



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 07:32 PM UTC

PDB ID : 6NZB / pdb_00006nzb
Title : Crystal structure of E. coli fumarase C S318A variant with closed SS Loop at 1.37 angstrom resolution
Authors : Weaver, T.M.; May, J.F.; Bhattacharyya, B.
Deposited on : 2019-02-13
Resolution : 1.37 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

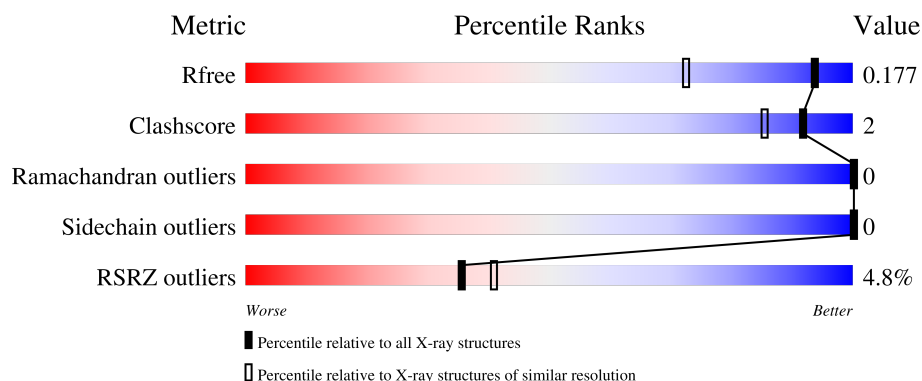
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.37 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))
R_{free}	180053	4403 (1.40-1.36)
Clashscore	190562	4528 (1.40-1.36)
Ramachandran outliers	187476	4459 (1.40-1.36)
Sidechain outliers	187428	4458 (1.40-1.36)
RSRZ outliers	180081	4399 (1.40-1.36)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	472	% 96% ..
1	B	472	8% 92% 5% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8050 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.

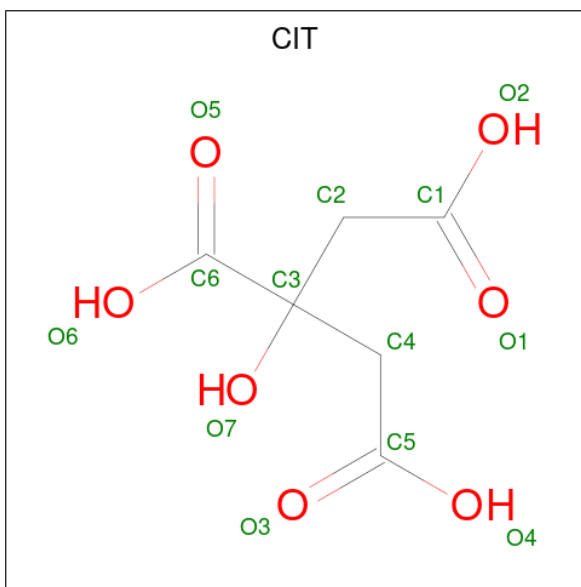
- Molecule 1 is a protein called Fumarate hydratase class II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	462	Total	C	N	O	S	0	10	0
			3542	2215	628	675	24			
1	B	459	Total	C	N	O	S	0	15	0
			3551	2227	629	672	23			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	318	ALA	SER	engineered mutation	UNP P05042
A	468	HIS	-	expression tag	UNP P05042
A	469	HIS	-	expression tag	UNP P05042
A	470	HIS	-	expression tag	UNP P05042
A	471	HIS	-	expression tag	UNP P05042
A	472	HIS	-	expression tag	UNP P05042
B	318	ALA	SER	engineered mutation	UNP P05042
B	468	HIS	-	expression tag	UNP P05042
B	469	HIS	-	expression tag	UNP P05042
B	470	HIS	-	expression tag	UNP P05042
B	471	HIS	-	expression tag	UNP P05042
B	472	HIS	-	expression tag	UNP P05042

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		

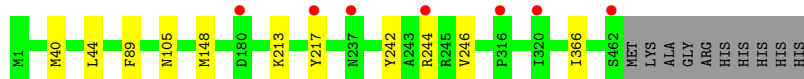
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	501	Total	O	0	0
			501	501		
3	B	404	Total	O	0	0
			404	404		

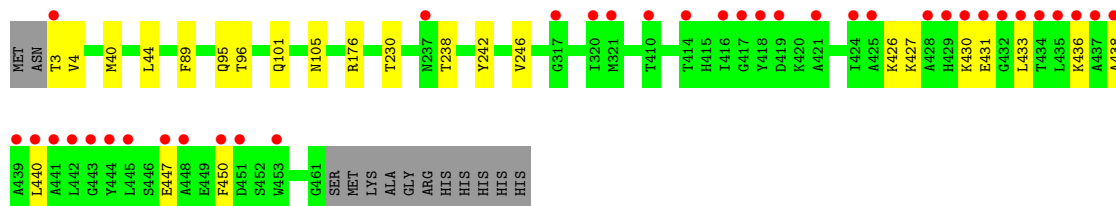
3 Residue-property plots [i](#)

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 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.

- Molecule 1: Fumarate hydratase class II



- Molecule 1: Fumarate hydratase class II



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	102.80Å 216.58Å 86.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.08 – 1.37 59.08 – 1.37	Depositor EDS
% Data completeness (in resolution range)	98.2 (59.08-1.37) 98.3 (59.08-1.37)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 1.37Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.147 , 0.177 0.147 , 0.177	Depositor DCC
R_{free} test set	9783 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	12.2	Xtriage
Anisotropy	0.868	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	8050	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: CIT

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	0.22	0/3630	0.46	0/4918
1	B	0.21	0/3651	0.44	0/4947
All	All	0.21	0/7281	0.45	0/9865

There are no bond length outliers.

There are no bond angle outliers.

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	3542	0	3588	6	0
1	B	3551	0	3616	17	0
2	A	26	0	10	0	0
2	B	26	0	10	0	0
3	A	501	0	0	0	0
3	B	404	0	0	0	0
All	All	8050	0	7224	23	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 2.

All (23) 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:89:PHE:HA	1:A:105:ASN:HD21	1.64	0.63
1:B:89:PHE:HA	1:B:105:ASN:HD21	1.67	0.58
1:B:440:LEU:HD11	1:B:447:GLU:HG3	1.85	0.58
1:B:436:LYS:HD3	1:B:450:PHE:CD2	2.38	0.58
1:B:436:LYS:HD2	1:B:447:GLU:HG2	1.85	0.57
1:B:427:LYS:HG2	1:B:438:ALA:HB1	1.91	0.53
1:B:40:MET:SD	1:B:44[B]:LEU:HD23	2.52	0.50
1:B:431:GLU:HB2	1:B:433:LEU:HD23	1.94	0.50
1:A:242:TYR:O	1:A:246[B]:VAL:HG23	2.12	0.49
1:B:3:THR:HG23	1:B:4:VAL:HG13	1.93	0.49
1:B:242:TYR:O	1:B:246[B]:VAL:HG23	2.12	0.48
1:A:244:ARG:HG2	1:A:244:ARG:HH11	1.77	0.48
1:B:230:THR:HG21	1:B:238:THR:HG21	1.96	0.47
1:A:148:MET:HE3	1:A:366:ILE:HB	1.98	0.46
1:B:436:LYS:HZ2	1:B:436:LYS:HB3	1.79	0.46
1:B:96[B]:THR:HG21	1:B:101[B]:GLN:OE1	2.16	0.46
1:A:213:LYS:HD2	1:A:217:TYR:CE1	2.54	0.43
1:B:426:LYS:HG2	1:B:430:LYS:HD2	2.01	0.43
1:A:40:MET:SD	1:A:44[B]:LEU:HD23	2.60	0.42
1:B:95:GLN:HB2	1:B:101[A]:GLN:NE2	2.35	0.42
1:B:176:ARG:HA	1:B:176:ARG:HD2	1.79	0.41
1:B:230:THR:HG21	1:B:238:THR:CG2	2.50	0.41
1:B:96[A]:THR:OG1	1:B:101[A]:GLN:OE1	2.39	0.40

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	470/472 (100%)	461 (98%)	9 (2%)	0	100	100
1	B	472/472 (100%)	460 (98%)	12 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	942/944 (100%)	921 (98%)	21 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	382/380 (100%)	382 (100%)	0	100	100
1	B	384/380 (101%)	384 (100%)	0	100	100
All	All	766/760 (101%)	766 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	163	GLN
1	A	211	ASN
1	A	237	ASN
1	A	355	ASN
1	A	384	ASN
1	A	429	HIS
1	B	32	HIS
1	B	84	GLN
1	B	105	ASN
1	B	384	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](#)

4 ligands 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	$\# Z > 2$
2	CIT	B	501	-	12,12,12	1.07	0	17,17,17	1.39	1 (5%)
2	CIT	A	501	-	12,12,12	1.04	0	17,17,17	1.64	1 (5%)
2	CIT	A	502	-	12,12,12	1.08	0	17,17,17	1.66	5 (29%)
2	CIT	B	502	-	12,12,12	1.06	0	17,17,17	1.45	1 (5%)

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
2	CIT	B	501	-	-	5/16/16/16	-
2	CIT	A	501	-	-	7/16/16/16	-
2	CIT	A	502	-	-	1/16/16/16	-
2	CIT	B	502	-	-	0/16/16/16	-

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	CIT	O6-C6-C3	4.63	122.03	113.14
2	B	502	CIT	O6-C6-C3	3.94	120.70	113.14
2	A	502	CIT	O6-C6-C3	3.88	120.58	113.14
2	B	501	CIT	O6-C6-C3	3.61	120.07	113.14
2	A	502	CIT	O4-C5-C4	2.30	121.64	114.35
2	A	502	CIT	C4-C3-C2	2.26	115.10	109.31
2	A	502	CIT	O2-C1-O1	-2.22	117.62	123.33
2	A	502	CIT	O4-C5-O3	-2.08	117.98	123.33

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	CIT	C4-C3-C6-O6
2	A	501	CIT	O7-C3-C6-O6
2	A	501	CIT	C4-C3-C6-O5
2	A	501	CIT	C1-C2-C3-O7
2	A	502	CIT	O7-C3-C4-C5
2	A	501	CIT	C2-C3-C6-O6
2	B	501	CIT	C4-C3-C6-O6
2	B	501	CIT	C1-C2-C3-O7
2	A	501	CIT	C2-C3-C6-O5
2	B	501	CIT	C2-C3-C6-O6
2	A	501	CIT	O7-C3-C6-O5
2	B	501	CIT	O7-C3-C6-O6
2	B	501	CIT	C4-C3-C6-O5

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	462/472 (97%)	-0.27	7 (1%) 72 78	8, 15, 24, 42	10 (2%)
1	B	459/472 (97%)	0.12	37 (8%) 18 21	7, 16, 48, 59	15 (3%)
All	All	921/944 (97%)	-0.08	44 (4%) 35 41	7, 15, 36, 59	25 (2%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	433	LEU	6.3
1	B	442	LEU	4.7
1	B	444	TYR	4.4
1	B	432	GLY	4.3
1	B	440	LEU	4.2
1	B	435	LEU	4.1
1	B	434	THR	4.1
1	B	237	ASN	4.0
1	B	414	THR	3.9
1	B	439	ALA	3.8
1	B	410	THR	3.7
1	B	441	ALA	3.7
1	B	453	TRP	3.6
1	B	416	ILE	3.6
1	A	462	SER	3.5
1	B	443	GLY	3.5
1	B	428	ALA	3.5
1	B	445	LEU	3.4
1	B	430	LYS	3.4
1	B	448	ALA	3.1
1	B	418	TYR	3.1
1	B	3	THR	3.1
1	B	429	HIS	3.1
1	B	417	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	437	ALA	3.0
1	B	421	ALA	3.0
1	B	321	MET	2.8
1	B	425	ALA	2.7
1	B	438	ALA	2.7
1	B	424	ILE	2.7
1	B	320	ILE	2.6
1	B	451	ASP	2.5
1	B	450	PHE	2.5
1	B	431	GLU	2.5
1	B	447	GLU	2.4
1	A	217	TYR	2.4
1	A	320	ILE	2.4
1	A	180	ASP	2.4
1	A	244	ARG	2.2
1	B	317	GLY	2.2
1	A	237	ASN	2.2
1	A	316	PRO	2.1
1	B	436	LYS	2.1
1	B	419	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CIT	B	501	13/13	0.79	0.14	25,33,37,38	0
2	CIT	A	502	13/13	0.92	0.09	18,22,29,31	0
2	CIT	B	502	13/13	0.92	0.11	22,26,43,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CIT	A	501	13/13	0.96	0.06	15,17,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.