



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:47 AM UTC

PDB ID : 3EFY / pdb_00003efy
Title : Structure of the Cyclomodulin Cif from Pathogenic Escherichia coli
Authors : Stebbins, C.E.; Hsu, Y.
Deposited on : 2008-09-10
Resolution : 1.70 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
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

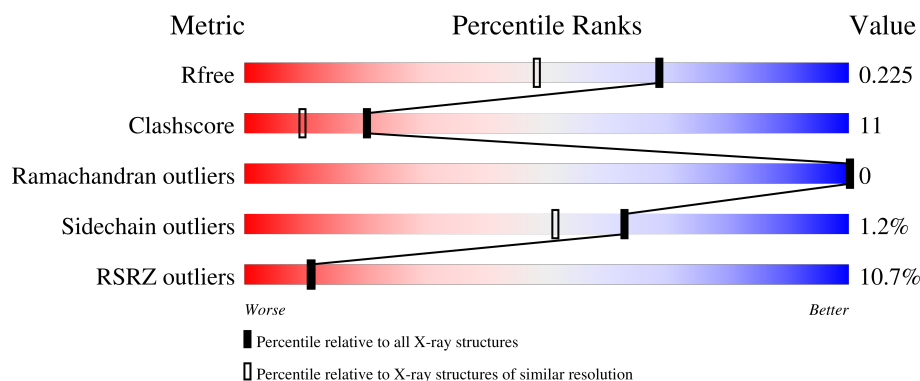
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
R_{free}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. 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	195	
1	B	195	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3667 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 Cif (Cell cycle inhibiting factor).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	183	Total	C	N	O	S	0	0	0
			1463	923	242	285	13			
1	B	182	Total	C	N	O	S	0	0	0
			1453	917	239	284	13			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	283	GLY	-	expression tag	UNP Q7WRZ5
A	284	ALA	-	expression tag	UNP Q7WRZ5
A	285	ALA	-	expression tag	UNP Q7WRZ5
A	286	ALA	-	expression tag	UNP Q7WRZ5
A	287	LEU	-	expression tag	UNP Q7WRZ5
A	288	GLU	-	expression tag	UNP Q7WRZ5
A	289	HIS	-	expression tag	UNP Q7WRZ5
A	290	HIS	-	expression tag	UNP Q7WRZ5
A	291	HIS	-	expression tag	UNP Q7WRZ5
A	292	HIS	-	expression tag	UNP Q7WRZ5
A	293	HIS	-	expression tag	UNP Q7WRZ5
A	294	HIS	-	expression tag	UNP Q7WRZ5
B	283	GLY	-	expression tag	UNP Q7WRZ5
B	284	ALA	-	expression tag	UNP Q7WRZ5
B	285	ALA	-	expression tag	UNP Q7WRZ5
B	286	ALA	-	expression tag	UNP Q7WRZ5
B	287	LEU	-	expression tag	UNP Q7WRZ5
B	288	GLU	-	expression tag	UNP Q7WRZ5
B	289	HIS	-	expression tag	UNP Q7WRZ5
B	290	HIS	-	expression tag	UNP Q7WRZ5
B	291	HIS	-	expression tag	UNP Q7WRZ5
B	292	HIS	-	expression tag	UNP Q7WRZ5
B	293	HIS	-	expression tag	UNP Q7WRZ5
B	294	HIS	-	expression tag	UNP Q7WRZ5

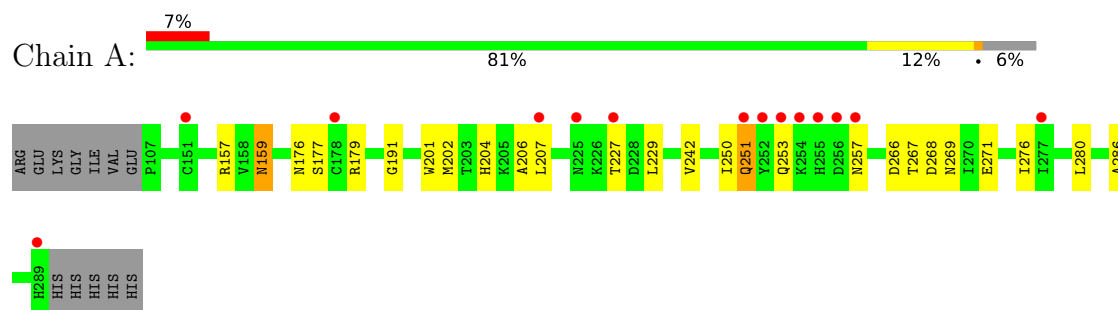
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	358	Total 358	O 358	0	0
2	B	393	Total 393	O 393	0	0

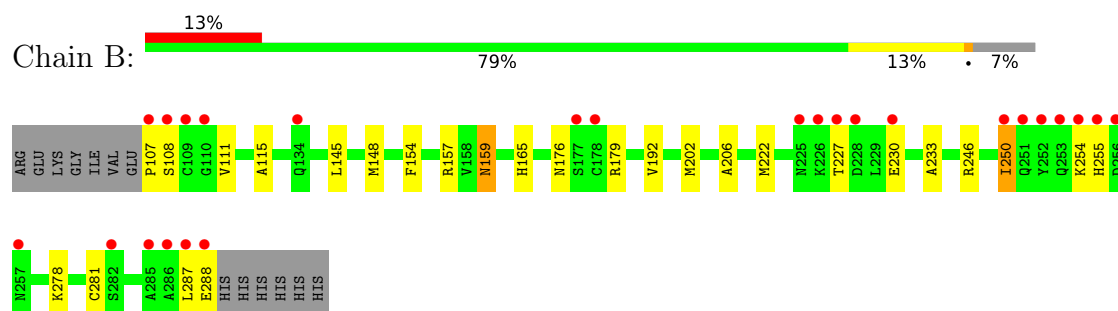
3 Residue-property plots [i](#)

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: Cif (Cell cycle inhibiting factor)



- Molecule 1: Cif (Cell cycle inhibiting factor)



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 2 2	Depositor
Cell constants a, b, c, α , β , γ	111.77Å 111.77Å 107.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.33 – 1.70 45.33 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (45.33-1.70) 98.9 (45.33-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.181 , 0.222 0.186 , 0.225	Depositor DCC
R_{free} test set	3761 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.009 for -h,-l,-k 0.005 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3667	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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](#)

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	1.00	0/1490	0.94	0/2007
1	B	1.03	3/1479 (0.2%)	0.98	1/1992 (0.1%)
All	All	1.01	3/2969 (0.1%)	0.96	1/3999 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	HIS	N-CA	-6.67	1.38	1.46
1	B	165	HIS	CA-C	5.82	1.59	1.52
1	B	233	ALA	CA-CB	5.08	1.61	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	165	HIS	N-CA-CB	-8.29	96.95	110.71

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	1463	0	1422	35	0
1	B	1453	0	1415	34	0
2	A	358	0	0	21	2
2	B	393	0	0	12	0
All	All	3667	0	2837	65	2

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 11.

All (65) 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)
2:A:521:HOH:O	1:B:287:LEU:HD22	1.38	1.18
1:A:207:LEU:HD23	2:A:495:HOH:O	1.49	1.12
1:B:148:MET:SD	2:B:727:HOH:O	2.14	1.05
2:A:483:HOH:O	1:B:281:CYS:SG	2.32	0.87
1:A:253:GLN:H	1:A:257:ASN:HD21	1.28	0.80
1:A:269:ASN:HB2	2:A:524:HOH:O	1.87	0.74
2:A:498:HOH:O	1:B:287:LEU:HD12	1.89	0.73
1:B:227:THR:N	2:B:474:HOH:O	2.25	0.68
1:A:253:GLN:HE21	1:A:257:ASN:HD22	1.44	0.65
1:A:207:LEU:HD21	2:B:590:HOH:O	1.97	0.65
2:A:483:HOH:O	1:B:281:CYS:CB	2.47	0.61
1:A:267:THR:HG23	2:A:509:HOH:O	2.02	0.60
1:A:176:ASN:HD21	1:A:179:ARG:HH11	1.49	0.58
1:A:227:THR:HG21	1:A:250:ILE:HD13	1.85	0.58
1:B:222:MET:O	1:B:222:MET:HE3	2.04	0.57
1:B:254:LYS:HB2	2:B:448:HOH:O	2.04	0.56
2:A:498:HOH:O	1:B:287:LEU:CD1	2.51	0.56
1:A:253:GLN:NE2	1:A:257:ASN:HD22	2.04	0.56
1:B:192:VAL:HG22	1:B:250:ILE:HG12	1.88	0.56
1:A:251:GLN:HG2	2:A:443:HOH:O	2.05	0.55
1:B:288:GLU:OE1	2:B:735:HOH:O	2.18	0.55
1:A:227:THR:CG2	2:A:499:HOH:O	2.54	0.55
1:A:227:THR:HG21	2:A:501:HOH:O	2.07	0.55
1:A:271:GLU:HG2	2:B:567:HOH:O	2.06	0.54
1:A:266:ASP:OD1	2:A:469:HOH:O	2.19	0.54
1:B:176:ASN:HD21	1:B:179:ARG:HH11	1.55	0.53
1:A:176:ASN:ND2	1:A:179:ARG:HH11	2.09	0.50
1:B:157:ARG:HH12	1:B:159:ASN:ND2	2.09	0.50
1:B:230:GLU:HG3	2:B:576:HOH:O	2.11	0.48
1:A:157:ARG:HH12	1:A:159:ASN:ND2	2.12	0.48
1:A:227:THR:CG2	1:A:250:ILE:HD13	2.43	0.47
1:A:227:THR:HG23	2:A:499:HOH:O	2.11	0.47
1:A:269:ASN:CB	2:A:524:HOH:O	2.54	0.47
1:A:229:LEU:HB3	1:A:242:VAL:HG23	1.97	0.47
1:A:286:ALA:HB3	1:B:202:MET:HE3	1.97	0.47
1:A:227:THR:HG22	2:A:499:HOH:O	2.15	0.47
1:B:176:ASN:ND2	1:B:179:ARG:HH11	2.13	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:ILE:HD13	1:B:250:ILE:HG23	1.66	0.46
1:B:192:VAL:CG2	1:B:250:ILE:HG12	2.45	0.46
1:A:253:GLN:HG2	1:A:257:ASN:ND2	2.31	0.46
1:B:145:LEU:HD23	1:B:148:MET:CE	2.45	0.46
2:A:498:HOH:O	1:B:287:LEU:HA	2.15	0.45
1:B:107:PRO:N	2:B:543:HOH:O	2.49	0.45
1:A:268:ASP:OD1	2:A:509:HOH:O	2.21	0.45
1:B:157:ARG:HH12	1:B:159:ASN:HD22	1.65	0.45
1:B:246:ARG:NH1	2:B:565:HOH:O	2.50	0.44
1:B:108:SER:HB2	2:B:610:HOH:O	2.16	0.44
1:A:280:LEU:HD11	1:B:115:ALA:HB1	1.98	0.44
1:A:157:ARG:HH12	1:A:159:ASN:HD22	1.65	0.43
1:A:177:SER:O	2:A:515:HOH:O	2.21	0.43
1:A:202:MET:HA	1:A:206:ALA:HB3	2.01	0.42
1:A:253:GLN:HE21	1:A:257:ASN:ND2	2.14	0.42
1:B:202:MET:HA	1:B:206:ALA:HB3	2.01	0.42
1:B:288:GLU:HB3	2:B:490:HOH:O	2.19	0.42
1:A:204:HIS:C	2:A:503:HOH:O	2.62	0.42
1:B:145:LEU:HD23	1:B:148:MET:HE3	2.01	0.42
1:A:191:GLY:HA3	2:A:361:HOH:O	2.20	0.41
1:B:278:LYS:NZ	2:B:507:HOH:O	2.52	0.41
1:A:276:ILE:HD11	1:B:111:VAL:HG11	2.03	0.41
1:A:276:ILE:HD11	1:B:111:VAL:CG1	2.51	0.41
1:B:148:MET:HG3	1:B:154:PHE:CE2	2.56	0.41
1:B:176:ASN:HD22	1:B:176:ASN:HA	1.73	0.40
1:A:201:TRP:CD1	1:A:206:ALA:HB2	2.56	0.40
1:A:207:LEU:HA	2:A:495:HOH:O	2.22	0.40
1:B:254:LYS:HG3	1:B:255:HIS:CD2	2.56	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:463:HOH:O	2:A:637:HOH:O[2_655]	2.06	0.14
2:A:451:HOH:O	2:A:637:HOH:O[2_655]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone

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	181/195 (93%)	177 (98%)	4 (2%)	0	100	100
1	B	180/195 (92%)	176 (98%)	4 (2%)	0	100	100
All	All	361/390 (93%)	353 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	164/175 (94%)	162 (99%)	2 (1%)	63	51
1	B	163/175 (93%)	161 (99%)	2 (1%)	63	51
All	All	327/350 (93%)	323 (99%)	4 (1%)	63	51

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	ASN
1	A	251	GLN
1	B	159	ASN
1	B	250	ILE

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	159	ASN
1	A	176	ASN
1	A	251	GLN
1	A	257	ASN
1	A	269	ASN
1	B	159	ASN
1	B	176	ASN
1	B	217	ASN
1	B	253	GLN
1	B	255	HIS
1	B	269	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

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	183/195 (93%)	0.46	14 (7%) 19 21	17, 26, 39, 56	0
1	B	182/195 (93%)	0.85	25 (13%) 6 6	20, 28, 43, 60	0
All	All	365/390 (93%)	0.65	39 (10%) 11 11	17, 27, 43, 60	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	285	ALA	7.1
1	B	254	LYS	7.1
1	B	253	GLN	6.0
1	B	286	ALA	6.0
1	B	288	GLU	5.6
1	B	282	SER	5.6
1	B	227	THR	5.5
1	B	287	LEU	5.2
1	B	255	HIS	5.1
1	B	107	PRO	4.8
1	B	226	LYS	4.7
1	A	253	GLN	4.6
1	B	178	CYS	4.4
1	B	252	TYR	4.3
1	A	254	LYS	4.2
1	B	109	CYS	4.2
1	B	256	ASP	4.1
1	A	255	HIS	3.9
1	B	177	SER	3.6
1	A	256	ASP	3.6
1	A	252	TYR	3.3
1	B	230	GLU	3.2
1	A	207	LEU	3.2
1	B	108	SER	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	225	ASN	2.8
1	B	251	GLN	2.7
1	A	227	THR	2.6
1	A	251	GLN	2.4
1	B	228	ASP	2.4
1	A	257	ASN	2.4
1	A	225	ASN	2.3
1	A	289	HIS	2.3
1	B	110	GLY	2.2
1	A	151	CYS	2.2
1	A	277	ILE	2.2
1	B	250	ILE	2.1
1	B	257	ASN	2.1
1	A	178	CYS	2.1
1	B	134	GLN	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.