



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 9GFP / pdb\_00009gfp  
Title : The crystal structure of CsvR from Escherichia coli  
Authors : Moche, M.; Joffre, E.; Ampah-Korsah, H.; Nyman, T.; Sjoling, A.; Sun, L.  
Deposited on : 2024-08-12  
Resolution : 3.03 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

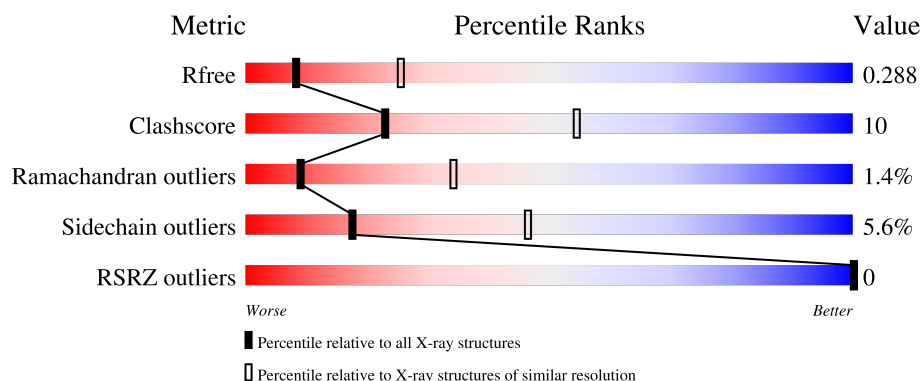
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.03 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))
$R_{free}$	164625	3418 (3.08-3.00)
Clashscore	180529	3811 (3.08-3.00)
Ramachandran outliers	177936	3656 (3.08-3.00)
Sidechain outliers	177891	3658 (3.08-3.00)
RSRZ outliers	164620	3430 (3.08-3.00)

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  $\geq 3$ , 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	267	
1	B	267	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4056 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 HTH-type transcriptional activator CsvR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2044	1315	350	365	14			
1	B	244	Total	C	N	O	S	0	0	0
			2003	1290	340	359	14			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	PRO	-	expression tag	UNP P43460
A	258	LYS	-	expression tag	UNP P43460
A	259	GLN	-	expression tag	UNP P43460
A	260	PHE	-	expression tag	UNP P43460
A	261	PHE	-	expression tag	UNP P43460
A	262	ASN	-	expression tag	UNP P43460
A	263	TYR	-	expression tag	UNP P43460
A	264	PHE	-	expression tag	UNP P43460
A	265	LYS	-	expression tag	UNP P43460
A	266	GLY	-	expression tag	UNP P43460
A	267	GLY	-	expression tag	UNP P43460
B	257	PRO	-	expression tag	UNP P43460
B	258	LYS	-	expression tag	UNP P43460
B	259	GLN	-	expression tag	UNP P43460
B	260	PHE	-	expression tag	UNP P43460
B	261	PHE	-	expression tag	UNP P43460
B	262	ASN	-	expression tag	UNP P43460
B	263	TYR	-	expression tag	UNP P43460
B	264	PHE	-	expression tag	UNP P43460
B	265	LYS	-	expression tag	UNP P43460
B	266	GLY	-	expression tag	UNP P43460
B	267	GLY	-	expression tag	UNP P43460

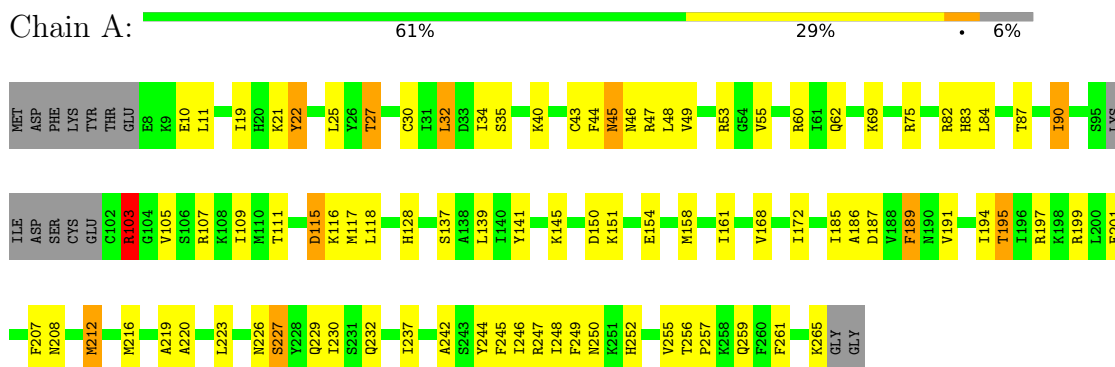
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	8	Total 8	O 8	0	0
2	B	1	Total 1	O 1	0	0

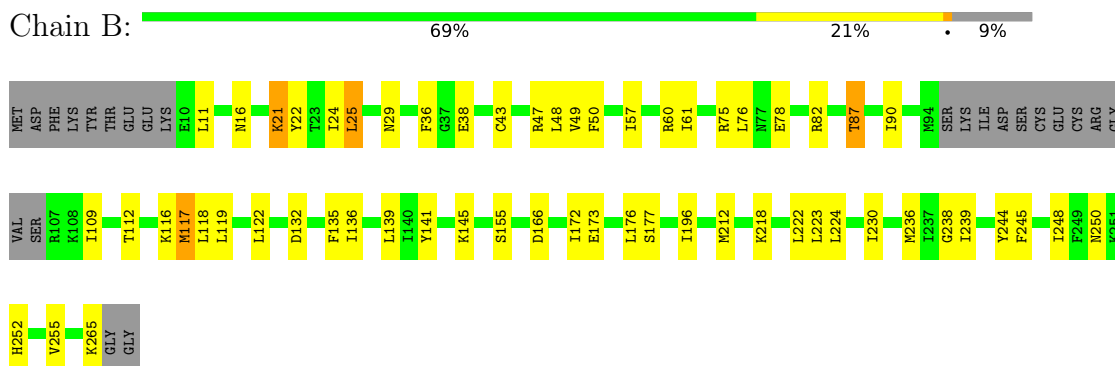
### 3 Residue-property plots [i](#)

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: HTH-type transcriptional activator CsvR



- Molecule 1: HTH-type transcriptional activator CsvR



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.61Å 77.60Å 184.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.32 – 3.03 48.32 – 3.03	Depositor EDS
% Data completeness (in resolution range)	69.7 (48.32-3.03) 69.7 (48.32-3.03)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.212 , 0.298 0.215 , 0.288	Depositor DCC
$R_{free}$ test set	403 reflections (3.21%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	102.6	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 122.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4056	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	151.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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	0.63	0/2075	1.32	8/2786 (0.3%)
1	B	0.51	0/2034	1.13	2/2730 (0.1%)
All	All	0.57	0/4109	1.23	10/5516 (0.2%)

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
1	B	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	87	THR	CA-CB-OG1	-8.52	96.82	109.60
1	A	195	THR	CA-CB-OG1	-8.20	97.31	109.60
1	A	139	LEU	N-CA-CB	-6.96	99.86	110.16
1	A	189	PHE	CA-CB-CG	-6.90	106.90	113.80
1	A	69	LYS	CB-CA-C	6.44	118.67	109.08

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	103	ARG	Sidechain
1	B	38	GLU	Peptide
1	B	47	ARG	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	2044	0	2108	47	0
1	B	2003	0	2078	38	0
2	A	8	0	0	1	0
2	B	1	0	0	0	0
All	All	4056	0	4186	84	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 10.

The worst 5 of 84 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:250:ASN:HA	1:A:255:VAL:O	1.78	0.83
1:B:132:ASP:O	1:B:136:ILE:HG13	1.89	0.72
1:A:244:TYR:CE2	1:A:248:ILE:HD11	2.25	0.72
1:A:87:THR:O	1:A:90:ILE:HG13	1.93	0.69
1:A:248:ILE:O	2:A:301:HOH:O	2.14	0.65

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	248/267 (93%)	226 (91%)	16 (6%)	6 (2%)	5 22
1	B	240/267 (90%)	231 (96%)	8 (3%)	1 (0%)	30 62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	488/534 (91%)	457 (94%)	24 (5%)	7 (1%)	9	34

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	105	VAL
1	A	227	SER
1	A	45	ASN
1	A	22	TYR

### 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	231/250 (92%)	214 (93%)	17 (7%)	11	36
1	B	230/250 (92%)	221 (96%)	9 (4%)	27	59
All	All	461/500 (92%)	435 (94%)	26 (6%)	17	46

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	194	ILE
1	B	21	LYS
1	B	166	ASP
1	A	212	MET
1	B	25	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	209	GLN
1	B	15	ASN

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Mol	Chain	Res	Type
1	B	62	GLN
1	B	213	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](#)

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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	252/267 (94%)	-0.71	0 100 100	54, 95, 158, 196	0
1	B	244/267 (91%)	-0.48	0 100 100	111, 192, 294, 369	0
All	All	496/534 (92%)	-0.60	0 100 100	54, 136, 281, 369	0

There are no RSRZ outliers to report.

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.