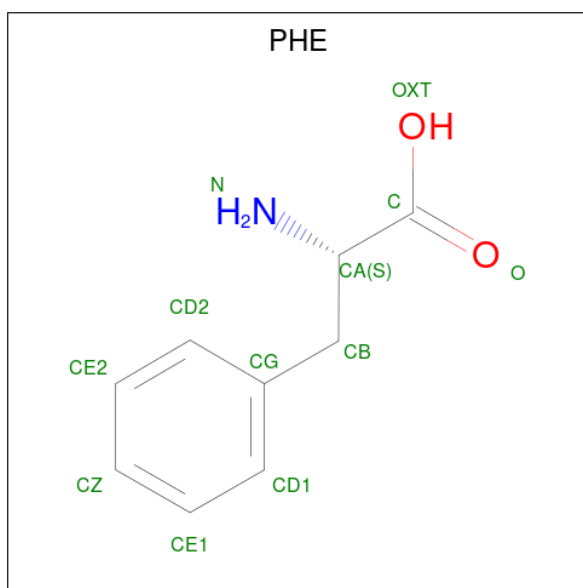
- Molecule 2 is a protein called OF ELONGATION FACTOR TU (EF-TU).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	405	Total	C	N	O	S	0	0	0
			3144	1986	548	598	12			
2	B	405	Total	C	N	O	S	0	0	0
			3144	1986	548	598	12			
2	C	405	Total	C	N	O	S	0	0	0
			3144	1986	548	598	12			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

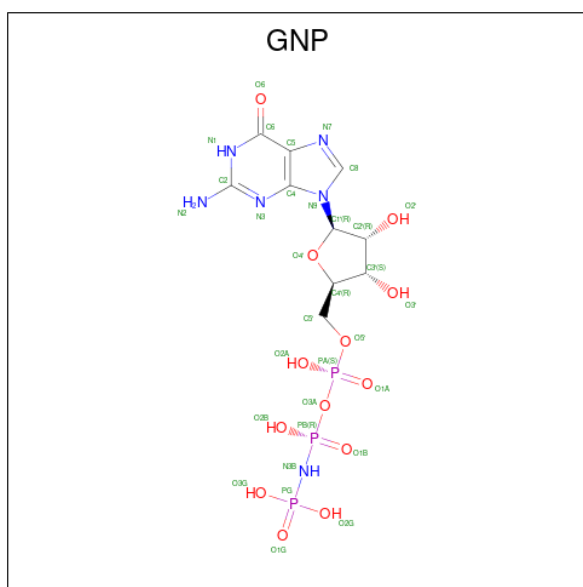
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	N	O	0	0
			11	9	1	1		
4	E	1	Total	C	N	O	0	0
			11	9	1	1		
4	F	1	Total	C	N	O	0	0
			11	9	1	1		

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



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

- Molecule 6 is water.

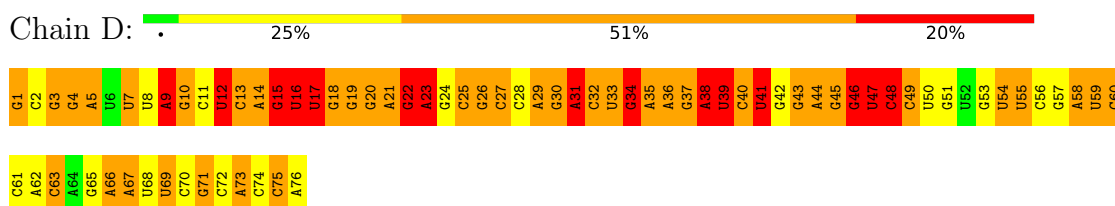
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	6	Total	O	0	0
			6	6		
6	E	2	Total	O	0	0
			2	2		
6	F	1	Total	O	0	0
			1	1		
6	A	21	Total	O	0	0
			21	21		
6	B	13	Total	O	0	0
			13	13		
6	C	7	Total	O	0	0
			7	7		

3 Residue-property plots

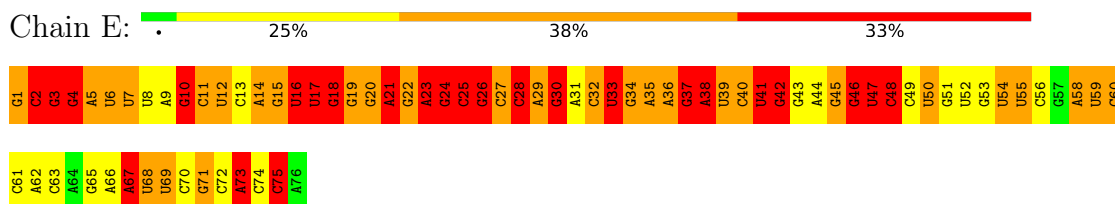
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

Note EDS was not executed.

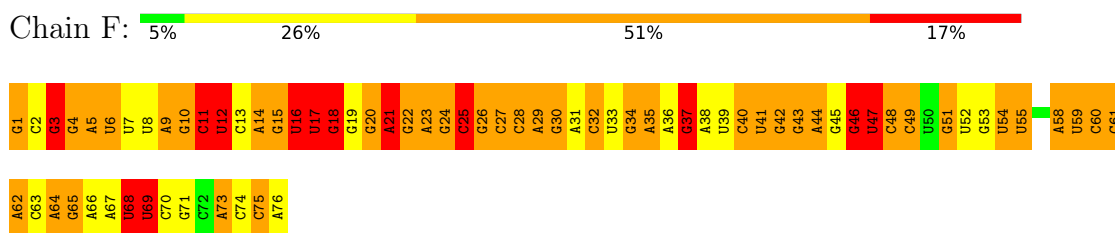
- Molecule 1: TRANSFER RIBONUCLEIC ACID (YEAST, PHE)



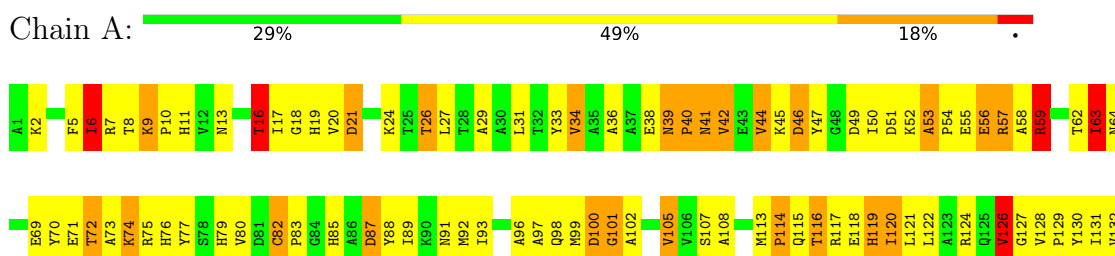
- Molecule 1: TRANSFER RIBONUCLEIC ACID (YEAST, PHE)

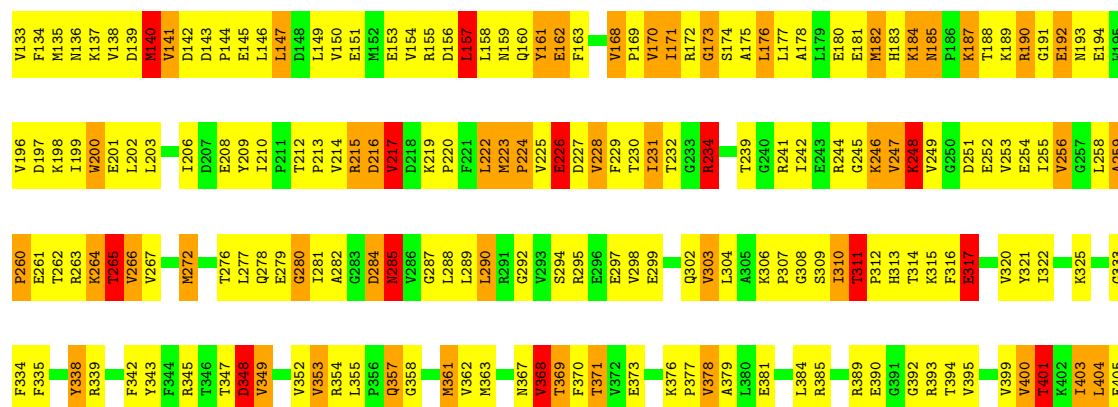


- Molecule 1: TRANSFER RIBONUCLEIC ACID (YEAST, PHE)



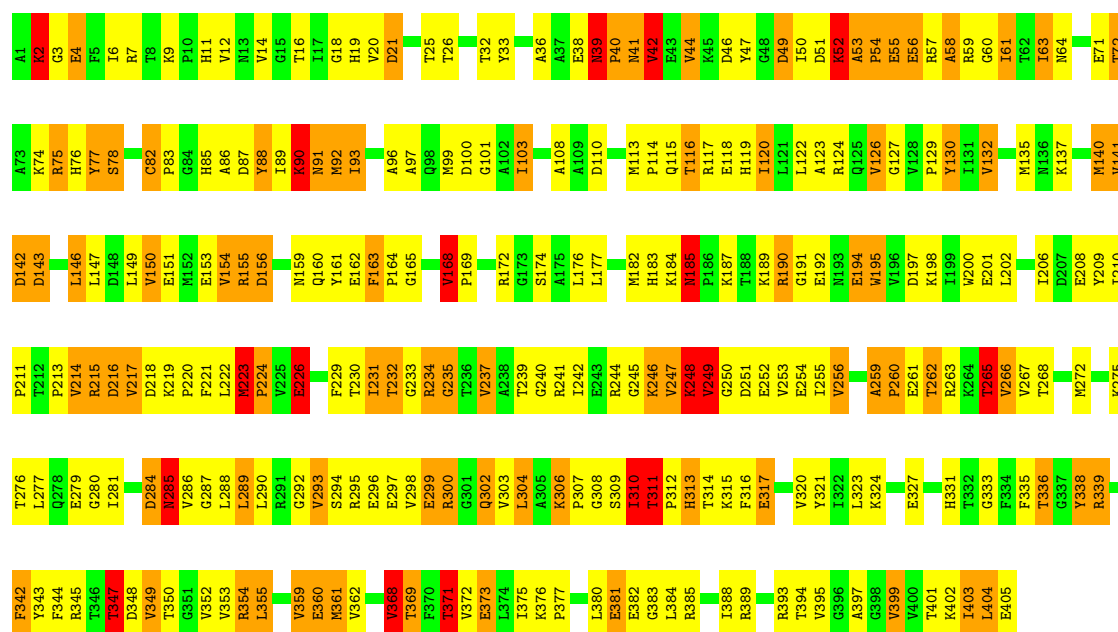
- Molecule 2: OF ELONGATION FACTOR TU (EF-TU)





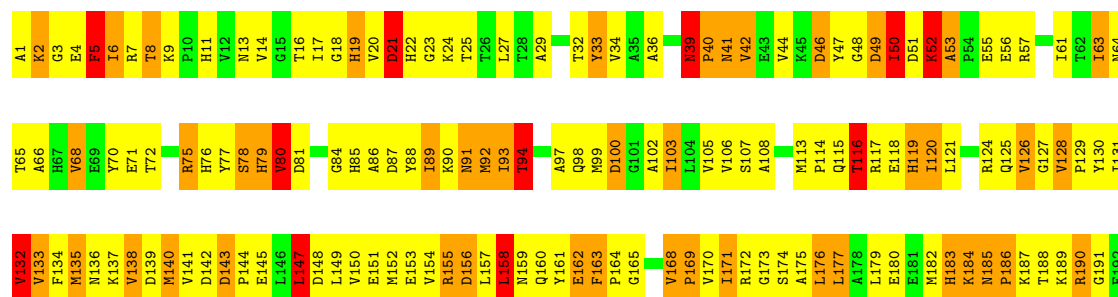
• Molecule 2: OF ELONGATION FACTOR TU (EF-TU)

Chain B: 33% 42% 21%



• Molecule 2: OF ELONGATION FACTOR TU (EF-TU)

Chain C: 23% 49% 23% 6%





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	206.84Å 122.35Å 151.55Å 90.00° 126.30° 90.00°	Depositor
Resolution (Å)	25.00 – 2.70	Depositor
% Data completeness (in resolution range)	91.1 (25.00-2.70)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.206 , 0.290	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14573	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: H2U, OMC, M2G, GNP, PSU, 5MC, 2MG, MG, YYG, 7MG, OMG, 5MU, 1MA

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	D	0.46	0/1487	1.97	84/2315 (3.6%)
1	E	0.45	0/1487	1.92	82/2315 (3.5%)
1	F	0.47	0/1487	1.94	89/2315 (3.8%)
2	A	1.14	8/3204 (0.2%)	2.00	119/4345 (2.7%)
2	B	1.14	5/3204 (0.2%)	1.95	109/4345 (2.5%)
2	C	1.11	6/3204 (0.2%)	2.02	131/4345 (3.0%)
All	All	0.97	19/14073 (0.1%)	1.97	614/19980 (3.1%)

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	F	2	0
2	A	2	0
All	All	4	0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	400	VAL	CA-CB	-8.62	1.43	1.54
2	B	61	ILE	CA-CB	-7.06	1.48	1.55
2	C	6	ILE	CA-CB	-6.92	1.45	1.54
2	A	120	ILE	CA-CB	-6.91	1.46	1.54
2	C	388	ILE	CA-CB	-6.84	1.46	1.54

The worst 5 of 614 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	21	A	N9-C1'-C2'	-16.07	87.90	112.00
1	D	22	G	O4'-C1'-N9	15.49	131.74	108.50
1	D	22	G	N9-C1'-C2'	-15.08	89.38	112.00
1	F	11	C	C3'-C2'-O2'	14.28	132.11	110.70
2	A	163	PHE	N-CA-C	-14.07	90.28	110.40

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	11	C	C3',C2'
2	A	232	THR	CA
2	A	311	THR	CA

There are no planarity outliers.

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	D	1652	0	856	118	0
1	E	1652	0	855	115	0
1	F	1652	0	856	110	0
2	A	3144	0	3161	294	0
2	B	3144	0	3160	314	0
2	C	3144	0	3162	370	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	D	11	0	8	2	0
4	E	11	0	8	1	0
4	F	11	0	8	1	0
5	A	32	0	13	6	0
5	B	32	0	13	7	0
5	C	32	0	13	7	0
6	A	21	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	13	0	0	0	0
6	C	7	0	0	1	0
6	D	6	0	0	0	0
6	E	2	0	0	1	0
6	F	1	0	0	0	0
All	All	14573	0	12113	1294	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 50.

The worst 5 of 1294 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:E:9:A:H5'	1:E:46:7MG:H1'	1.22	1.15
2:A:217:VAL:HG12	2:A:246:LYS:HD3	1.28	1.11
2:A:54:PRO:HA	2:A:57:ARG:HG3	1.21	1.08
2:A:389:ARG:HG2	2:A:394:THR:HA	1.32	1.05
2:A:101:GLY:HA3	2:A:210:ILE:HD13	1.40	1.02

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	
2	A	403/405 (100%)	362 (90%)	35 (9%)	6 (2%)	8	22
2	B	403/405 (100%)	359 (89%)	31 (8%)	13 (3%)	3	7
2	C	403/405 (100%)	353 (88%)	36 (9%)	14 (4%)	3	6
All	All	1209/1215 (100%)	1074 (89%)	102 (8%)	33 (3%)	4	10

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	40	PRO
2	B	2	LYS
2	B	53	ALA
2	B	54	PRO
2	C	5	PHE

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	
2	A	338/338 (100%)	283 (84%)	55 (16%)	2	6
2	B	338/338 (100%)	281 (83%)	57 (17%)	2	6
2	C	338/338 (100%)	276 (82%)	62 (18%)	2	5
All	All	1014/1014 (100%)	840 (83%)	174 (17%)	2	6

5 of 174 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	46	ASP
2	C	247	VAL
2	C	68	VAL
2	C	147	LEU
2	C	286	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	85	HIS
2	C	119	HIS
2	C	341	GLN
2	A	357	GLN
2	A	341	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D	75/76 (98%)	27 (36%)	5 (6%)
1	E	75/76 (98%)	32 (42%)	11 (14%)
1	F	75/76 (98%)	26 (34%)	6 (8%)
All	All	225/228 (98%)	85 (37%)	22 (9%)

5 of 85 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D	4	G
1	D	5	A
1	D	9	A
1	D	12	U
1	D	14	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	47	U
1	F	11	C
1	F	3	G
1	F	16	H2U
1	E	16	H2U

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

42 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	$\# Z > 2$
1	1MA	D	58	1	21,25,26	0.80	1 (4%)	30,37,40	0.89	3 (10%)
1	2MG	E	10	1	23,26,27	0.39	0	33,38,41	0.90	2 (6%)
1	M2G	D	26	1	24,27,28	0.36	0	33,40,43	1.42	5 (15%)
1	H2U	F	17	1	18,21,22	1.13	1 (5%)	19,30,33	1.41	4 (21%)
1	OMG	F	34	1	23,26,27	0.40	0	32,38,41	1.15	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	7MG	E	46	1	23,26,27	2.69	3 (13%)	27,39,42	2.10	4 (14%)
1	1MA	E	58	1	21,25,26	0.76	1 (4%)	30,37,40	0.97	3 (10%)
1	2MG	F	10	1	23,26,27	0.38	0	33,38,41	0.84	2 (6%)
1	OMC	D	32	1	19,22,23	0.38	0	25,31,34	1.02	2 (8%)
1	OMC	F	32	1	19,22,23	0.37	0	25,31,34	0.86	1 (4%)
1	5MC	D	40	1	19,22,23	1.93	1 (5%)	26,32,35	1.35	4 (15%)
1	OMC	E	32	1	19,22,23	0.35	0	25,31,34	1.21	2 (8%)
1	PSU	D	39	1	18,21,22	0.66	0	21,30,33	1.07	2 (9%)
1	5MC	E	49	1	19,22,23	0.47	0	26,32,35	0.86	2 (7%)
1	PSU	E	55	1	18,21,22	0.64	0	21,30,33	1.17	2 (9%)
1	5MC	F	40	1	19,22,23	2.92	1 (5%)	26,32,35	3.64	4 (15%)
1	M2G	E	26	1	24,27,28	0.41	0	33,40,43	2.75	7 (21%)
1	YYG	E	37	1	38,42,43	1.62	8 (21%)	45,62,65	2.24	17 (37%)
1	M2G	F	26	1	24,27,28	0.34	0	33,40,43	0.55	0
1	7MG	D	46	1	23,26,27	3.01	4 (17%)	27,39,42	2.06	6 (22%)
1	PSU	E	39	1	18,21,22	0.87	1 (5%)	21,30,33	1.04	1 (4%)
1	H2U	D	16	1	18,21,22	0.74	0	19,30,33	1.96	4 (21%)
1	5MC	E	40	1	19,22,23	2.57	1 (5%)	26,32,35	1.33	3 (11%)
1	1MA	F	58	1	21,25,26	0.79	1 (4%)	30,37,40	0.66	1 (3%)
1	5MC	F	49	1	19,22,23	1.04	1 (5%)	26,32,35	0.98	2 (7%)
1	OMG	D	34	1	23,26,27	0.42	0	32,38,41	0.88	2 (6%)
1	H2U	E	17	1	18,21,22	1.16	2 (11%)	19,30,33	2.91	5 (26%)
1	PSU	F	39	1	18,21,22	0.82	0	21,30,33	1.58	2 (9%)
1	H2U	E	16	1	18,21,22	0.62	0	19,30,33	2.98	8 (42%)
1	H2U	D	17	1	18,21,22	0.72	1 (5%)	19,30,33	1.49	4 (21%)
1	5MC	D	49	1	19,22,23	0.59	1 (5%)	26,32,35	2.09	5 (19%)
1	5MU	D	54	1	19,22,23	4.53	1 (5%)	27,32,35	3.58	5 (18%)
1	YYG	D	37	1	38,42,43	1.73	7 (18%)	45,62,65	2.77	17 (37%)
1	H2U	F	16	1	18,21,22	1.10	1 (5%)	19,30,33	2.90	10 (52%)
1	PSU	D	55	1	18,21,22	0.75	0	21,30,33	1.04	2 (9%)
1	7MG	F	46	1	23,26,27	2.71	3 (13%)	27,39,42	2.14	5 (18%)
1	5MU	E	54	1	19,22,23	1.93	1 (5%)	27,32,35	0.91	2 (7%)
1	OMG	E	34	1	23,26,27	0.38	0	32,38,41	1.47	4 (12%)
1	YYG	F	37	1	38,42,43	1.50	5 (13%)	45,62,65	2.48	17 (37%)
1	2MG	D	10	1	23,26,27	0.34	0	33,38,41	0.71	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MU	F	54	1	19,22,23	1.51	1 (5%)	27,32,35	0.71	1 (3%)
1	PSU	F	55	1	18,21,22	0.78	0	21,30,33	1.00	1 (4%)

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
1	1MA	D	58	1	-	2/7/25/26	0/3/3/3
1	2MG	E	10	1	-	1/9/27/28	0/3/3/3
1	M2G	D	26	1	-	0/11/29/30	0/3/3/3
1	H2U	F	17	1	-	4/7/38/39	0/2/2/2
1	OMG	F	34	1	-	1/9/27/28	0/3/3/3
1	7MG	E	46	1	-	1/7/37/38	0/3/3/3
1	1MA	E	58	1	-	0/7/25/26	0/3/3/3
1	2MG	F	10	1	-	0/9/27/28	0/3/3/3
1	OMC	D	32	1	-	1/9/27/28	0/2/2/2
1	OMC	F	32	1	-	0/9/27/28	0/2/2/2
1	5MC	D	40	1	-	0/7/25/26	0/2/2/2
1	OMC	E	32	1	-	2/9/27/28	0/2/2/2
1	PSU	D	39	1	-	4/7/25/26	0/2/2/2
1	5MC	E	49	1	-	0/7/25/26	0/2/2/2
1	PSU	E	55	1	-	2/7/25/26	0/2/2/2
1	5MC	F	40	1	-	0/7/25/26	0/2/2/2
1	M2G	E	26	1	-	3/11/29/30	0/3/3/3
1	YYG	E	37	1	-	14/24/42/43	0/4/4/4
1	M2G	F	26	1	-	1/11/29/30	0/3/3/3
1	7MG	D	46	1	-	2/7/37/38	0/3/3/3
1	PSU	E	39	1	-	0/7/25/26	0/2/2/2
1	H2U	D	16	1	-	6/7/38/39	0/2/2/2
1	5MC	E	40	1	-	2/7/25/26	0/2/2/2
1	1MA	F	58	1	-	2/7/25/26	0/3/3/3
1	5MC	F	49	1	-	0/7/25/26	0/2/2/2
1	OMG	D	34	1	-	2/9/27/28	0/3/3/3
1	H2U	E	17	1	-	2/7/38/39	0/2/2/2
1	PSU	F	39	1	-	0/7/25/26	0/2/2/2
1	H2U	E	16	1	-	5/7/38/39	0/2/2/2
1	H2U	D	17	1	-	6/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	D	49	1	-	0/7/25/26	0/2/2/2
1	5MU	D	54	1	-	0/7/25/26	0/2/2/2
1	YYG	D	37	1	-	9/24/42/43	0/4/4/4
1	H2U	F	16	1	-	0/7/38/39	0/2/2/2
1	PSU	D	55	1	-	1/7/25/26	0/2/2/2
1	7MG	F	46	1	-	0/7/37/38	0/3/3/3
1	5MU	E	54	1	-	0/7/25/26	0/2/2/2
1	OMG	E	34	1	-	3/9/27/28	0/3/3/3
1	YYG	F	37	1	-	4/24/42/43	0/4/4/4
1	2MG	D	10	1	-	2/9/27/28	0/3/3/3
1	5MU	F	54	1	-	0/7/25/26	0/2/2/2
1	PSU	F	55	1	-	1/7/25/26	0/2/2/2

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	54	5MU	C5M-C5	-19.68	1.02	1.50
1	D	46	7MG	C8-N9	-13.33	1.37	1.45
1	F	40	5MC	CM5-C5	-12.66	1.19	1.50
1	F	46	7MG	C8-N9	-12.34	1.37	1.45
1	E	46	7MG	C8-N9	-12.31	1.37	1.45

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	40	5MC	CM5-C5-C6	-14.23	103.59	122.85
1	D	54	5MU	C5M-C5-C4	12.85	132.50	118.78
1	D	54	5MU	C5M-C5-C6	-11.18	107.72	122.85
1	F	40	5MC	CM5-C5-C4	11.06	138.68	120.51
1	E	26	M2G	CM1-N2-C2	9.34	139.72	120.61

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	16	H2U	O4'-C1'-N1-C6
1	D	16	H2U	C2'-C1'-N1-C2
1	D	17	H2U	O4'-C4'-C5'-O5'
1	D	32	OMC	C3'-C2'-O2'-CM2
1	D	37	YYG	O23-C21-N20-C15

There are no ring outliers.

38 monomers are involved in 152 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	58	1MA	2	0
1	E	10	2MG	9	0
1	D	26	M2G	11	0
1	F	17	H2U	1	0
1	F	34	OMG	4	0
1	E	46	7MG	2	0
1	E	58	1MA	1	0
1	F	10	2MG	9	0
1	D	32	OMC	2	0
1	F	32	OMC	1	0
1	D	40	5MC	4	0
1	E	32	OMC	3	0
1	D	39	PSU	6	0
1	E	55	PSU	1	0
1	F	40	5MC	3	0
1	E	26	M2G	9	0
1	E	37	YYG	10	0
1	F	26	M2G	7	0
1	D	46	7MG	2	0
1	E	39	PSU	2	0
1	D	16	H2U	5	0
1	F	49	5MC	1	0
1	D	34	OMG	2	0
1	E	17	H2U	3	0
1	E	16	H2U	5	0
1	D	17	H2U	3	0
1	D	49	5MC	1	0
1	D	54	5MU	1	0
1	D	37	YYG	8	0
1	F	16	H2U	5	0
1	D	55	PSU	1	0
1	F	46	7MG	4	0
1	E	54	5MU	2	0
1	E	34	OMG	3	0
1	F	37	YYG	20	0
1	D	10	2MG	4	0
1	F	54	5MU	1	0
1	F	55	PSU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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
5	GNP	B	406	3	34,34,34	1.86	3 (8%)	47,54,54	1.70	8 (17%)
4	PHE	D	77	1	10,11,12	1.18	1 (10%)	8,13,15	0.41	0
4	PHE	F	77	1	10,11,12	1.35	2 (20%)	8,13,15	0.30	0
4	PHE	E	77	1	10,11,12	1.09	1 (10%)	8,13,15	0.64	0
5	GNP	A	406	3	34,34,34	2.03	7 (20%)	47,54,54	2.84	15 (31%)
5	GNP	C	406	3	34,34,34	2.53	4 (11%)	47,54,54	3.10	13 (27%)

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	GNP	B	406	3	-	9/18/38/38	0/3/3/3
4	PHE	D	77	1	-	0/5/6/8	0/1/1/1
4	PHE	F	77	1	-	1/5/6/8	0/1/1/1
4	PHE	E	77	1	-	1/5/6/8	0/1/1/1
5	GNP	A	406	3	-	9/18/38/38	0/3/3/3
5	GNP	C	406	3	-	5/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	406	GNP	PA-O3A	-9.80	1.48	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	406	GNP	PB-O3A	-8.02	1.49	1.59
5	A	406	GNP	PA-O3A	-7.82	1.51	1.59
5	B	406	GNP	PA-O3A	-7.45	1.51	1.59
5	B	406	GNP	PB-O3A	-6.27	1.51	1.59

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	406	GNP	O2B-PB-O1B	10.89	133.22	109.87
5	A	406	GNP	C1'-N9-C8	-10.22	97.70	126.73
5	A	406	GNP	C1'-N9-C4	9.51	154.59	126.49
5	C	406	GNP	C1'-N9-C8	9.09	152.55	126.73
5	C	406	GNP	C1'-N9-C4	-8.65	100.94	126.49

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	77	PHE	O-C-CA-CB
4	F	77	PHE	O-C-CA-CB
5	A	406	GNP	PB-N3B-PG-O1G
5	A	406	GNP	PG-N3B-PB-O1B
5	A	406	GNP	PA-O3A-PB-O2B

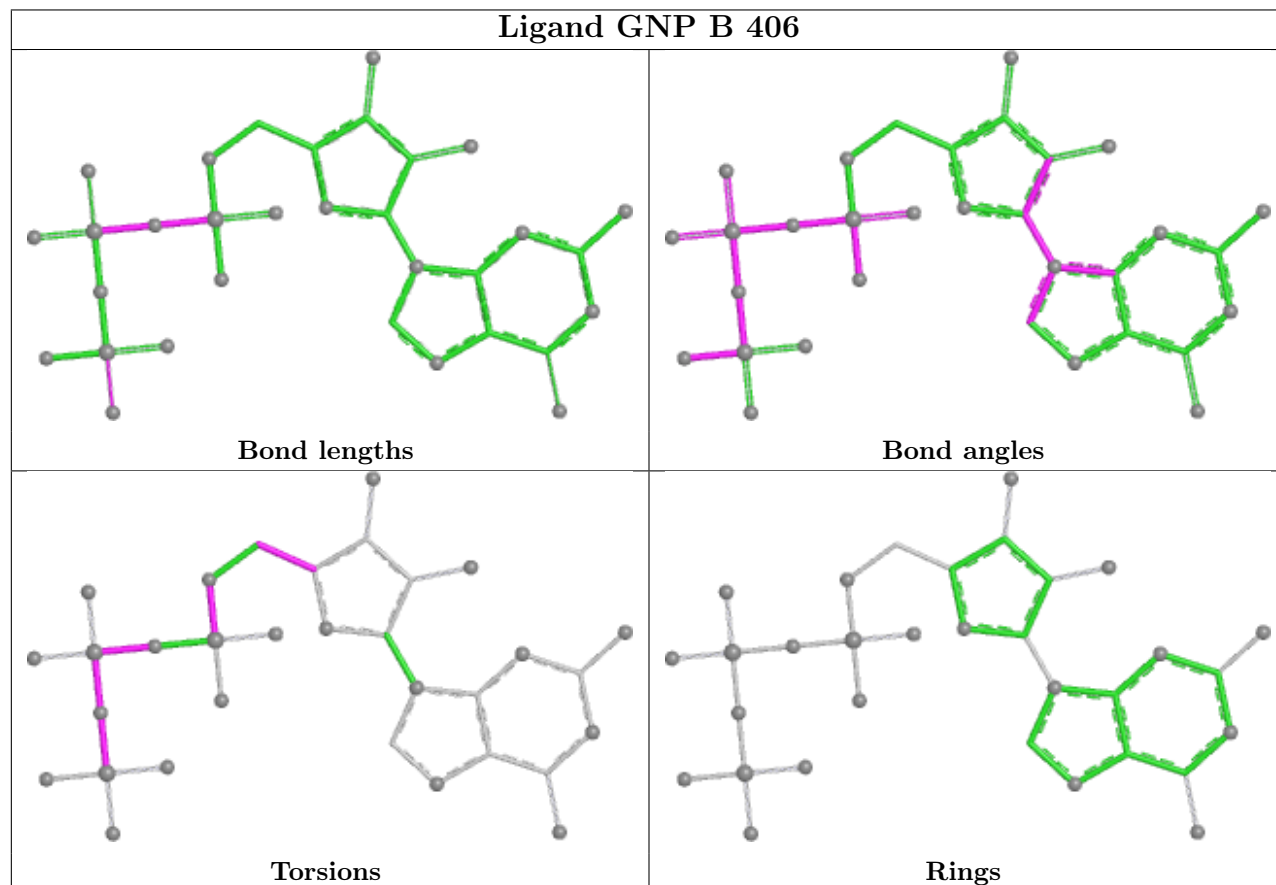
There are no ring outliers.

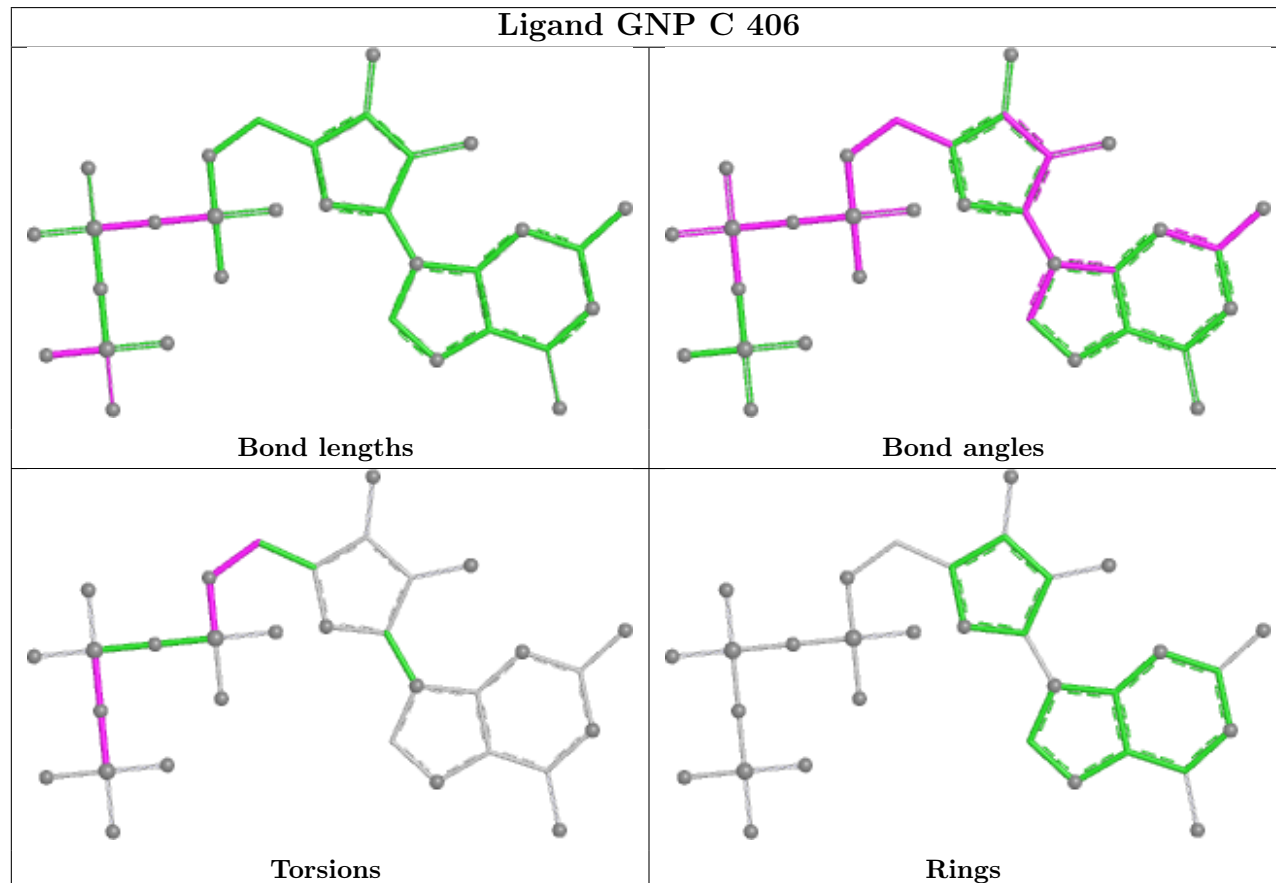
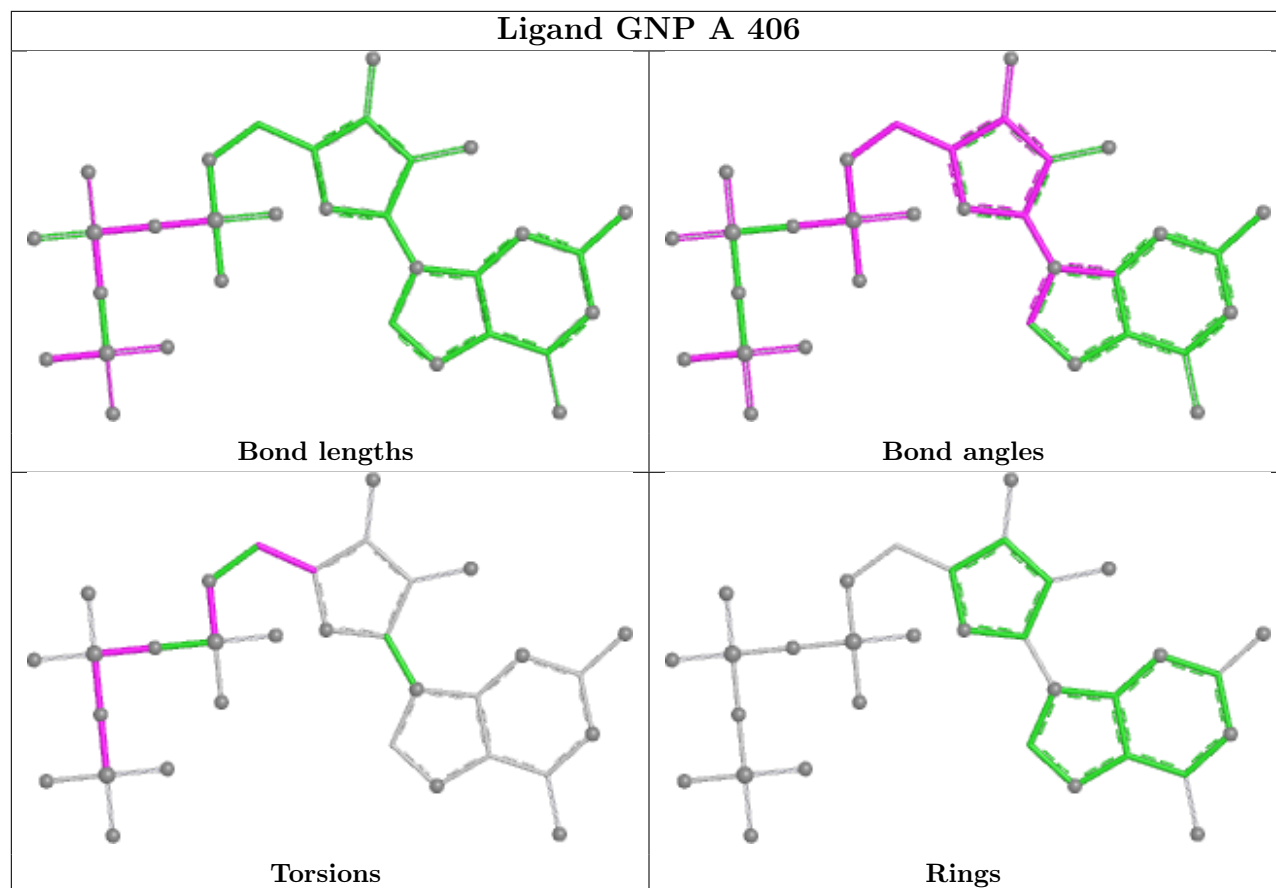
6 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	406	GNP	7	0
4	D	77	PHE	2	0
4	F	77	PHE	1	0
4	E	77	PHE	1	0
5	A	406	GNP	6	0
5	C	406	GNP	7	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.