



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 25, 2024 – 03:38 PM EST

PDB ID : 1UV7  
Title : periplasmic domain of EpsM from Vibrio cholerae  
Authors : Abendroth, J.; Hol, W.G.J.  
Deposited on : 2004-01-15  
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](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 : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.21  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.004 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

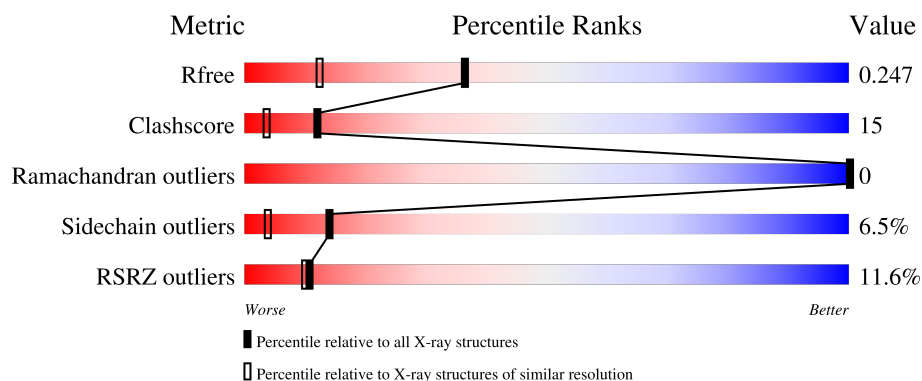
# 1 Overall quality at a glance

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))
$R_{free}$	164625	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	110	<div> <div>11%</div> <div>56%</div> <div>10%</div> <div>••</div> <div>31%</div> </div>
1	B	110	<div> <div>5%</div> <div>49%</div> <div>15%</div> <div>•</div> <div>33%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1314 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 GENERAL SECRETION PATHWAY PROTEIN M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	76	Total	C	N	O	Se	0	2	0
			626	398	114	110	4			
1	B	74	Total	C	N	O	Se	0	2	0
			618	394	112	108	4			

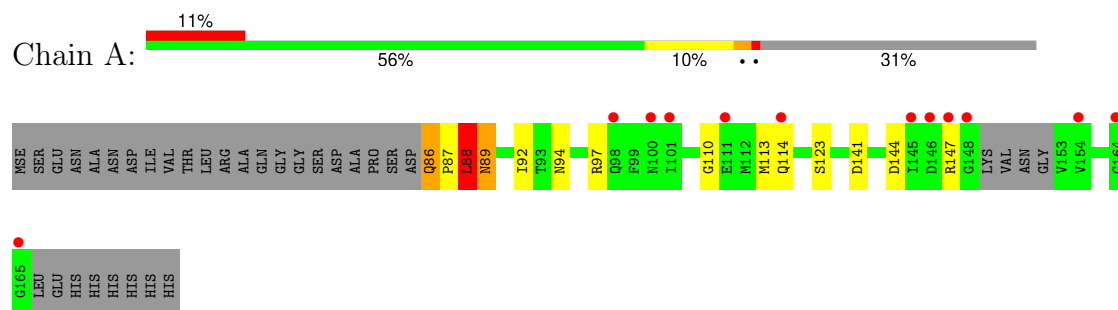
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	35	Total	O	0	0
			35	35		
2	B	35	Total	O	0	0
			35	35		

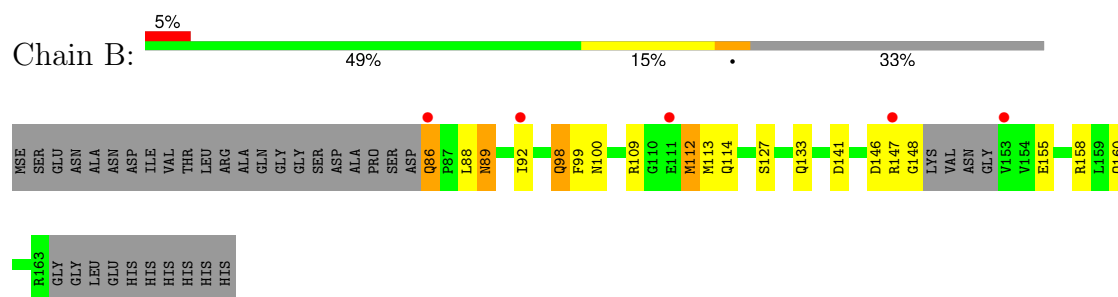
### 3 Residue-property plots [i](#)

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. 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.

#### • Molecule 1: GENERAL SECRETION PATHWAY PROTEIN M



#### • Molecule 1: GENERAL SECRETION PATHWAY PROTEIN M



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.88Å 52.88Å 112.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.70 20.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-1.70) 99.8 (20.00-1.70)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.196 , 0.242 0.209 , 0.247	Depositor DCC
$R_{free}$ test set	390 reflections (1.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.6	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 50.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	1314	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.25% 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	1/640 (0.2%)	1.21	4/858 (0.5%)
1	B	0.57	0/632	1.28	5/848 (0.6%)
All	All	0.60	1/1272 (0.1%)	1.25	9/1706 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	110	GLY	N-CA	8.68	1.59	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	141	ASP	CB-CG-OD2	6.91	124.52	118.30
1	A	141	ASP	CB-CG-OD1	6.42	124.08	118.30
1	A	144	ASP	CB-CG-OD2	6.25	123.92	118.30
1	B	146	ASP	CB-CG-OD2	6.10	123.79	118.30
1	A	147	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	B	158	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	B	147	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	A	88	LEU	CB-CG-CD2	5.24	119.90	111.00
1	B	127	SER	CB-CA-C	5.11	119.80	110.10

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	626	0	646	14	0
1	B	618	0	640	26	0
2	A	35	0	0	0	0
2	B	35	0	0	3	0
All	All	1314	0	1286	39	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 15.

All (39) 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:89:ASN:CA	1:B:113[B]:MSE:HE1	1.97	0.93
1:B:89:ASN:HA	1:B:113[B]:MSE:HE1	1.49	0.93
1:B:100:ASN:HB3	2:B:2004:HOH:O	1.75	0.85
1:B:92:ILE:HD12	1:B:113[A]:MSE:SE	2.28	0.84
1:A:88:LEU:HD13	1:A:113[B]:MSE:CG	2.11	0.81
1:B:112[B]:MSE:HE2	1:B:160:GLN:OE1	1.82	0.79
1:B:109:ARG:NH1	1:B:114:GLN:HE21	1.83	0.77
1:A:88:LEU:HD13	1:A:113[B]:MSE:HG2	1.66	0.76
1:B:92:ILE:HD12	1:B:113[B]:MSE:HE2	1.68	0.74
1:B:114:GLN:HE22	1:B:160:GLN:HE21	1.35	0.72
1:B:89:ASN:HB2	1:B:113[A]:MSE:HE1	1.72	0.72
1:B:89:ASN:CB	1:B:113[B]:MSE:HE1	2.20	0.72
1:A:89:ASN:HD22	1:A:89:ASN:H	1.42	0.65
1:A:92:ILE:HD12	1:A:113[B]:MSE:HG3	1.79	0.65
1:B:109:ARG:HH11	1:B:112[B]:MSE:HE1	1.61	0.64
1:B:109:ARG:NH1	1:B:114:GLN:NE2	2.47	0.63
1:B:89:ASN:HB2	1:B:113[B]:MSE:CE	2.30	0.61
1:A:86:GLN:N	1:A:87:PRO:CD	2.65	0.59
1:B:100:ASN:CB	2:B:2004:HOH:O	2.42	0.59
1:B:113[B]:MSE:SE	2:B:2010:HOH:O	2.70	0.59
1:B:89:ASN:HB2	1:B:113[B]:MSE:HE1	1.85	0.58
1:B:114:GLN:HE22	1:B:160:GLN:NE2	2.02	0.57
1:B:89:ASN:HA	1:B:113[B]:MSE:CE	2.32	0.55
1:A:88:LEU:HB3	1:A:113[B]:MSE:HE3	1.90	0.54
1:A:86:GLN:N	1:A:87:PRO:HD3	2.23	0.53
1:A:88:LEU:HD13	1:A:113[B]:MSE:HG3	1.92	0.52
1:A:94:ASN:HA	1:A:97:ARG:NH1	2.26	0.51
1:A:123:SER:HA	1:B:133:GLN:HE22	1.76	0.50
1:B:86:GLN:NE2	1:B:86:GLN:HA	2.27	0.49
1:B:112[B]:MSE:HE2	1:B:160:GLN:CD	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ILE:CD1	1:A:113[B]:MSE:HG3	2.44	0.47
1:A:89:ASN:HD22	1:A:89:ASN:N	2.13	0.46
1:B:98:GLN:HG2	1:B:99:PHE:CD1	2.51	0.45
1:B:92:ILE:CD1	1:B:113[A]:MSE:SE	3.07	0.45
1:B:109:ARG:HH12	1:B:114:GLN:NE2	2.14	0.43
1:A:92:ILE:HD12	1:A:113[A]:MSE:HG3	2.01	0.43
1:A:92:ILE:HD12	1:A:113[A]:MSE:CE	2.50	0.41
1:B:148:GLY:HA2	1:B:155:GLU:CG	2.51	0.41
1:B:112[B]:MSE:SE	1:B:160:GLN:HB3	2.70	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	74/110 (67%)	74 (100%)	0	0	100	100
1	B	72/110 (66%)	72 (100%)	0	0	100	100
All	All	146/220 (66%)	146 (100%)	0	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	71/94 (76%)	67 (94%)	4 (6%)	17	6
1	B	71/94 (76%)	65 (92%)	6 (8%)	8	2
All	All	142/188 (76%)	132 (93%)	10 (7%)	14	3

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	GLN
1	A	88	LEU
1	A	89	ASN
1	A	114	GLN
1	B	86	GLN
1	B	88	LEU
1	B	89	ASN
1	B	98	GLN
1	B	112[A]	MSE
1	B	112[B]	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	90	GLN
1	B	86	GLN
1	B	114	GLN
1	B	133	GLN
1	B	136	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

**Warning:** The R factor obtained from EDS is 0.2516, which does not match the depositor's R factor of 0.196. Please interpret the results in this section carefully.

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	74/110 (67%)	0.86	12 (16%) 5 5	13, 23, 33, 37	0
1	B	72/110 (65%)	0.56	5 (6%) 24 25	11, 21, 35, 44	0
All	All	146/220 (66%)	0.71	17 (11%) 11 10	11, 22, 34, 44	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	111	GLU	3.4
1	A	146	ASP	3.2
1	A	148	GLY	3.1
1	A	164	GLY	2.9
1	B	147	ARG	2.7
1	A	101	ILE	2.6
1	A	165	GLY	2.6
1	B	153	VAL	2.6
1	B	86	GLN	2.3
1	A	98	GLN	2.3
1	A	145	ILE	2.3
1	A	100	ASN	2.3
1	A	154	VAL	2.2
1	B	92	ILE	2.1
1	A	114	GLN	2.1
1	A	111	GLU	2.1
1	A	147	ARG	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 monosaccharides 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.