



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:29 PM GMT

PDB ID : 1TTT
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

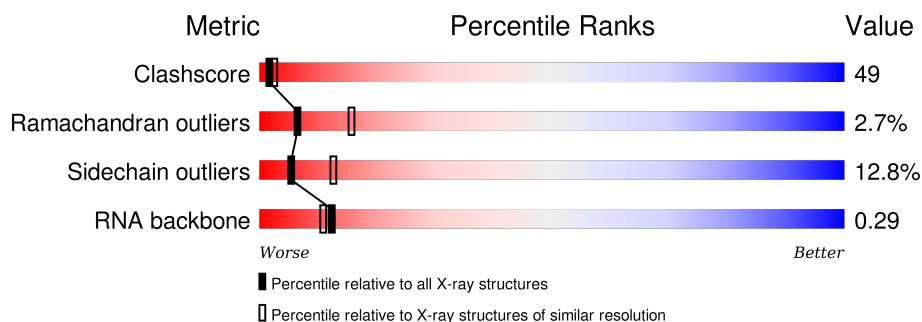
1 Overall quality at a glance

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	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RNA backbone	2183	1069 (3.10-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	D	76	<div> <div></div> <div>28%</div> <div>55%</div> <div>14%</div> </div>
1	E	76	<div> <div>8%</div> <div>25%</div> <div>39%</div> <div>28%</div> </div>
1	F	76	<div> <div>28%</div> <div>51%</div> <div>17%</div> </div>
2	A	405	<div> <div>34%</div> <div>53%</div> <div>12%</div> </div>
2	B	405	<div> <div>39%</div> <div>49%</div> <div>12%</div> </div>
2	C	405	<div> <div>29%</div> <div>54%</div> <div>15%</div> </div>

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			

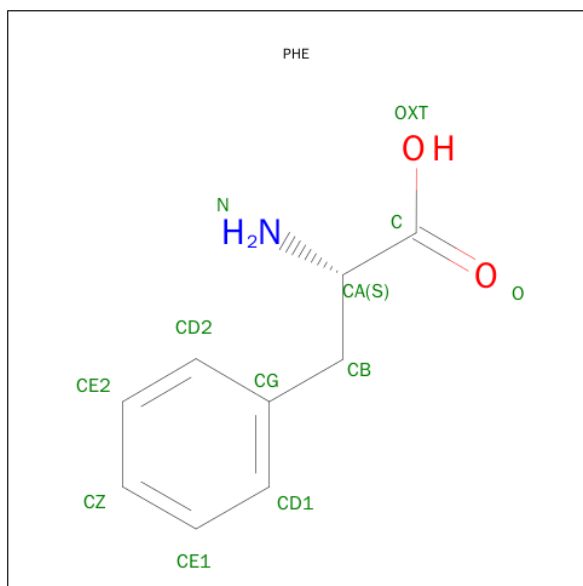
- Molecule 2 is a protein called OF ELONGATION FACTOR TU (EF-TU).

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 (three-letter code: MG) (formula: Mg).

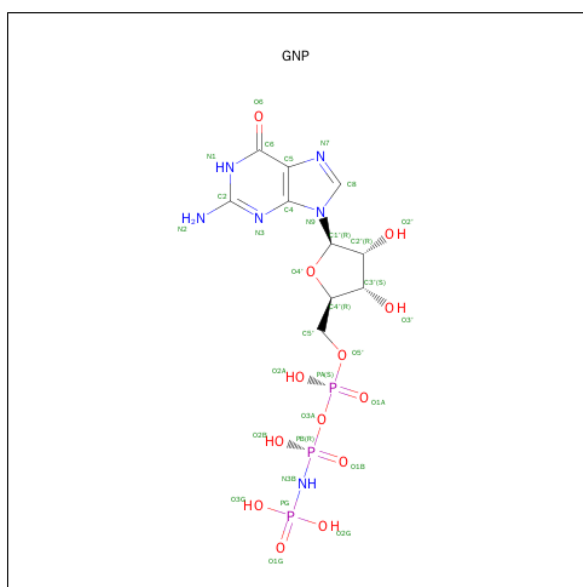
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHENYLALANINE (three-letter code: 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 (three-letter code: 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.

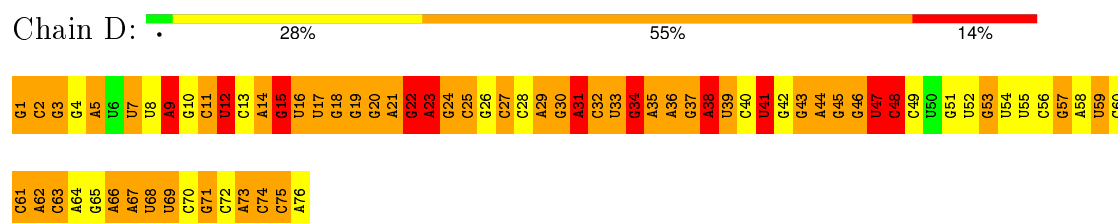
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	21	Total	O	0	0
			21	21		
6	B	13	Total	O	0	0
			13	13		
6	C	7	Total	O	0	0
			7	7		
6	D	6	Total	O	0	0
			6	6		
6	E	2	Total	O	0	0
			2	2		
6	F	1	Total	O	0	0
			1	1		

3 Residue-property plots

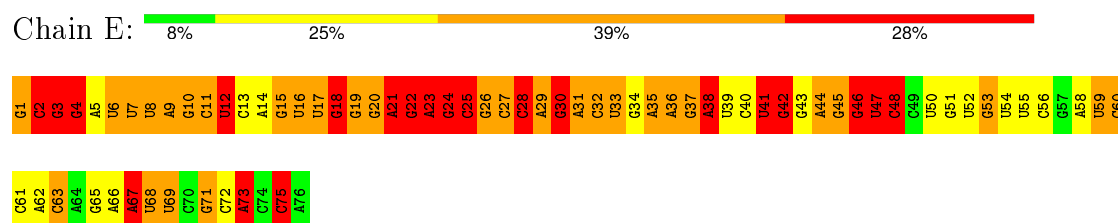
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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.

Note EDS was not executed.

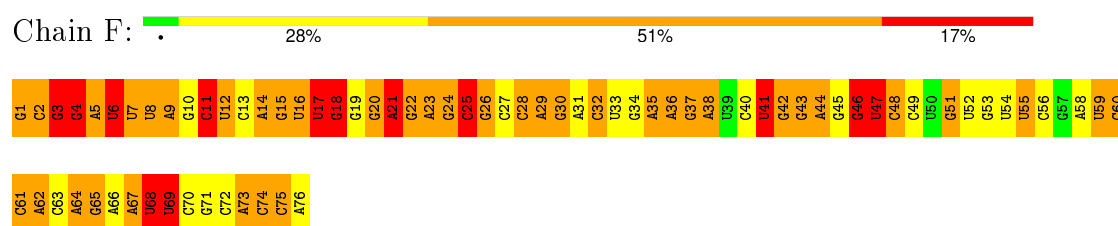
• Molecule 1: TRANSFER RIBONUCLEIC ACID (YEAST, PHE)



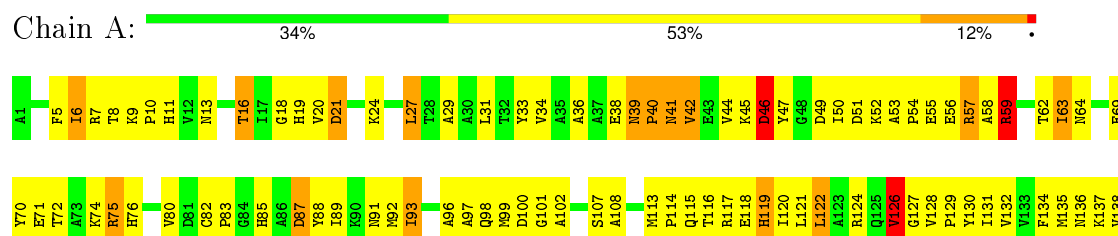
• Molecule 1: TRANSFER RIBONUCLEIC ACID (YEAST, PHE)

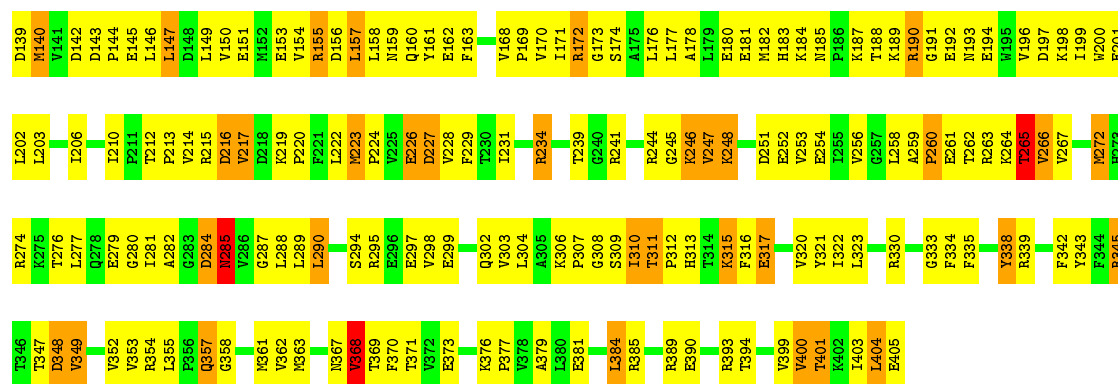


• Molecule 1: TRANSFER RIBONUCLEIC ACID (YEAST, PHE)



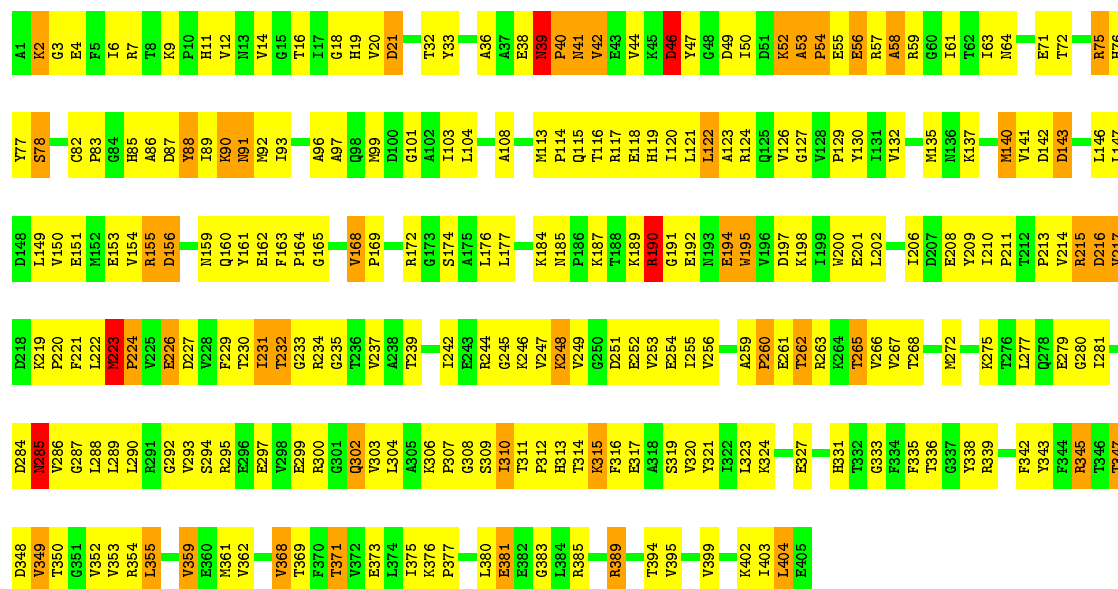
• Molecule 2: OF ELONGATION FACTOR TU (EF-TU)





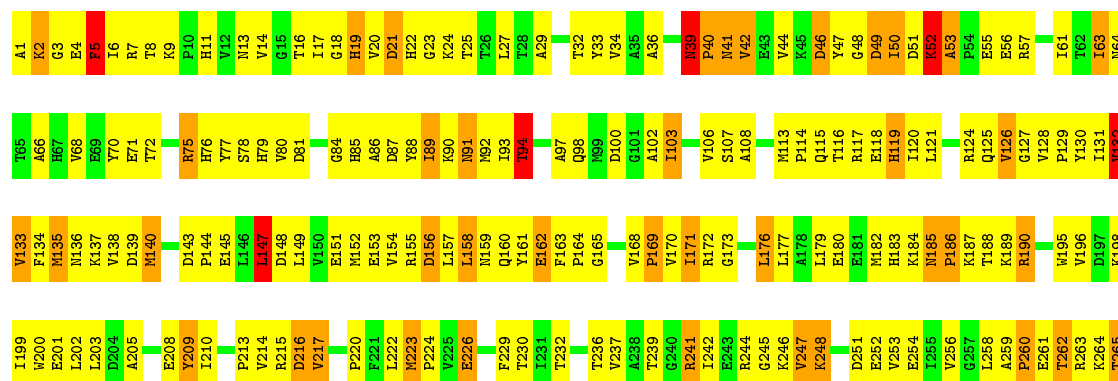
• Molecule 2: OF ELONGATION FACTOR TU (EF-TU)

Chain B: 39% 49% 12%



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

Chain C: 29% 54% 15%





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be 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: OMC, 5MU, GNP, OMG, H2U, MG, YYG, 2MG, 5MC, 1MA, M2G, 7MG, 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	D	0.46	1/1487 (0.1%)	2.28	87/2315 (3.8%)
1	E	0.47	1/1487 (0.1%)	2.25	92/2315 (4.0%)
1	F	0.45	0/1487	2.21	108/2315 (4.7%)
2	A	0.87	1/3204 (0.0%)	1.52	43/4345 (1.0%)
2	B	0.87	0/3204	1.47	27/4345 (0.6%)
2	C	0.86	0/3204	1.52	35/4345 (0.8%)
All	All	0.76	3/14073 (0.0%)	1.80	392/19980 (2.0%)

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	F	2	0
2	A	2	0
All	All	4	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	1	G	OP3-P	-7.83	1.51	1.61
1	D	1	G	OP3-P	-5.69	1.54	1.61
2	A	400	VAL	CA-CB	-5.18	1.43	1.54

The worst 5 of 392 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	22	G	O4'-C1'-N9	29.42	131.74	108.20
1	D	33	U	O4'-C1'-N1	20.76	124.81	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	18	G	O4'-C1'-N9	20.70	124.76	108.20
2	A	39	ASN	C-N-CD	-20.57	75.34	120.60
1	D	21	A	N9-C1'-C2'	-20.07	87.90	114.00

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	11	C	C2',C3'
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	116	0
1	E	1652	0	855	131	0
1	F	1652	0	856	108	0
2	A	3144	0	3161	282	0
2	B	3144	0	3160	302	0
2	C	3144	0	3162	362	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
6	B	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	1273	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 49.

The worst 5 of 1273 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%)	13	32
2	B	403/405 (100%)	359 (89%)	31 (8%)	13 (3%)	5	12
2	C	403/405 (100%)	353 (88%)	36 (9%)	14 (4%)	4	10
All	All	1209/1215 (100%)	1074 (89%)	102 (8%)	33 (3%)	6	16

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 ⓘ

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%)	297 (88%)	41 (12%)	6	14
2	B	338/338 (100%)	299 (88%)	39 (12%)	7	16
2	C	338/338 (100%)	288 (85%)	50 (15%)	4	9
All	All	1014/1014 (100%)	884 (87%)	130 (13%)	5	12

5 of 130 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	223	MET
2	B	317	GLU
2	C	319	SER
2	B	231	ILE
2	B	285	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	64	ASN
2	B	119	HIS
2	C	183	HIS
2	B	115	GLN
2	B	160	GLN

5.3.3 RNA ⓘ

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%)	24 (32%)	6 (8%)
All	All	225/228 (98%)	83 (36%)	22 (9%)

5 of 83 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	22	G
1	E	30	G
1	F	22	G
1	E	25	C
1	E	27	C

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	2MG	D	10	1	17,26,27	1.06	1 (5%)	21,38,41	2.94	6 (28%)
1	H2U	D	16	1	17,21,22	0.89	0	23,30,33	2.65	7 (30%)
1	H2U	D	17	1	17,21,22	0.74	1 (5%)	23,30,33	2.06	6 (26%)
1	M2G	D	26	1	17,27,28	1.12	1 (5%)	22,40,43	3.38	7 (31%)
1	OMC	D	32	1	13,22,23	0.79	0	20,31,34	1.31	3 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	D	34	1	17,26,27	1.13	1 (5%)	21,38,41	2.68	5 (23%)
1	YYG	D	37	1	27,42,43	1.99	6 (22%)	29,62,65	3.65	11 (37%)
1	PSU	D	39	1	13,21,22	1.36	2 (15%)	18,30,33	6.16	6 (33%)
1	5MC	D	40	1	13,22,23	2.92	2 (15%)	15,32,35	1.77	3 (20%)
1	7MG	D	46	1	19,26,27	2.33	4 (21%)	24,39,42	2.37	5 (20%)
1	5MC	D	49	1	13,22,23	1.10	2 (15%)	15,32,35	2.05	3 (20%)
1	5MU	D	54	1	12,22,23	7.17	4 (33%)	14,32,35	5.60	6 (42%)
1	PSU	D	55	1	13,21,22	1.78	3 (23%)	18,30,33	6.21	7 (38%)
1	1MA	D	58	1	14,25,26	1.07	1 (7%)	15,37,40	1.56	2 (13%)
1	2MG	E	10	1	17,26,27	1.08	1 (5%)	21,38,41	2.85	6 (28%)
1	H2U	E	16	1	17,21,22	0.68	0	23,30,33	3.39	10 (43%)
1	H2U	E	17	1	17,21,22	1.15	2 (11%)	23,30,33	2.19	6 (26%)
1	M2G	E	26	1	17,27,28	1.22	2 (11%)	22,40,43	5.48	8 (36%)
1	OMC	E	32	1	13,22,23	0.75	0	20,31,34	1.35	3 (15%)
1	OMG	E	34	1	17,26,27	1.10	1 (5%)	21,38,41	2.91	5 (23%)
1	YYG	E	37	1	27,42,43	1.82	6 (22%)	29,62,65	2.68	12 (41%)
1	PSU	E	39	1	13,21,22	1.98	4 (30%)	18,30,33	6.45	7 (38%)
1	5MC	E	40	1	13,22,23	3.83	2 (15%)	15,32,35	0.68	0
1	7MG	E	46	1	19,26,27	1.67	3 (15%)	24,39,42	2.57	5 (20%)
1	5MC	E	49	1	13,22,23	0.93	1 (7%)	15,32,35	1.14	2 (13%)
1	5MU	E	54	1	12,22,23	3.22	3 (25%)	14,32,35	4.44	3 (21%)
1	PSU	E	55	1	13,21,22	1.53	3 (23%)	18,30,33	6.19	6 (33%)
1	1MA	E	58	1	14,25,26	1.01	1 (7%)	15,37,40	1.38	2 (13%)
1	2MG	F	10	1	17,26,27	1.05	1 (5%)	21,38,41	2.91	6 (28%)
1	H2U	F	16	1	17,21,22	1.09	2 (11%)	23,30,33	3.13	12 (52%)
1	H2U	F	17	1	17,21,22	1.12	2 (11%)	23,30,33	1.89	8 (34%)
1	M2G	F	26	1	17,27,28	1.17	1 (5%)	22,40,43	2.29	4 (18%)
1	OMC	F	32	1	13,22,23	0.74	0	20,31,34	1.29	2 (10%)
1	OMG	F	34	1	17,26,27	1.11	1 (5%)	21,38,41	2.78	4 (19%)
1	YYG	F	37	1	27,42,43	1.75	3 (11%)	29,62,65	2.78	11 (37%)
1	PSU	F	39	1	13,21,22	1.85	3 (23%)	18,30,33	6.34	7 (38%)
1	5MC	F	40	1	13,22,23	4.36	2 (15%)	15,32,35	2.11	2 (13%)
1	7MG	F	46	1	19,26,27	1.70	3 (15%)	24,39,42	2.49	5 (20%)
1	5MC	F	49	1	13,22,23	1.54	2 (15%)	15,32,35	1.18	1 (6%)
1	5MU	F	54	1	12,22,23	2.63	3 (25%)	14,32,35	4.41	2 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	F	55	1	13,21,22	2.12	3 (23%)	18,30,33	6.29	5 (27%)
1	1MA	F	58	1	14,25,26	1.04	1 (7%)	15,37,40	1.16	1 (6%)

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	2MG	D	10	1	-	0/5/27/28	0/3/3/3
1	H2U	D	16	1	-	0/7/38/39	0/2/2/2
1	H2U	D	17	1	-	0/7/38/39	0/2/2/2
1	M2G	D	26	1	-	0/7/29/30	0/3/3/3
1	OMC	D	32	1	-	0/5/27/28	0/2/2/2
1	OMG	D	34	1	-	0/5/27/28	0/3/3/3
1	YYG	D	37	1	-	0/20/42/43	0/4/4/4
1	PSU	D	39	1	-	0/7/25/26	0/2/2/2
1	5MC	D	40	1	-	0/3/25/26	0/2/2/2
1	7MG	D	46	1	-	0/7/37/38	0/3/3/3
1	5MC	D	49	1	-	0/3/25/26	0/2/2/2
1	5MU	D	54	1	-	0/3/25/26	0/2/2/2
1	PSU	D	55	1	-	0/7/25/26	0/2/2/2
1	1MA	D	58	1	-	0/3/25/26	0/3/3/3
1	2MG	E	10	1	-	0/5/27/28	0/3/3/3
1	H2U	E	16	1	-	0/7/38/39	0/2/2/2
1	H2U	E	17	1	-	0/7/38/39	0/2/2/2
1	M2G	E	26	1	-	0/7/29/30	0/3/3/3
1	OMC	E	32	1	-	0/5/27/28	0/2/2/2
1	OMG	E	34	1	-	0/5/27/28	0/3/3/3
1	YYG	E	37	1	-	0/20/42/43	0/4/4/4
1	PSU	E	39	1	-	0/7/25/26	0/2/2/2
1	5MC	E	40	1	-	0/3/25/26	0/2/2/2
1	7MG	E	46	1	-	0/7/37/38	0/3/3/3
1	5MC	E	49	1	-	0/3/25/26	0/2/2/2
1	5MU	E	54	1	-	0/3/25/26	0/2/2/2
1	PSU	E	55	1	-	0/7/25/26	0/2/2/2
1	1MA	E	58	1	-	0/3/25/26	0/3/3/3
1	2MG	F	10	1	-	0/5/27/28	0/3/3/3
1	H2U	F	16	1	-	0/7/38/39	0/2/2/2
1	H2U	F	17	1	-	0/7/38/39	0/2/2/2
1	M2G	F	26	1	-	0/7/29/30	0/3/3/3
1	OMC	F	32	1	-	0/5/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	F	34	1	-	0/5/27/28	0/3/3/3
1	YYG	F	37	1	-	0/20/42/43	0/4/4/4
1	PSU	F	39	1	-	0/7/25/26	0/2/2/2
1	5MC	F	40	1	-	0/3/25/26	0/2/2/2
1	7MG	F	46	1	-	0/7/37/38	0/3/3/3
1	5MC	F	49	1	-	0/3/25/26	0/2/2/2
1	5MU	F	54	1	-	0/3/25/26	0/2/2/2
1	PSU	F	55	1	-	0/7/25/26	0/2/2/2
1	1MA	F	58	1	-	0/3/25/26	0/3/3/3

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	54	5MU	C5M-C5	-24.46	1.02	1.51
1	F	40	5MC	CM5-C5	-15.37	1.19	1.51
1	E	40	5MC	CM5-C5	-13.42	1.23	1.51
1	E	54	5MU	C5M-C5	-10.30	1.30	1.51
1	D	40	5MC	CM5-C5	-10.06	1.30	1.51

The worst 5 of 222 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	39	PSU	N1-C2-N3	-20.92	114.99	128.33
1	F	55	PSU	N1-C2-N3	-20.91	114.99	128.33
1	E	55	PSU	N1-C2-N3	-20.90	115.00	128.33
1	E	39	PSU	N1-C2-N3	-20.89	115.00	128.33
1	D	55	PSU	N1-C2-N3	-20.86	115.03	128.33

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

38 monomers are involved in 156 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	10	2MG	4	0
1	D	16	H2U	5	0
1	D	17	H2U	3	0
1	D	26	M2G	11	0
1	D	32	OMC	2	0
1	D	34	OMG	2	0
1	D	37	YYG	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	39	PSU	5	0
1	D	40	5MC	4	0
1	D	46	7MG	2	0
1	D	49	5MC	1	0
1	D	54	5MU	1	0
1	D	55	PSU	1	0
1	D	58	1MA	3	0
1	E	10	2MG	12	0
1	E	16	H2U	4	0
1	E	17	H2U	3	0
1	E	26	M2G	11	0
1	E	32	OMC	3	0
1	E	34	OMG	3	0
1	E	37	YYG	12	0
1	E	39	PSU	2	0
1	E	46	7MG	2	0
1	E	54	5MU	3	0
1	E	55	PSU	1	0
1	E	58	1MA	1	0
1	F	10	2MG	9	0
1	F	16	H2U	5	0
1	F	17	H2U	1	0
1	F	26	M2G	7	0
1	F	32	OMC	1	0
1	F	34	OMG	4	0
1	F	37	YYG	17	0
1	F	40	5MC	3	0
1	F	46	7MG	4	0
1	F	49	5MC	1	0
1	F	54	5MU	1	0
1	F	55	PSU	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	A	406	3	28,34,34	1.85	7 (25%)	33,54,54	4.48	16 (48%)
5	GNP	B	406	3	28,34,34	1.66	3 (10%)	33,54,54	2.76	8 (24%)
5	GNP	C	406	3	28,34,34	2.38	5 (17%)	33,54,54	5.11	13 (39%)
4	PHE	D	77	1	10,11,12	1.02	1 (10%)	10,13,15	2.15	2 (20%)
4	PHE	E	77	1	10,11,12	0.93	1 (10%)	10,13,15	1.51	2 (20%)
4	PHE	F	77	1	10,11,12	1.15	1 (10%)	10,13,15	2.01	2 (20%)

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	A	406	3	-	1/12/38/38	0/3/3/3
5	GNP	B	406	3	-	1/12/38/38	0/3/3/3
5	GNP	C	406	3	-	1/12/38/38	0/3/3/3
4	PHE	D	77	1	-	0/4/6/8	0/1/1/1
4	PHE	E	77	1	-	0/4/6/8	0/1/1/1
4	PHE	F	77	1	-	0/4/6/8	0/1/1/1

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	PB-O3A	-7.99	1.49	1.59
5	B	406	GNP	PB-O3A	-6.26	1.51	1.59
5	A	406	GNP	PB-O3A	-4.79	1.53	1.59
5	A	406	GNP	PB-O2B	-3.50	1.46	1.56
5	C	406	GNP	PG-O2G	-3.34	1.47	1.56

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	406	GNP	C1'-N9-C4	-17.24	100.94	126.94
5	C	406	GNP	C2'-C1'-N9	-11.76	96.32	114.29
5	C	406	GNP	O3A-PA-O5'	-10.70	74.56	102.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	406	GNP	C5-C6-N1	-9.38	110.76	123.59
5	B	406	GNP	C5-C6-N1	-9.22	110.99	123.59

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	406	GNP	O1B-PB-N3B-PG
5	C	406	GNP	O1B-PB-N3B-PG
5	B	406	GNP	O1B-PB-N3B-PG

There are no ring outliers.

6 monomers are involved in 24 short contacts:

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

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.