



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2021 – 10:53 AM EDT

PDB ID : 2TMG
Title : THERMOTOGA MARITIMA GLUTAMATE DEHYDROGENASE MUTANT S128R, T158E, N117R, S160E
Authors : Knapp, S.; Lebbink, J.H.G.; van der Oost, J.; de Vos, W.M.; Rice, D.; Ladenstein, R.
Deposited on : 1998-12-04
Resolution : 2.90 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 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 : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

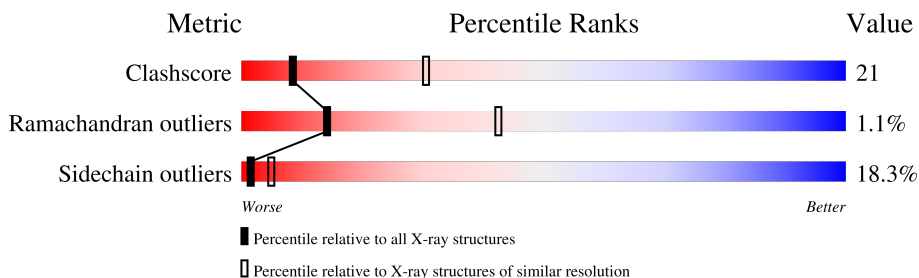
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 19032 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
			Total	C	N	O	S			
1	A	408	3172	2013	556	590	13	0	0	0
1	B	408	3172	2013	556	590	13	0	0	0
1	C	408	3172	2013	556	590	13	0	0	0
1	D	408	3172	2013	556	590	13	0	0	0
1	E	408	3172	2013	556	590	13	0	0	0
1	F	408	3172	2013	556	590	13	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	ARG	ASN	engineered mutation	UNP P96110
A	128	ARG	SER	engineered mutation	UNP P96110
A	158	GLU	THR	engineered mutation	UNP P96110
A	160	GLU	SER	engineered mutation	UNP P96110
B	117	ARG	ASN	engineered mutation	UNP P96110
B	128	ARG	SER	engineered mutation	UNP P96110
B	158	GLU	THR	engineered mutation	UNP P96110
B	160	GLU	SER	engineered mutation	UNP P96110
C	117	ARG	ASN	engineered mutation	UNP P96110
C	128	ARG	SER	engineered mutation	UNP P96110
C	158	GLU	THR	engineered mutation	UNP P96110
C	160	GLU	SER	engineered mutation	UNP P96110
D	117	ARG	ASN	engineered mutation	UNP P96110
D	128	ARG	SER	engineered mutation	UNP P96110
D	158	GLU	THR	engineered mutation	UNP P96110
D	160	GLU	SER	engineered mutation	UNP P96110
E	117	ARG	ASN	engineered mutation	UNP P96110

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Chain	Residue	Modelled	Actual	Comment	Reference
E	128	ARG	SER	engineered mutation	UNP P96110
E	158	GLU	THR	engineered mutation	UNP P96110
E	160	GLU	SER	engineered mutation	UNP P96110
F	117	ARG	ASN	engineered mutation	UNP P96110
F	128	ARG	SER	engineered mutation	UNP P96110
F	158	GLU	THR	engineered mutation	UNP P96110
F	160	GLU	SER	engineered mutation	UNP P96110

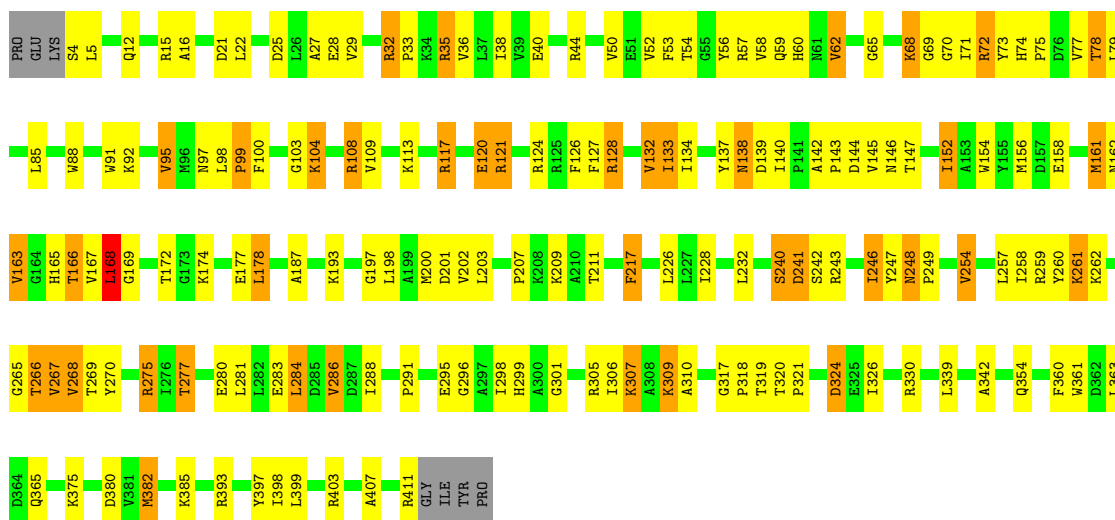
3 Residue-property plots

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.

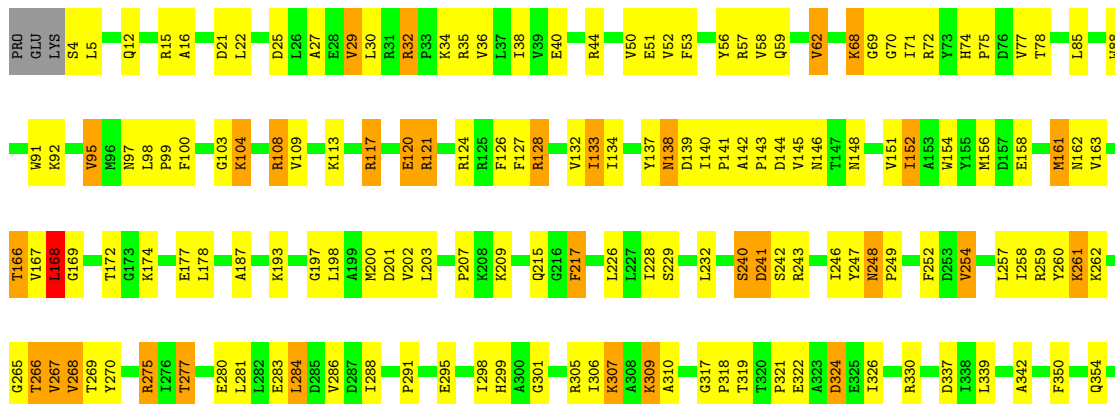
- Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)

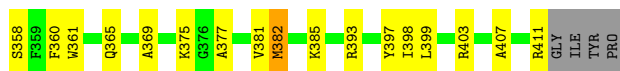
Chain A: 



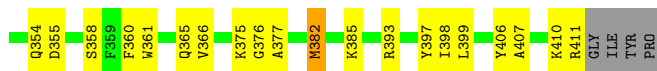
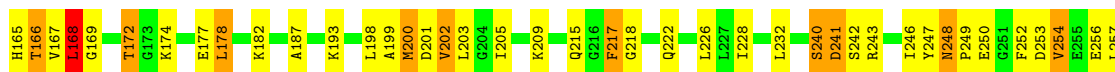
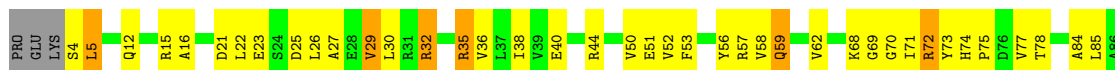
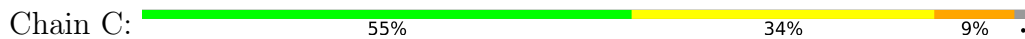
- Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)

Chain B: 

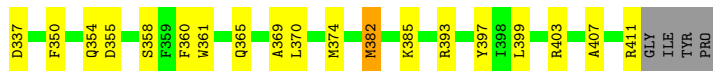
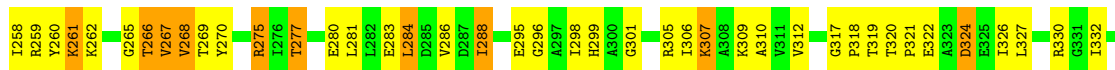
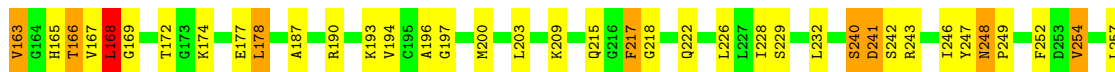




• Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)

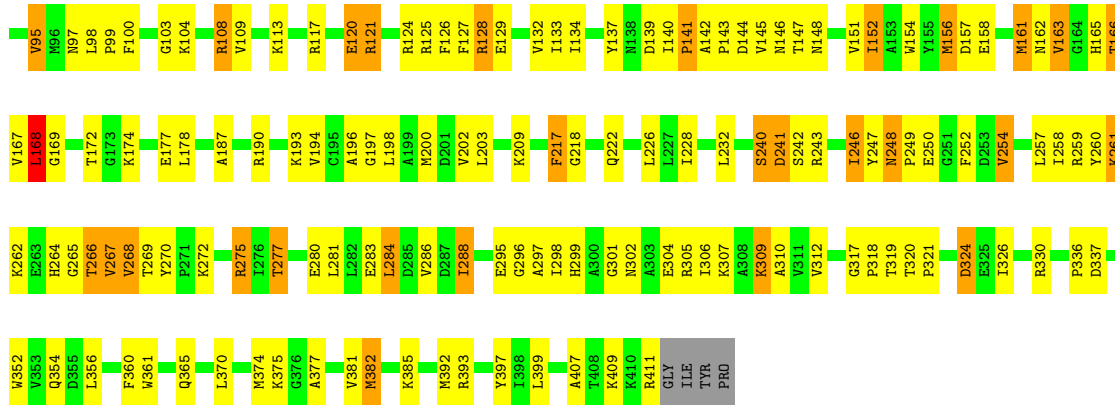


• Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)

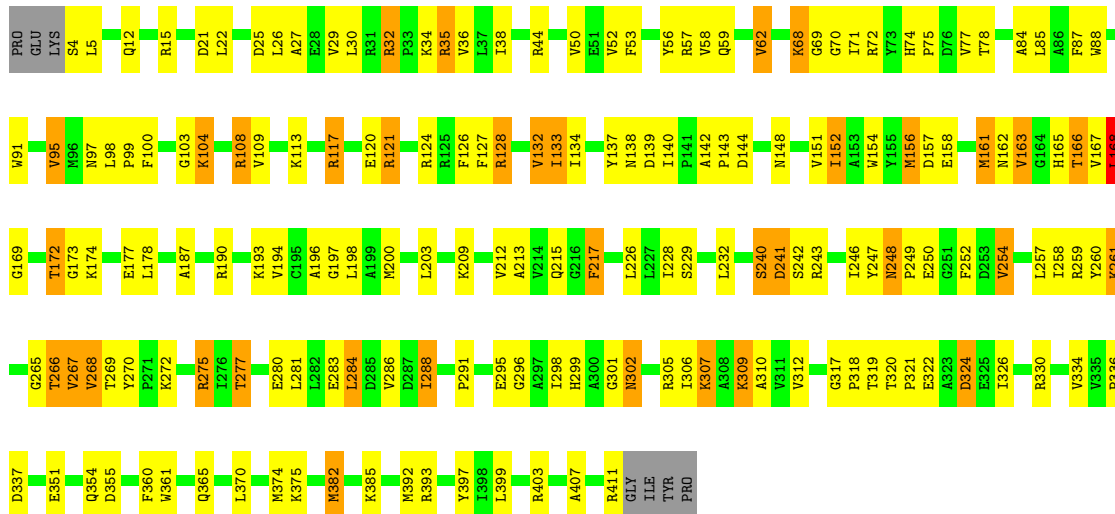


• Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)





● Molecule 1: PROTEIN (GLUTAMATE DEHYDROGENASE)



4 Data and refinement statistics

Xtrriage (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, α , β , γ	145.10Å 145.10Å 272.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.90	Depositor
% Data completeness (in resolution range)	98.0 (8.00-2.90)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.04	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.211 , 0.274	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	19032	wwPDB-VP
Average B, all atoms (Å ²)	52.0	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	0.42	0/3231	0.60	1/4371 (0.0%)
1	B	0.37	0/3231	0.58	1/4371 (0.0%)
1	C	0.39	0/3231	0.60	2/4371 (0.0%)
1	D	0.37	0/3231	0.58	1/4371 (0.0%)
1	E	0.41	0/3231	0.60	1/4371 (0.0%)
1	F	0.41	0/3231	0.59	1/4371 (0.0%)
All	All	0.39	0/19386	0.59	7/26226 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	168	LEU	CA-CB-CG	6.39	130.00	115.30
1	A	168	LEU	CA-CB-CG	6.31	129.81	115.30
1	E	168	LEU	CA-CB-CG	6.26	129.70	115.30
1	D	168	LEU	CA-CB-CG	6.17	129.50	115.30
1	F	168	LEU	CA-CB-CG	6.14	129.42	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	3172	0	3196	133	0
1	B	3172	0	3196	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3172	0	3196	135	0
1	D	3172	0	3196	140	0
1	E	3172	0	3196	148	0
1	F	3172	0	3196	136	0
All	All	19032	0	19176	793	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 21.

The worst 5 of 793 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:D:243:ARG:HD3	1:D:266:THR:HG21	1.24	1.16
1:A:243:ARG:HD3	1:A:266:THR:HG21	1.29	1.13
1:B:243:ARG:HD3	1:B:266:THR:HG21	1.29	1.12
1:C:243:ARG:HD3	1:C:266:THR:HG21	1.25	1.09
1:F:243:ARG:HD3	1:F:266:THR:HG21	1.32	1.08

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	406/415 (98%)	363 (89%)	39 (10%)	4 (1%)	15	45
1	B	406/415 (98%)	364 (90%)	36 (9%)	6 (2%)	10	34
1	C	406/415 (98%)	362 (89%)	40 (10%)	4 (1%)	15	45
1	D	406/415 (98%)	371 (91%)	30 (7%)	5 (1%)	13	40
1	E	406/415 (98%)	366 (90%)	35 (9%)	5 (1%)	13	40
1	F	406/415 (98%)	369 (91%)	33 (8%)	4 (1%)	15	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2436/2490 (98%)	2195 (90%)	213 (9%)	28 (1%)	14	42

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	ALA
1	A	265	GLY
1	B	187	ALA
1	B	265	GLY
1	C	187	ALA

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	332/338 (98%)	272 (82%)	60 (18%)	1	5
1	B	332/338 (98%)	271 (82%)	61 (18%)	1	5
1	C	332/338 (98%)	271 (82%)	61 (18%)	1	5
1	D	332/338 (98%)	271 (82%)	61 (18%)	1	5
1	E	332/338 (98%)	271 (82%)	61 (18%)	1	5
1	F	332/338 (98%)	271 (82%)	61 (18%)	1	5
All	All	1992/2028 (98%)	1627 (82%)	365 (18%)	1	5

5 of 365 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	268	VAL
1	E	254	VAL
1	D	305	ARG
1	E	104	LYS
1	E	305	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	299	HIS
1	F	162	ASN
1	D	162	ASN
1	F	138	ASN
1	F	365	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 monosaccharides 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 [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.