



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:31 AM UTC

PDB ID : 2QG9 / pdb_00002qg9
Title : Structure of a regulatory subunit mutant D19A of ATCase from E. coli
Authors : Stec, B.; Williams, M.K.; Stieglitz, K.A.; Kantrowitz, E.R.
Deposited on : 2007-06-28
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

<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
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

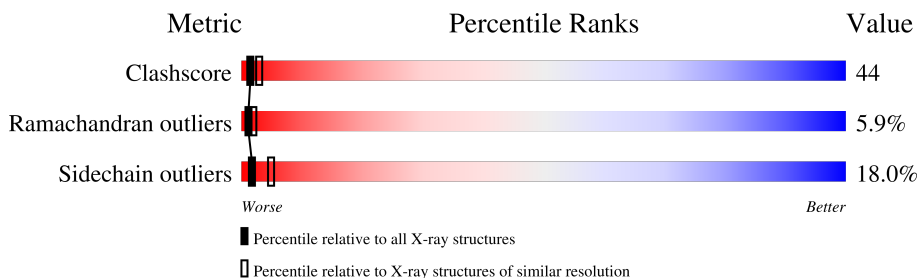
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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	310	28% 48% 22% .
1	C	310	35% 48% 16% .
2	B	153	20% 59% 18% .
2	D	153	24% 54% 20% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7436 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 Aspartate carbamoyltransferase catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2415	1527	423	456	9			
1	C	310	Total	C	N	O	S	0	0	0
			2415	1527	423	456	9			

- Molecule 2 is a protein called Aspartate carbamoyltransferase regulatory chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1198	751	213	228	6			
2	D	153	Total	C	N	O	S	0	0	0
			1198	751	213	228	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	19	ALA	ASP	engineered mutation	UNP P0A7F3
D	19	ALA	ASP	engineered mutation	UNP P0A7F3

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	97	Total	O	0	0
			97	97		

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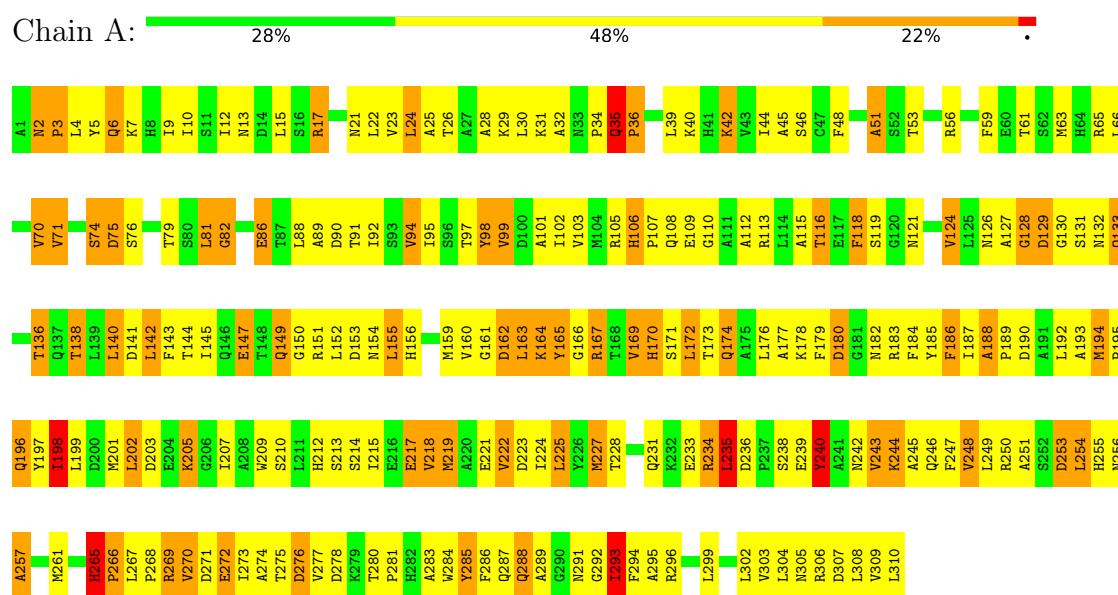
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	23	Total 23	O 23	0	0
4	C	70	Total 70	O 70	0	0
4	D	18	Total 18	O 18	0	0

3 Residue-property plots

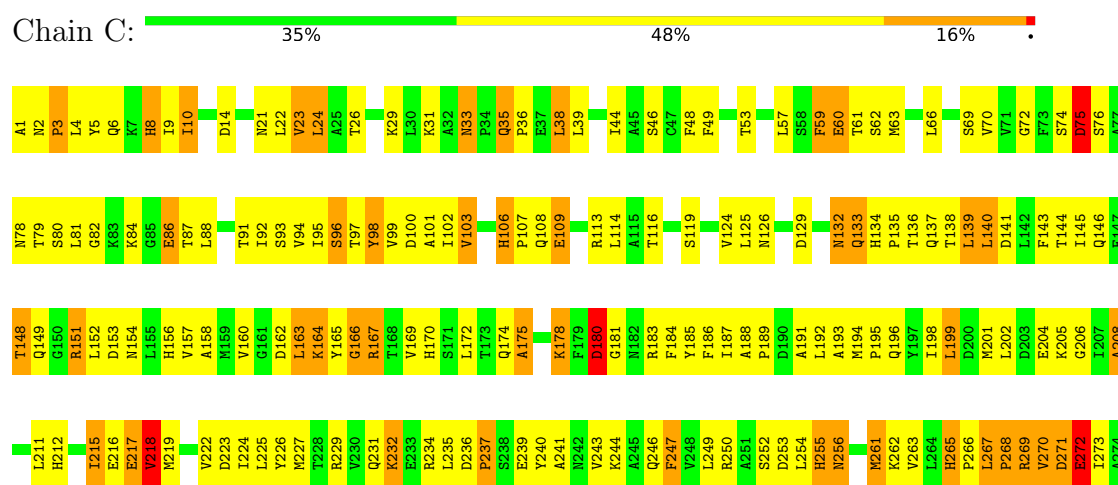
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Aspartate carbamoyltransferase catalytic chain

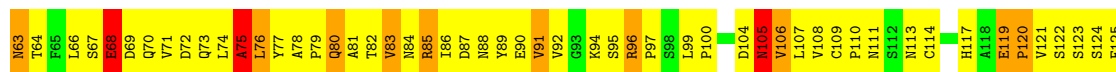
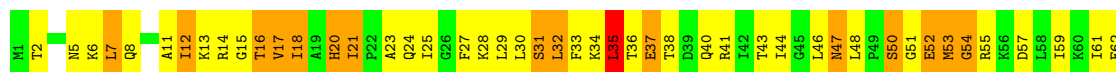


- Molecule 1: Aspartate carbamoyltransferase catalytic chain

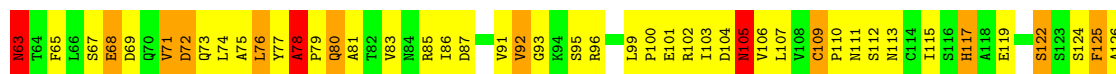
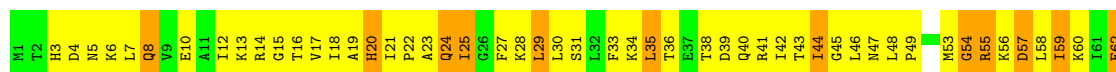




• Molecule 2: Aspartate carbamoyltransferase regulatory chain



• Molecule 2: Aspartate carbamoyltransferase regulatory chain



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.29Å 122.29Å 142.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (35.00-2.70)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.191 , 0.244	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7436	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	1.05	5/2461 (0.2%)	1.54	43/3339 (1.3%)
1	C	1.09	2/2461 (0.1%)	1.46	31/3339 (0.9%)
2	B	0.85	1/1216 (0.1%)	1.43	17/1643 (1.0%)
2	D	0.93	0/1216	1.47	28/1643 (1.7%)
All	All	1.02	8/7354 (0.1%)	1.49	119/9964 (1.2%)

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	A	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	194	MET	SD-CE	6.37	1.95	1.79
1	A	170	HIS	N-CA	6.20	1.53	1.46
1	C	175	ALA	CA-CB	-6.00	1.43	1.53
1	A	291	ASN	CG-OD1	5.88	1.34	1.23
2	B	21	ILE	CA-C	-5.44	1.48	1.53

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	204	GLU	N-CA-C	-12.08	98.09	111.14
2	B	78	ALA	CA-C-N	9.74	129.37	119.24
2	B	78	ALA	C-N-CA	9.74	129.37	119.24
1	C	160	VAL	N-CA-C	9.38	121.12	108.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ASP	N-CA-C	9.27	124.24	110.52

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	98	TYR	Sidechain

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	2415	0	2422	224	0
1	C	2415	0	2422	194	0
2	B	1198	0	1220	121	0
2	D	1198	0	1220	121	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	97	0	0	6	0
4	B	23	0	0	1	0
4	C	70	0	0	4	0
4	D	18	0	0	2	0
All	All	7436	0	7284	639	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 44.

The worst 5 of 639 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:A:109:GLU:HG3	1:A:130:GLY:HA3	1.39	1.04
2:D:30:LEU:HA	2:D:35:LEU:HD12	1.47	0.96
2:B:99:LEU:HD12	2:B:100:PRO:HD2	1.46	0.96
1:C:10:ILE:CD1	1:C:113:ARG:HA	1.97	0.94
2:B:105:ASN:HA	2:B:123:SER:OG	1.68	0.93

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	308/310 (99%)	246 (80%)	44 (14%)	18 (6%)	1	2
1	C	308/310 (99%)	243 (79%)	47 (15%)	18 (6%)	1	2
2	B	151/153 (99%)	124 (82%)	15 (10%)	12 (8%)	1	1
2	D	151/153 (99%)	118 (78%)	27 (18%)	6 (4%)	2	5
All	All	918/926 (99%)	731 (80%)	133 (14%)	54 (6%)	1	2

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	GLN
1	A	244	LYS
1	A	270	VAL
2	B	51	GLY
2	B	63	ASN

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	261/261 (100%)	205 (78%)	56 (22%)	1	3
1	C	261/261 (100%)	222 (85%)	39 (15%)	3	8
2	B	136/136 (100%)	111 (82%)	25 (18%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	136/136 (100%)	113 (83%)	23 (17%)	2	6
All	All	794/794 (100%)	651 (82%)	143 (18%)	2	5

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	278	ASP
1	C	308	LEU
2	D	63	ASN
1	A	265	HIS
1	A	254	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	182	ASN
2	D	113	ASN
1	C	288	GLN
2	D	24	GLN
2	B	24	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.