



# wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 02:11 AM GMT

PDB ID : 2FMT  
Title : METHIONYL-TRNAFMET FORMYLTRANSFERASE COMPLEXED  
WITH FORMYL-METHIONYL-TRNAFMET  
Authors : Schmitt, E.; Mechulam, Y.; Blanquet, S.  
Deposited on : 1998-07-29  
Resolution : 2.80 Å(reported)

This is a wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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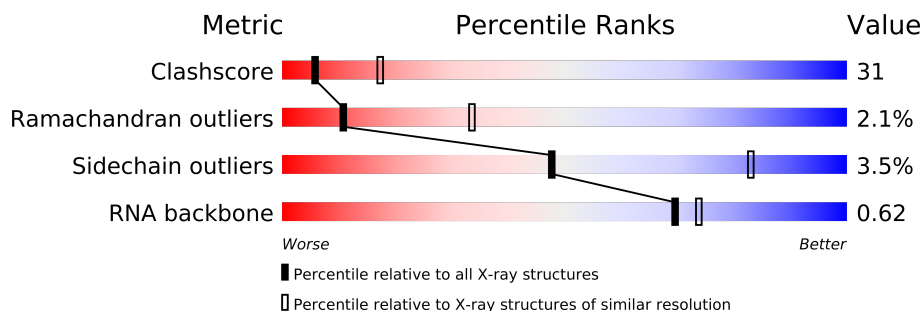
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.80 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	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RNA backbone	1838	1076 (3.30-2.30)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	77	
1	D	77	
2	A	314	
2	B	314	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8179 atoms, of which 0 are hydrogen and 0 are deuterium.

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 FORMYL-METHIONYL-TRNAFMET2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	77	Total	C	N	O	P	S	0	0	0
			1645	734	297	536	77	1			
1	D	77	Total	C	N	O	P	S	0	0	0
			1645	734	297	536	77	1			

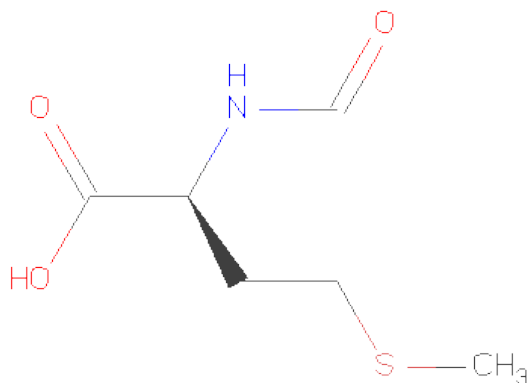
- Molecule 2 is a protein called METHIONYL-TRNA FMET FORMYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	314	Total	C	N	O	S	0	0	0
			2392	1517	414	450	11			
2	B	314	Total	C	N	O	S	0	0	0
			2392	1517	414	450	11			

- 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	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: C<sub>6</sub>H<sub>11</sub>NO<sub>3</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
4	D	1	Total	C	N	O	S	0	0
			10	6	1	2	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	17	Total	O	0	0
			17	17		
5	D	13	Total	O	0	0
			13	13		
5	A	35	Total	O	0	0
			35	35		
5	B	18	Total	O	0	0
			18	18		

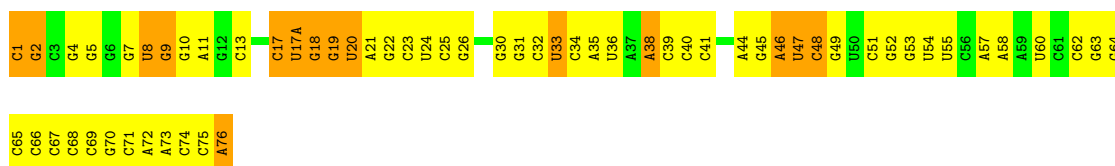
### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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.

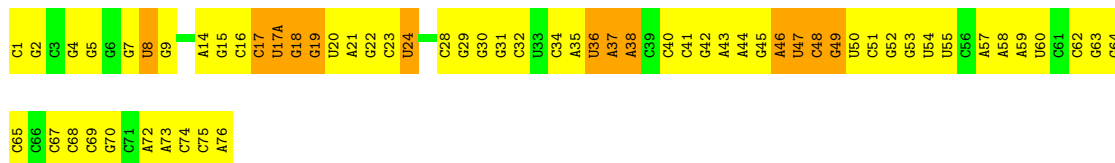
#### • Molecule 1: FORMYL-METHIONYL-TRNAFMET2

Chain C: 



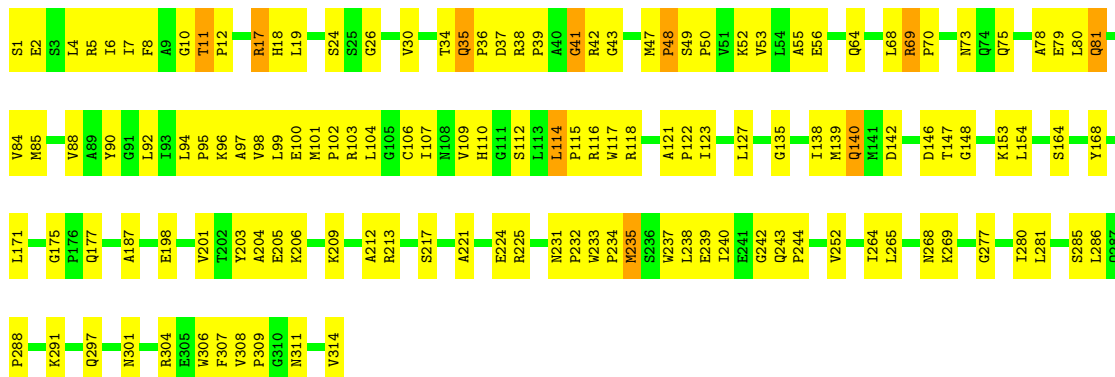
#### • Molecule 1: FORMYL-METHIONYL-TRNAFMET2

Chain D: 



#### • Molecule 2: METHIONYL-TRNA FMET FORMYLTRANSFERASE

Chain A: 



#### • Molecule 2: METHIONYL-TRNA FMET FORMYLTRANSFERASE

Chain B: 

A260	P261	G262	T263	T264	L265	I272	Q273	V274	A275	T276	G277	D278	G279	T280	L281	N282	L283	L284	S285	L286	A289	S302	R303	R304	E305	W306	F307	V308	N311	R312	L313	V314																						
D83	S164	Y168	L171	G175	P176	L179	L186	A187	A191	E198	V201	T202	Y203	A204	L207	S208	K209	A212	D215	W216	S217	L218	S219	Q222	L223	E224	R225	N231	P232	W233	P234	M235	S236	W237	L238	E239	T240	E241	G242	Q243	P244	T253	A256											
R83	V84	N85	V86	V87	Y90	G91	L92	T93	L94	P95	K96	A97	V98	L99	E100	M101	P102	R103	L104	C106	I107	M108	V109	H110	G111	S112	L113	L114	P115	R116	W117	R118	G119	A120	A121	P122	I123	Q124	R125	S126	L127	W128	G135	M139	Q140	N141	D142	V143	G144	L145	D146	T147	G148	I158
S1	E2	S3	L4	R5	I6	I7	G10	T11	P12	R17	H18	M28	V29	V30	G31	T34	Q35	P36	D37	R38	P39	A40	G41	R42	M47	P48	S49	P50	V51	K52	A55	E56	P61	V62	F63	Q64	P65	V66	S67	L68	R69	P70	N73	Q74	Q75	A78	E79	L80	Q81	A82				

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	201.71Å 68.06Å 86.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.00 – 2.80	Depositor
% Data completeness (in resolution range)	87.2 (19.00-2.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	CNS 0.3C	Depositor
R, $R_{free}$	0.247 , 0.292	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8179	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	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, MG, FME, H2U, 4SU, 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	C	0.52	2/1725 (0.1%)	0.73	2/2687 (0.1%)
1	D	0.51	1/1725 (0.1%)	0.76	2/2687 (0.1%)
2	A	0.49	0/2439	0.77	1/3317 (0.0%)
2	B	0.48	0/2439	0.76	2/3317 (0.1%)
All	All	0.50	3/8328 (0.0%)	0.76	7/12008 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1	C	OP3-P	-7.45	1.52	1.61
1	C	1	C	OP3-P	-6.99	1.52	1.61
1	C	76	A	C3'-O3'	5.93	1.50	1.42

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1	C	OP2-P-O3'	6.52	119.53	105.20
1	C	1	C	OP1-P-O3'	6.11	118.64	105.20
2	B	41	GLY	N-CA-C	5.87	127.77	113.10
2	A	41	GLY	N-CA-C	5.70	127.34	113.10
1	D	2	G	O5'-P-OP2	-5.24	100.99	105.70



There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	24	U	Sidechain

## 5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1645	0	839	89	0
1	D	1645	0	839	75	0
2	A	2392	0	2442	140	0
2	B	2392	0	2442	176	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	C	10	0	10	1	0
4	D	10	0	10	1	0
5	A	35	0	0	0	0
5	B	18	0	0	0	0
5	C	17	0	0	0	0
5	D	13	0	0	0	0
All	All	8179	0	6582	459	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 31.

The worst 5 of 459 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:32:OMC:O2'	1:C:32:OMC:CM2	1.68	1.42
1:C:32:OMC:O2'	1:C:32:OMC:C2'	1.68	1.41
1:D:32:OMC:CM2	1:D:32:OMC:O2'	1.71	1.37
1:C:1:C:H3'	1:C:2:G:C5'	1.78	1.13
1:C:1:C:C3'	1:C:2:G:H5'	1.80	1.10

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	312/314 (99%)	262 (84%)	45 (14%)	5 (2%)	14	44
2	B	312/314 (99%)	264 (85%)	40 (13%)	8 (3%)	8	26
All	All	624/628 (99%)	526 (84%)	85 (14%)	13 (2%)	11	33

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	256	ALA
2	B	175	GLY
2	A	11	THR
2	B	42	ARG
2	A	235	MET

### 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	257/257 (100%)	248 (96%)	9 (4%)	48	83
2	B	257/257 (100%)	248 (96%)	9 (4%)	48	83
All	All	514/514 (100%)	496 (96%)	18 (4%)	48	83

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	268	ASN
2	B	17	ARG
2	B	140	GLN
2	A	205	GLU

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Mol	Chain	Res	Type
2	A	232	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	297	GLN
2	B	27	HIS
2	B	243	GLN
2	A	282	ASN
2	B	222	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	76/77 (98%)	14 (18%)	3 (3%)
1	D	76/77 (98%)	14 (18%)	4 (5%)
All	All	152/154 (98%)	28 (18%)	7 (4%)

5 of 28 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	2	G
1	C	8	4SU
1	C	9	G
1	C	17	C
1	C	17(A)	U

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	D	17	C
1	D	46	A
1	D	17(A)	U
1	C	17(A)	U
1	D	36	U

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

10 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	H2U	C	20	1	19,21,22	0.83	1 (5%)	27,30,33	1.25	1 (3%)
1	OMC	C	32	1	20,22,23	2.96	4 (20%)	25,31,34	1.20	2 (8%)
1	5MU	C	54	1	20,22,23	0.84	1 (5%)	25,32,35	1.26	3 (12%)
1	PSU	C	55	1	19,21,22	2.06	3 (15%)	23,30,33	2.95	3 (13%)
1	4SU	C	8	1	19,21,22	4.80	2 (10%)	23,30,33	26.69	1 (4%)
1	H2U	D	20	1	19,21,22	1.06	1 (5%)	27,30,33	1.26	1 (3%)
1	OMC	D	32	1	20,22,23	2.32	4 (20%)	25,31,34	1.04	2 (8%)
1	5MU	D	54	1	20,22,23	0.95	2 (10%)	25,32,35	1.24	2 (8%)
1	PSU	D	55	1	19,21,22	2.12	3 (15%)	23,30,33	2.90	3 (13%)
1	4SU	D	8	1	19,21,22	5.11	2 (10%)	23,30,33	26.71	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	H2U	C	20	1	-	0/8/38/39	0/2/2/2
1	OMC	C	32	1	-	0/8/27/28	0/2/2/2
1	5MU	C	54	1	-	0/6/25/26	0/2/2/2
1	PSU	C	55	1	-	0/8/25/26	0/2/2/2
1	4SU	C	8	1	-	0/6/25/26	0/2/2/2
1	H2U	D	20	1	-	0/8/38/39	0/2/2/2
1	OMC	D	32	1	-	0/8/27/28	0/2/2/2
1	5MU	D	54	1	-	0/6/25/26	0/2/2/2
1	PSU	D	55	1	-	0/8/25/26	0/2/2/2
1	4SU	D	8	1	-	0/6/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	8	4SU	C4-S4	-21.87	1.25	1.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	8	4SU	C4-S4	-20.46	1.27	1.67
1	C	32	OMC	O2'-C2'	10.31	1.68	1.42
1	D	55	PSU	C6-N1	-8.39	1.24	1.32
1	C	55	PSU	C6-N1	-8.18	1.24	1.32

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	8	4SU	C4-N3-C2	128.09	127.08	121.60
1	C	8	4SU	C4-N3-C2	127.95	127.07	121.60
1	C	55	PSU	O4'-C1'-C5	13.23	126.01	109.55
1	D	55	PSU	O4'-C1'-C5	12.96	125.68	109.55
1	C	20	H2U	C5-C6-N1	5.66	117.05	110.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	FME	C	585	1	9,9,10	8.10	4 (44%)	6,9,11	1.21	1 (16%)
4	FME	D	586	1	9,9,10	5.64	2 (22%)	6,9,11	1.52	1 (16%)

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	FME	C	585	1	-	1/7/9/11	0/0/0/0
4	FME	D	586	1	-	1/7/9/11	0/0/0/0

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	585	FME	O-C	23.87	1.27	1.11
4	D	586	FME	O-C	16.45	1.22	1.11
4	D	586	FME	CA-C	2.93	1.53	1.48
4	C	585	FME	CA-C	2.91	1.53	1.48
4	C	585	FME	CN-N	2.47	1.42	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	586	FME	CB-CA-N	-3.40	105.36	111.26
4	C	585	FME	CB-CA-N	-2.24	107.36	111.26

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	586	FME	O1-CN-N-CA
4	C	585	FME	O1-CN-N-CA

There are no ring outliers.

## 5.7 Other polymers ⓘ

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 ⓘ

### 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.