



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 16, 2018 – 07:08 am GMT

PDB ID : 1B3B  
Title : THERMOTOGA MARITIMA GLUTAMATE DEHYDROGENASE MUTANT N97D, G376K  
Authors : Knapp, S.; Lebbink, J.H.G.; Van Der Oost, J.; Devos, W.M.; Rice, D.; Ladenstein, R.  
Deposited on : 1998-12-07  
Resolution : 3.10 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.

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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  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

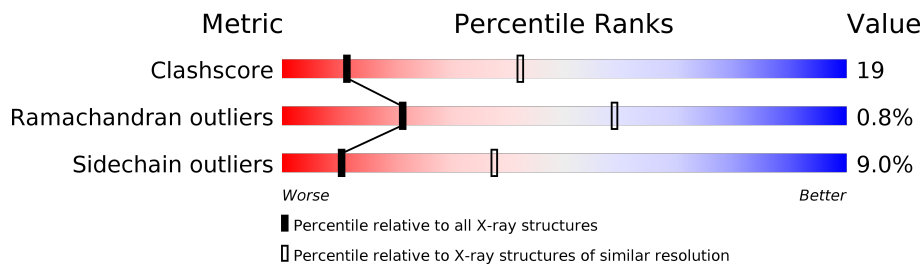
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	122078	1042 (3.10-3.10)
Ramachandran outliers	120005	1010 (3.10-3.10)
Sidechain outliers	119972	1010 (3.10-3.10)

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. 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	A	415	
1	B	415	
1	C	415	
1	D	415	
1	E	415	
1	F	415	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 19008 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 PROTEIN (GLUTAMATE DEHYDROGENASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	B	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	C	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	D	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	E	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			
1	F	409	Total	C	N	O	S	0	0	0
			3168	2011	552	592	13			

There are 12 discrepancies between the modelled and reference sequences:

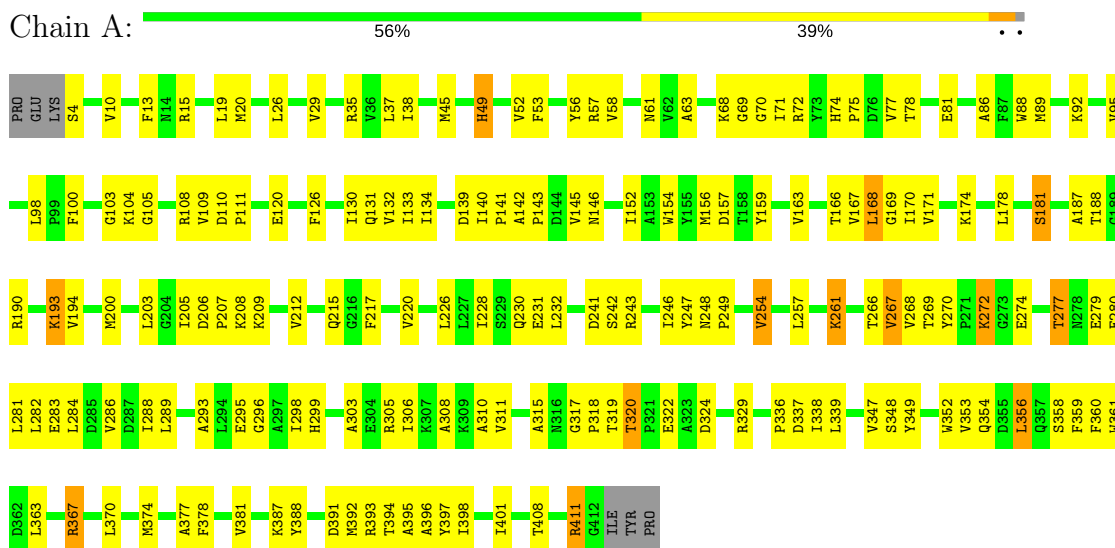
Chain	Residue	Modelled	Actual	Comment	Reference
A	97	ASP	ASN	ENGINEERED	UNP P96110
A	376	LYS	GLY	ENGINEERED	UNP P96110
B	97	ASP	ASN	ENGINEERED	UNP P96110
B	376	LYS	GLY	ENGINEERED	UNP P96110
C	97	ASP	ASN	ENGINEERED	UNP P96110
C	376	LYS	GLY	ENGINEERED	UNP P96110
D	97	ASP	ASN	ENGINEERED	UNP P96110
D	376	LYS	GLY	ENGINEERED	UNP P96110
E	97	ASP	ASN	ENGINEERED	UNP P96110
E	376	LYS	GLY	ENGINEERED	UNP P96110
F	97	ASP	ASN	ENGINEERED	UNP P96110
F	376	LYS	GLY	ENGINEERED	UNP P96110

### 3 Residue-property plots [i](#)

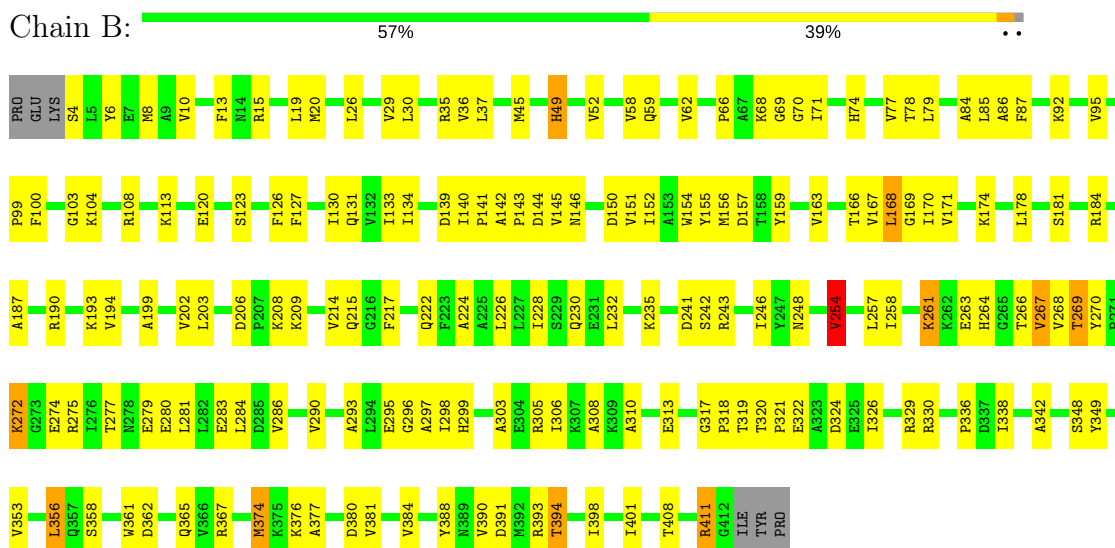
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

#### • Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)



#### • Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)



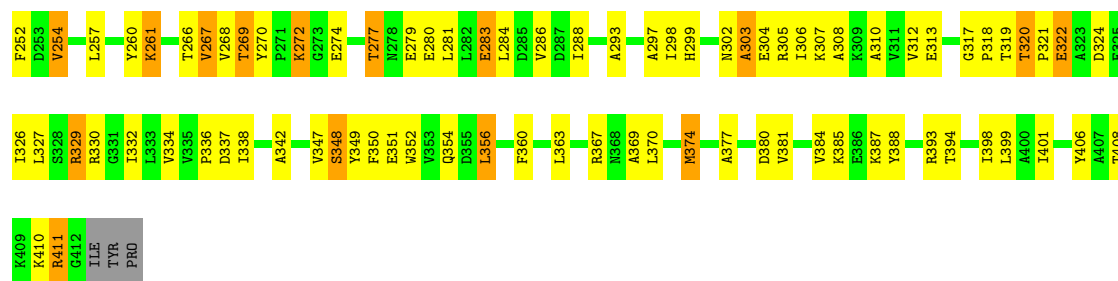
Chain C: 55% ●● 40%

PRO	GLU	LVS	S4	M8	A9	V10	F13	M14	R15	A16	L19	L26	A27	E28	V29	R35	V36	L37	R44	M45	G48	H49	V50	E51	V52	R57	V58	Q59	N61	V62	A63	K68	G69	G70	I71	R72	R73	H74	P75	D76	V77	T78	E81	L85	A86	F87	V88		
K92	V95	L98	P99	F100	G103	K104	G105	R108	V109	D110	P111	L114	S115	E120	R124	R125	F126	F127	I130	Q131	V132	I133	I134	D139	I140	P141	A142	P143	D144	V145	N146	L147	N148	A149	D150	V154	V155	M156	Y159	V163	T166	V167	L168	G169	I170				
L178	S181	R184	A187	R190	G191	V192	V194	G197	L198	A199	M200	V202	L203	G204	L205	D206	P207	K208	K209	V214	Q215	G216	F217	A224	A225	L226	L227	T228	S229	Q230	E231	L232	S240	D241	S242	R243	I246	N248	P249	E250	D253	V254	E255	E256	L257				
T258	R259	V260	K261	T266	V267	T269	Q270	P271	D272	G273	R275	L276	T277	E280	L281	L282	E283	L284	D285	V286	T287	L288	L289	V290	P291	A292	A293	L294	E295	T298	A303	K308	V309	A310	V311	V312	E313	G317	P318	T319	P320	T321	E322	A323	D324	E325	L326	L327	R330
P336	D337	I338	A342	S348	V349	Q354	D355	L356	Q357	S358	F359	F360	V361	D362	L363	R367	M374	K375	K376	A377	V381	K387	V388	D391	R393	T394	Y397	L398	L399	A400	I401	V406	A407	T408	K409	K410	R411	G412	ILE	TYR	PRO								

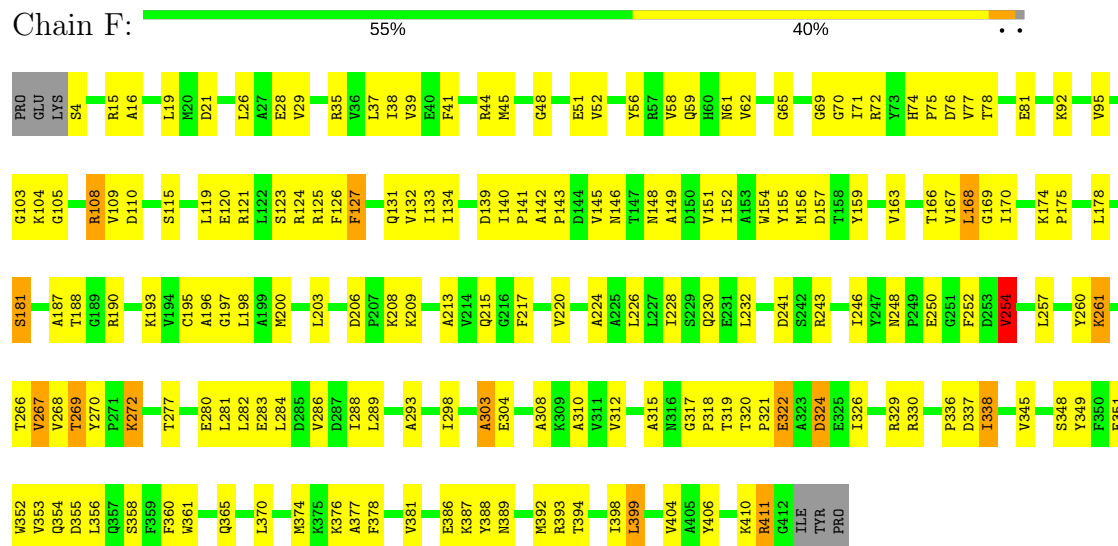
Chain D: 57% 39%

Category	Token Count
PRO	1
GLU	1
LVS	1
S4	1
I5	1
Y6	1
E7	1
M8	1
A9	1
V10	1
P11	1
R15	1
L19	1
M20	1
D21	1
L22	1
L26	1
A27	1
E28	1
V29	1
L30	1
R31	1
R32	1
R35	1
V36	1
L37	1
R44	1
G48	1
F53	1
V58	1
Q59	1
H60	1
N61	1
V62	1
A63	1
K68	1
G69	1
G70	1
I71	1
R72	1
Y73	1
H74	1
P75	1
D76	1
V77	1
T78	1
A86	1
F87	1
W88	1
Y90	1
V95	1
G103	1
K104	1
G105	1
R108	1
V109	1
D110	1
P111	1
L114	1
S115	1
E118	1
L119	1
E120	1
R121	1
L122	1
S123	1
F126	1
F127	1
I130	1
Q131	1
V132	1
I133	1
I134	1
D139	1
I140	1
P141	1
A142	1
P143	1
D144	1
V145	1
N146	1
T147	1
D150	1
V151	1
V154	1
L155	1
M156	1
D157	1
T158	1
V159	1
V163	1
T166	1
V167	1
L168	1
G169	1
I170	1
V171	1
K174	1
L178	1
S181	1
R184	1
A187	1
T188	1
G189	1
R190	1
K193	1
V194	1
G195	1
A196	1
G197	1
M200	1
D201	1
V202	1
L203	1
D206	1
P207	1
K208	1
K209	1
Q215	1
G216	1
F217	1
V220	1
L226	1
L227	1
I228	1
S229	1
Q230	1
P231	1
L232	1
S240	1
D241	1
S242	1
R243	1
T246	1
Y247	1
N248	1
P249	1
E250	1
G251	1
P252	1
D253	1
V254	1
L257	1
Y260	1
K261	1
T266	1
V267	1
V268	1
T269	1
P271	1
Y270	1
K272	1
G273	1
E274	1
T277	1
E280	1
L281	1
L282	1
E283	1
L284	1
D285	1
V286	1
P287	1
T288	1
A293	1
L294	1
E295	1
T298	1
H299	1
A303	1
K304	1
R305	1
L306	1
K307	1
A308	1
V312	1
E313	1
N316	1
G317	1
P318	1
T319	1
T320	1
P321	1
E322	1
A323	1
K324	1
E325	1
L326	1
L327	1
R330	1
G331	1
L332	1
P336	1

[illegible]



• Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.10 Å   145.10 Å   272.50 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	8.00 – 3.10	Depositor
% Data completeness (in resolution range)	94.0 (8.00-3.10)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, $R_{free}$	0.225 , 0.298	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	19008	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.34	0/3227	0.53	0/4367
1	B	0.33	0/3227	0.52	0/4367
1	C	0.33	0/3227	0.51	0/4367
1	D	0.31	0/3227	0.51	0/4367
1	E	0.35	0/3227	0.53	0/4367
1	F	0.33	0/3227	0.51	1/4367 (0.0%)
All	All	0.33	0/19362	0.52	1/26202 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	168	LEU	CA-CB-CG	5.21	127.29	115.30

There are no chirality outliers.

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	A	3168	0	3192	118	18
1	B	3168	0	3192	117	20
1	C	3168	0	3192	114	2
1	D	3168	0	3192	124	2
1	E	3168	0	3192	139	18
1	F	3168	0	3192	123	20

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	19008	0	19152	722	40

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 19.

The worst 5 of 722 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:248:ASN:HD21	1:E:272:LYS:HE2	1.22	1.03
1:F:248:ASN:HD21	1:F:272:LYS:HE2	1.32	0.95
1:A:248:ASN:HD21	1:A:272:LYS:HE2	1.38	0.88
1:E:224:ALA:O	1:E:228:ILE:HG13	1.74	0.88
1:C:354:GLN:HG2	1:C:360:PHE:HA	1.55	0.87

The worst 5 of 40 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:HIS:CG	1:E:304:GLU:OE1[6_655]	0.79	1.41
1:B:279:GLU:CG	1:F:330:ARG:O[6_665]	1.00	1.20
1:A:279:GLU:OE1	1:E:330:ARG:NE[6_655]	1.11	1.09
1:B:296:GLY:O	1:F:329:ARG:NH2[6_665]	1.20	1.00
1:A:299:HIS:ND1	1:E:304:GLU:OE1[6_655]	1.28	0.92

## 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	
1	A	407/415 (98%)	365 (90%)	39 (10%)	3 (1%)	24	61
1	B	407/415 (98%)	366 (90%)	37 (9%)	4 (1%)	17	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	407/415 (98%)	369 (91%)	35 (9%)	3 (1%)	24	61
1	D	407/415 (98%)	370 (91%)	33 (8%)	4 (1%)	17	53
1	E	407/415 (98%)	373 (92%)	32 (8%)	2 (0%)	31	68
1	F	407/415 (98%)	366 (90%)	37 (9%)	4 (1%)	17	53
All	All	2442/2490 (98%)	2209 (90%)	213 (9%)	20 (1%)	21	59

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	178	LEU
1	A	178	LEU
1	A	303	ALA
1	B	178	LEU
1	B	303	ALA

### 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	
1	A	333/339 (98%)	303 (91%)	30 (9%)	10	37
1	B	333/339 (98%)	303 (91%)	30 (9%)	10	37
1	C	333/339 (98%)	301 (90%)	32 (10%)	9	34
1	D	333/339 (98%)	303 (91%)	30 (9%)	10	37
1	E	333/339 (98%)	305 (92%)	28 (8%)	12	41
1	F	333/339 (98%)	304 (91%)	29 (9%)	11	40
All	All	1998/2034 (98%)	1819 (91%)	179 (9%)	10	37

5 of 179 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	283	GLU
1	D	166	THR

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Mol	Chain	Res	Type
1	F	269	THR
1	C	348	SER
1	C	408	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	365	GLN
1	D	61	ASN
1	E	215	GLN
1	C	357	GLN
1	E	357	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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.