



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1P9R
Title : Crystal Structure of Vibrio cholerae putative NTPase EpsE
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Deposited on : 2003-05-12
Resolution : 2.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

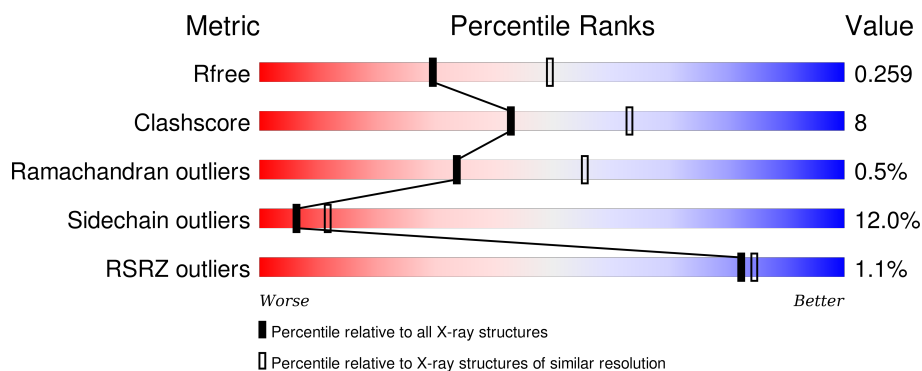
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	418	<div> <div></div> <div>65%</div> <div>23%</div> <div>• 10%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	A	602	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3045 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 E.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	378	Total	C	N	O	S	Se	0	0	0
			2932	1827	536	554	4	11			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	91	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	130	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	182	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	214	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	224	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	241	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	313	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	331	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	355	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	373	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	467	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	497	MSE	MET	MODIFIED RESIDUE	UNP P37093
A	499	GLY	-	EXPRESSION TAG	UNP P37093
A	500	SER	-	EXPRESSION TAG	UNP P37093
A	501	ARG	-	EXPRESSION TAG	UNP P37093
A	502	SER	-	EXPRESSION TAG	UNP P37093
A	503	HIS	-	EXPRESSION TAG	UNP P37093
A	504	HIS	-	EXPRESSION TAG	UNP P37093
A	505	HIS	-	EXPRESSION TAG	UNP P37093
A	506	HIS	-	EXPRESSION TAG	UNP P37093
A	507	HIS	-	EXPRESSION TAG	UNP P37093
A	508	HIS	-	EXPRESSION TAG	UNP P37093

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

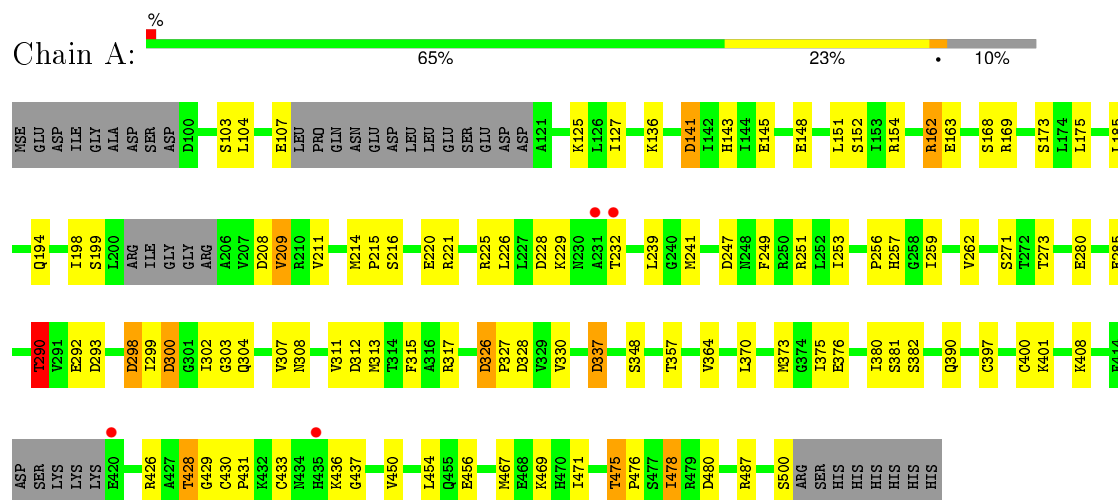
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	111	Total	O	0	0
			111	111		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: General secretion pathway protein E



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.61Å 103.61Å 166.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.50 49.46 – 2.50	Depositor EDS
% Data completeness (in resolution range)	84.9 (50.00-2.50) 84.9 (49.46-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.00 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.214 , 0.265 0.208 , 0.259	Depositor DCC
R_{free} test set	808 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 16070 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3045	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, CL

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	0.50	0/2957	0.85	14/3968 (0.4%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	A	326	ASP	CB-CG-OD2	5.86	123.57	118.30
1	A	208	ASP	CB-CG-OD2	5.75	123.47	118.30
1	A	162	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	337	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	312	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	141	ASP	CB-CG-OD2	5.45	123.20	118.30
1	A	480	ASP	CB-CG-OD2	5.34	123.11	118.30
1	A	293	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	228	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	300	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	298	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	290	THR	OG1-CB-CG2	-5.17	98.11	110.00
1	A	328	ASP	CB-CG-OD2	5.12	122.91	118.30

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	2932	0	3010	49	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	111	0	0	0	0
All	All	3045	0	3010	49	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 8.

All (49) 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:290:THR:HG23	1:A:304:GLN:HA	1.35	1.03
1:A:290:THR:CG2	1:A:304:GLN:HA	1.88	1.03
1:A:290:THR:HG22	1:A:303:GLY:O	1.77	0.84
1:A:430:CYS:HB2	1:A:431:PRO:HD2	1.60	0.83
1:A:290:THR:HG21	1:A:304:GLN:HG2	1.64	0.78
1:A:433:CYS:SG	1:A:437:GLY:HA2	2.25	0.76
1:A:273:THR:HG21	1:A:390:GLN:OE1	1.88	0.74
1:A:364:VAL:HB	1:A:467:MSE:HE2	1.69	0.73
1:A:241:MSE:HE1	1:A:249:PHE:HB2	1.79	0.64
1:A:313:MSE:HE2	1:A:313:MSE:HA	1.82	0.60
1:A:397:CYS:O	1:A:401:LYS:HB3	2.01	0.60
1:A:430:CYS:CB	1:A:431:PRO:HD2	2.30	0.60
1:A:143:HIS:ND1	1:A:221:ARG:NH2	2.46	0.58
1:A:247:ASP:O	1:A:251:ARG:HG3	2.04	0.57
1:A:239:LEU:HD13	1:A:273:THR:HG22	1.89	0.55
1:A:262:VAL:O	1:A:357:THR:HA	2.06	0.55
1:A:198:ILE:HB	1:A:209:VAL:HG13	1.92	0.52
1:A:256:PRO:HB2	1:A:257:HIS:CD2	2.45	0.52
1:A:433:CYS:HB2	1:A:436:LYS:O	2.10	0.52
1:A:154:ARG:HG2	1:A:163:GLU:HA	1.92	0.51
1:A:400:CYS:HB3	1:A:430:CYS:HB3	1.93	0.50
1:A:299:ILE:O	1:A:300:ASP:HB3	2.12	0.50
1:A:241:MSE:HE1	1:A:249:PHE:CB	2.40	0.50
1:A:298:ASP:HA	1:A:304:GLN:OE1	2.10	0.49
1:A:280:GLU:HG3	1:A:280:GLU:O	2.12	0.49
1:A:370:LEU:HA	1:A:373:MSE:HE2	1.95	0.49
1:A:326:ASP:N	1:A:327:PRO:HD3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:MSE:O	1:A:220:GLU:HA	2.14	0.48
1:A:290:THR:CG2	1:A:303:GLY:O	2.57	0.48
1:A:375:ILE:HG22	1:A:380:ILE:HG13	1.97	0.47
1:A:308:ASN:HD22	1:A:311:VAL:HG22	1.80	0.46
1:A:249:PHE:O	1:A:253:ILE:HG12	2.15	0.46
1:A:185:LEU:HB3	1:A:194:GLN:OE1	2.16	0.46
1:A:308:ASN:ND2	1:A:311:VAL:HG22	2.31	0.45
1:A:478:ILE:H	1:A:478:ILE:HG12	1.56	0.44
1:A:185:LEU:HD22	1:A:194:GLN:HB3	1.99	0.44
1:A:145:GLU:O	1:A:151:LEU:HD12	2.18	0.44
1:A:290:THR:OG1	1:A:292:GLU:HG3	2.18	0.43
1:A:214:MSE:HG3	1:A:215:PRO:HD2	2.00	0.43
1:A:225:ARG:HG3	1:A:225:ARG:O	2.18	0.43
1:A:299:ILE:HG21	1:A:302:ILE:HD12	2.00	0.43
1:A:127:ILE:HD11	1:A:175:LEU:HD22	2.01	0.43
1:A:450:VAL:HA	1:A:454:LEU:HD23	2.01	0.43
1:A:428:THR:OG1	1:A:429:GLY:N	2.48	0.42
1:A:370:LEU:HD23	1:A:373:MSE:HE1	2.02	0.42
1:A:475:THR:HA	1:A:476:PRO:HD3	1.88	0.42
1:A:151:LEU:HD12	1:A:152:SER:H	1.86	0.41
1:A:290:THR:CG2	1:A:304:GLN:CA	2.80	0.41
1:A:430:CYS:CB	1:A:431:PRO:CD	2.98	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	370/418 (88%)	358 (97%)	10 (3%)	2 (0%)	34 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	GLU
1	A	226	LEU

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	325/349 (93%)	286 (88%)	39 (12%)	6 12

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	SER
1	A	104	LEU
1	A	107	GLU
1	A	125	LYS
1	A	136	LYS
1	A	141	ASP
1	A	162	ARG
1	A	168	SER
1	A	169	ARG
1	A	173	SER
1	A	199	SER
1	A	209	VAL
1	A	211	VAL
1	A	216	SER
1	A	229	LYS
1	A	232	THR
1	A	259	ILE
1	A	271	SER
1	A	285	GLU
1	A	290	THR
1	A	307	VAL
1	A	315	PHE
1	A	317	ARG
1	A	330	VAL
1	A	337	ASP

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Mol	Chain	Res	Type
1	A	348	SER
1	A	376	GLU
1	A	381	SER
1	A	382	SER
1	A	408	LYS
1	A	426	ARG
1	A	428	THR
1	A	456	GLU
1	A	469	LYS
1	A	471	ILE
1	A	475	THR
1	A	478	ILE
1	A	487	ARG
1	A	500	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	410	GLN
1	A	434	ASN
1	A	455	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 carbohydrates 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

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](#)

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	367/418 (87%)	-0.09	4 (1%) 82 84	17, 38, 63, 73	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	435	HIS	3.6
1	A	232	THR	2.9
1	A	420	GLU	2.3
1	A	231	ALA	2.1

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	CL	A	602	1/1	0.89	0.38	13.57	42,42,42,42	0
2	ZN	A	601	1/1	0.99	0.10	-0.68	51,51,51,51	0

6.5 Other polymers

There are no such residues in this entry.