



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:56 PM UTC

PDB ID : 1GG4 / pdb_00001gg4
Title : CRYSTAL STRUCTURE OF ESCHERICHIA COLI UDP-MURNACTRIPEPTIDE D-ALANYL-D-ALANINE-ADDING ENZYME (MURF) AT 2.3 ANGSTROM RESOLUTION
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Deposited on : 2000-07-12
Resolution : 2.30 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
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

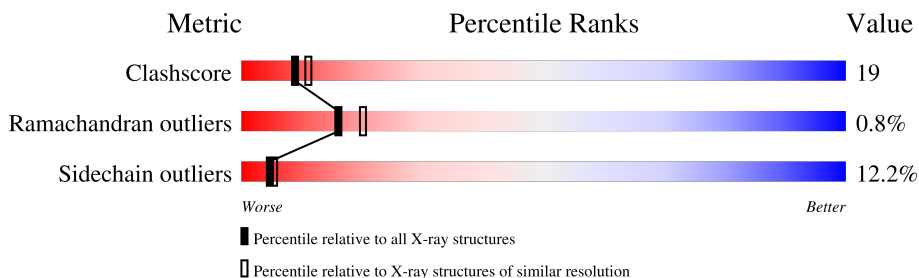
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 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	452	 61% 30% 6% •
1	B	452	 60% 29% 8% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6791 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 UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOPIMELATE-D-ALANYL-D-ALANYL LIGASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	439	Total	C	N	O	S	Se	0	0	0
			3242	2036	567	627	3	9			
1	B	439	Total	C	N	O	S	Se	0	0	0
			3242	2036	567	627	3	9			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P11880
A	117	MSE	MET	modified residue	UNP P11880
A	143	MSE	MET	modified residue	UNP P11880
A	217	MSE	MET	modified residue	UNP P11880
A	294	MSE	MET	modified residue	UNP P11880
A	340	MSE	MET	modified residue	UNP P11880
A	350	MSE	MET	modified residue	UNP P11880
A	361	MSE	MET	modified residue	UNP P11880
A	439	MSE	MET	modified residue	UNP P11880
B	501	MSE	MET	modified residue	UNP P11880
B	617	MSE	MET	modified residue	UNP P11880
B	643	MSE	MET	modified residue	UNP P11880
B	717	MSE	MET	modified residue	UNP P11880
B	794	MSE	MET	modified residue	UNP P11880
B	840	MSE	MET	modified residue	UNP P11880
B	850	MSE	MET	modified residue	UNP P11880
B	861	MSE	MET	modified residue	UNP P11880
B	939	MSE	MET	modified residue	UNP P11880

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	175	Total	O	0	0
			175	175		

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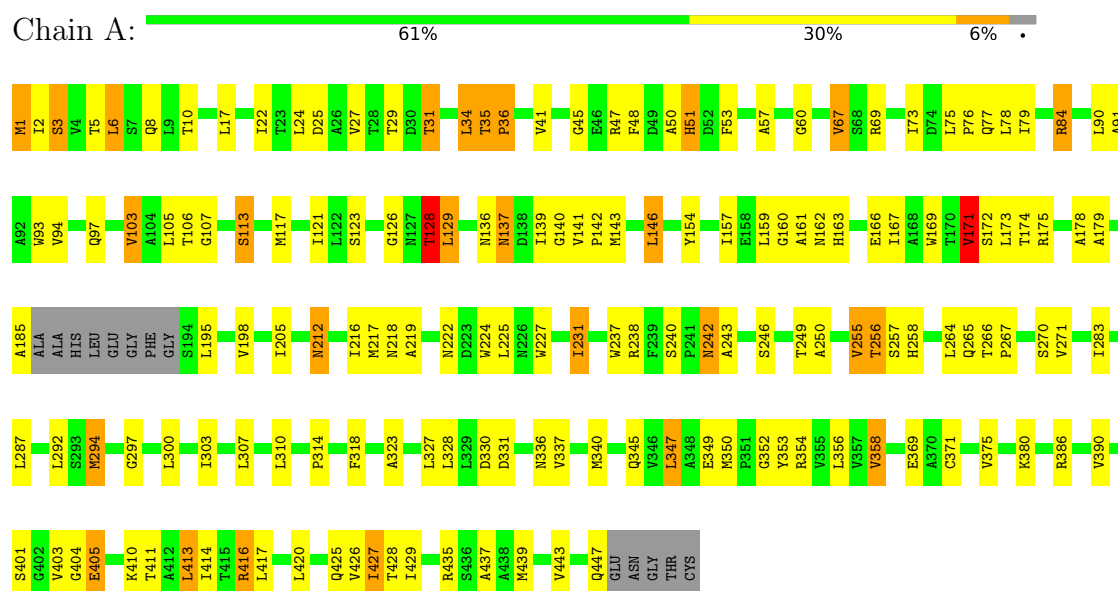
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	132	Total 132	O 132	0	0

3 Residue-property plots

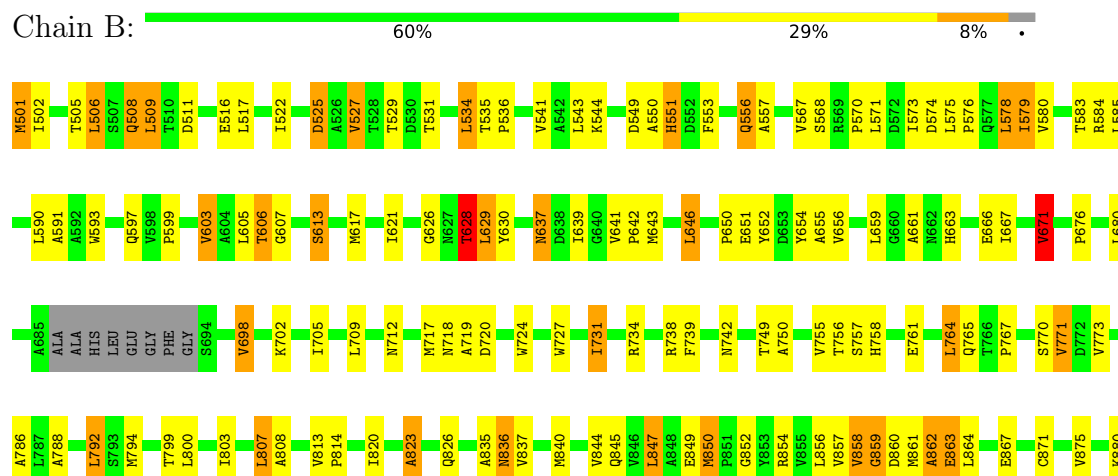
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: UDP-N-ACETYL MURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE-D-ALANYL-D-ALANYL LIGASE



- Molecule 1: UDP-N-ACETYL MURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE-D-ALANYL-D-ALANYL LIGASE





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	74.20Å 74.20Å 429.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	82.0 (8.00-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.203 , 0.280	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6791	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	0.62	1/3280 (0.0%)	1.06	12/4451 (0.3%)
1	B	0.61	0/3280	1.06	11/4451 (0.2%)
All	All	0.61	1/6560 (0.0%)	1.06	23/8902 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	294	MSE	SE-CE	-8.72	1.69	1.95

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	GLY	N-CA-C	8.49	125.07	114.37
1	A	323	ALA	N-CA-C	-7.23	99.34	108.45
1	B	551	HIS	N-CA-C	-7.15	103.52	111.82
1	A	358	VAL	N-CA-C	7.00	119.02	108.80
1	A	45	GLY	N-CA-C	-6.82	100.54	112.55

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	3242	0	3294	112	0
1	B	3242	0	3291	131	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	175	0	0	3	0
2	B	132	0	0	5	0
All	All	6791	0	6585	243	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 19.

The worst 5 of 243 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:B:852:GLY:HA3	1:B:926:VAL:HG12	1.53	0.90
1:B:767:PRO:HD2	1:B:794:MSE:HE1	1.58	0.86
1:A:50:ALA:HA	1:A:53:PHE:HD1	1.41	0.85
1:A:51:HIS:CE1	1:A:67:VAL:HG23	2.12	0.83
1:B:867:GLU:HG3	1:B:871:CYS:SG	2.20	0.82

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	435/452 (96%)	407 (94%)	26 (6%)	2 (0%)	24	31
1	B	435/452 (96%)	408 (94%)	22 (5%)	5 (1%)	11	13
All	All	870/904 (96%)	815 (94%)	48 (6%)	7 (1%)	16	20

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	525	ASP
1	B	863	GLU

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Mol	Chain	Res	Type
1	B	574	ASP
1	B	862	ALA
1	B	536	PRO

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	341/340 (100%)	302 (89%)	39 (11%)	5	6
1	B	341/340 (100%)	297 (87%)	44 (13%)	4	4
All	All	682/680 (100%)	599 (88%)	83 (12%)	5	5

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	606	THR
1	B	792	LEU
1	B	628	THR
1	B	698	VAL
1	B	886	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	742	ASN
1	B	947	GLN
1	B	836	ASN
1	B	556	GLN
1	B	721	ASN

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 oligosaccharides 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.