



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2GU1 / pdb_00002gu1
Title : Crystal structure of a zinc containing peptidase from vibrio cholerae
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Deposited on : 2006-04-28
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

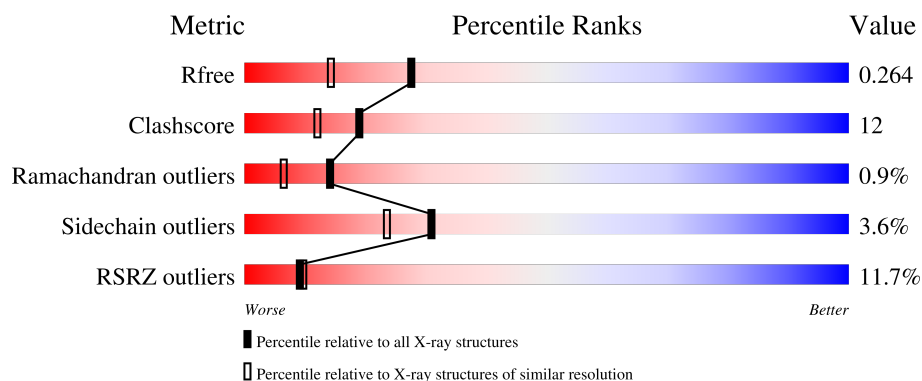
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	361	11% 68% 19% 10%

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	NA	A	363	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2688 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 Zinc peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	0	0
			2553	1621	453	471	8			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP Q9KUL5
A	2	SER	-	cloning artifact	UNP Q9KUL5
A	3	LEU	-	cloning artifact	UNP Q9KUL5
A	354	GLU	-	cloning artifact	UNP Q9KUL5
A	355	GLY	-	cloning artifact	UNP Q9KUL5
A	356	HIS	-	cloning artifact	UNP Q9KUL5
A	357	HIS	-	cloning artifact	UNP Q9KUL5
A	358	HIS	-	cloning artifact	UNP Q9KUL5
A	359	HIS	-	cloning artifact	UNP Q9KUL5
A	360	HIS	-	cloning artifact	UNP Q9KUL5
A	361	HIS	-	cloning artifact	UNP Q9KUL5

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 4 is water.

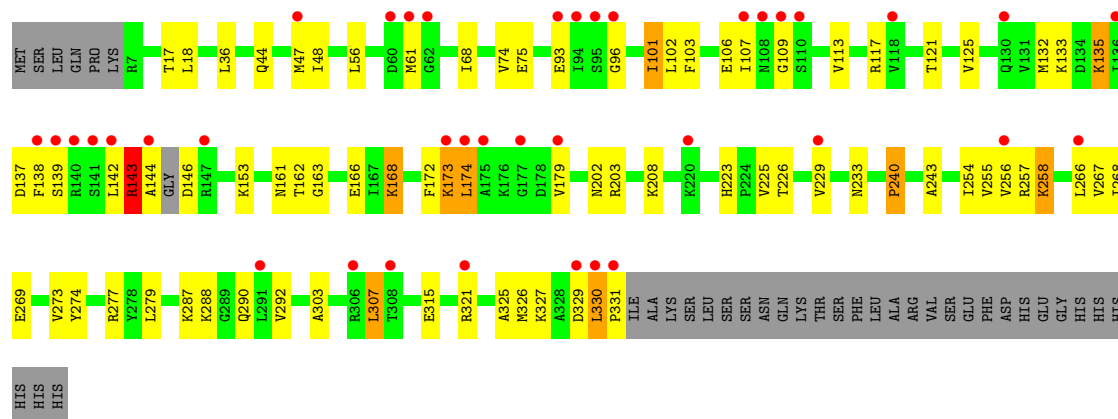
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	133	Total 133	O 133	0	0

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: Zinc peptidase

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.38Å 85.40Å 53.40Å 90.00° 112.96° 90.00°	Depositor
Resolution (Å)	32.24 – 1.90 32.24 – 1.90	Depositor EDS
% Data completeness (in resolution range)	89.8 (32.24-1.90) 89.9 (32.24-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 1.91Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.230 , 0.264 0.230 , 0.264	Depositor DCC
R_{free} test set	1987 reflections (6.70%)	wwPDB-VP
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2688	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.02% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, ZN

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	0.41	1/2604 (0.0%)	0.95	12/3512 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	143	ARG	CA-CB	-6.06	1.43	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	ARG	N-CA-C	12.70	137.86	110.80
1	A	109	GLY	N-CA-C	-9.66	90.28	113.18
1	A	274	TYR	N-CA-C	6.01	119.62	109.76
1	A	143	ARG	CA-C-O	5.57	128.47	120.51
1	A	240	PRO	N-CA-C	-5.49	103.23	111.57
1	A	133	LYS	N-CA-C	5.48	117.96	111.33
1	A	142	LEU	CA-C-N	5.43	131.91	121.54
1	A	142	LEU	C-N-CA	5.43	131.91	121.54
1	A	17	THR	N-CA-C	-5.37	101.20	109.52
1	A	273	VAL	N-CA-C	5.20	116.11	111.90
1	A	202	ASN	N-CA-C	-5.05	102.30	110.32
1	A	279	LEU	N-CA-C	5.03	117.54	110.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2553	0	2553	60	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	133	0	0	2	0
All	All	2688	0	2553	60	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 12.

All (60) 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:107:ILE:HB	1:A:143:ARG:CB	2.13	0.79
1:A:172:PHE:HB3	1:A:174:LEU:HD13	1.70	0.73
1:A:101:ILE:HD13	1:A:102:LEU:N	2.05	0.71
1:A:330:LEU:HD13	1:A:330:LEU:O	1.91	0.70
1:A:258:LYS:C	1:A:258:LYS:HD3	2.18	0.68
1:A:143:ARG:CB	1:A:146:ASP:N	2.58	0.67
1:A:173:LYS:HA	1:A:173:LYS:HZ3	1.60	0.66
1:A:172:PHE:HB3	1:A:174:LEU:CD1	2.29	0.62
1:A:267:VAL:HG22	1:A:277:ARG:HG2	1.80	0.62
1:A:233:ASN:O	1:A:315:GLU:HG2	2.00	0.61
1:A:161:ASN:ND2	1:A:163:GLY:H	1.98	0.60
1:A:257:ARG:HH11	1:A:257:ARG:HG2	1.67	0.59
1:A:106:GLU:OE2	1:A:144:ALA:O	2.21	0.58
1:A:256:VAL:HG22	1:A:266:LEU:CD1	2.33	0.58
1:A:161:ASN:HD22	1:A:162:THR:N	2.02	0.58
1:A:75:GLU:HG2	1:A:93:GLU:HG3	1.87	0.56
1:A:101:ILE:HD12	1:A:103:PHE:CE1	2.40	0.56
1:A:101:ILE:HD13	1:A:101:ILE:C	2.31	0.55
1:A:153:LYS:HD2	1:A:168:LYS:HE3	1.88	0.55
1:A:68:ILE:HD12	1:A:68:ILE:N	2.23	0.54
1:A:143:ARG:CB	1:A:146:ASP:HB2	2.38	0.54
1:A:254:ILE:HD13	1:A:269:GLU:HB2	1.91	0.53
1:A:287:LYS:HG2	1:A:288:LYS:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:GLU:OE1	1:A:168:LYS:HE2	2.09	0.52
1:A:330:LEU:HD22	1:A:331:PRO:O	2.10	0.52
1:A:255:VAL:HB	1:A:267:VAL:HB	1.93	0.51
1:A:256:VAL:HG22	1:A:266:LEU:HD12	1.90	0.51
1:A:161:ASN:HD22	1:A:161:ASN:C	2.19	0.51
1:A:203:ARG:CZ	1:A:330:LEU:HD11	2.40	0.51
1:A:74:VAL:HG23	1:A:75:GLU:HG3	1.92	0.51
1:A:330:LEU:HD22	1:A:330:LEU:C	2.37	0.50
1:A:240:PRO:HD2	1:A:243:ALA:HB2	1.92	0.50
1:A:287:LYS:H	1:A:290:GLN:HE21	1.60	0.50
1:A:203:ARG:NH1	1:A:330:LEU:HD11	2.26	0.49
1:A:137:ASP:C	1:A:139:SER:H	2.20	0.48
1:A:254:ILE:HG13	1:A:255:VAL:HG23	1.95	0.48
1:A:18:LEU:C	1:A:18:LEU:HD13	2.38	0.48
1:A:303:ALA:HA	1:A:307:LEU:HD21	1.96	0.47
1:A:113:VAL:O	1:A:117:ARG:HG3	2.14	0.47
1:A:132:MET:HE1	1:A:179:VAL:HG12	1.96	0.47
1:A:277:ARG:HB2	1:A:315:GLU:HB2	1.96	0.46
1:A:18:LEU:HD13	1:A:18:LEU:O	2.16	0.46
1:A:203:ARG:NH2	1:A:330:LEU:HD11	2.31	0.46
1:A:288:LYS:HB3	1:A:288:LYS:HE2	1.82	0.46
1:A:135:LYS:HZ2	1:A:179:VAL:HG13	1.79	0.46
1:A:321:ARG:HD2	4:A:394:HOH:O	2.16	0.45
1:A:223:HIS:HD2	1:A:226:THR:H	1.65	0.45
1:A:223:HIS:CD2	1:A:225:VAL:HB	2.51	0.45
1:A:121:THR:O	1:A:125:VAL:HG23	2.17	0.44
1:A:61:MET:HG2	1:A:61:MET:O	2.17	0.44
1:A:161:ASN:HD22	1:A:163:GLY:H	1.66	0.44
1:A:48:ILE:O	1:A:48:ILE:HG13	2.19	0.43
1:A:327:LYS:O	1:A:330:LEU:HD12	2.19	0.43
1:A:44:GLN:O	1:A:47:MET:HG2	2.19	0.42
1:A:325:ALA:C	1:A:326:MET:HE2	2.45	0.42
1:A:168:LYS:HA	1:A:168:LYS:HD2	1.83	0.41
1:A:229:VAL:O	1:A:229:VAL:HG23	2.20	0.41
1:A:268:ILE:HD13	1:A:292:VAL:HG21	2.03	0.41
1:A:208:LYS:HG3	4:A:384:HOH:O	2.21	0.41
1:A:329:ASP:O	1:A:330:LEU:HB3	2.21	0.40

There are no symmetry-related clashes.

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	320/361 (89%)	306 (96%)	11 (3%)	3 (1%)	14 6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	143	ARG
1	A	138	PHE
1	A	96	GLY

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	274/310 (88%)	264 (96%)	10 (4%)	31 23

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

Mol	Chain	Res	Type
1	A	36	LEU
1	A	56	LEU
1	A	101	ILE
1	A	135	LYS
1	A	168	LYS
1	A	173	LYS
1	A	174	LEU
1	A	258	LYS

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Mol	Chain	Res	Type
1	A	307	LEU
1	A	330	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	A	33	GLN
1	A	44	GLN
1	A	108	ASN
1	A	154	GLN
1	A	161	ASN
1	A	164	ASN
1	A	212	GLN
1	A	223	HIS
1	A	290	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](#)

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 [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	324/361 (89%)	0.78	38 (11%) 9 10	18, 31, 52, 66	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	331	PRO	9.0
1	A	144	ALA	7.8
1	A	330	LEU	6.9
1	A	108	ASN	5.1
1	A	142	LEU	4.9
1	A	329	ASP	4.1
1	A	139	SER	3.9
1	A	107	ILE	3.8
1	A	141	SER	3.5
1	A	140	ARG	3.5
1	A	109	GLY	3.5
1	A	61	MET	3.4
1	A	177	GLY	3.3
1	A	95	SER	3.1
1	A	138	PHE	2.8
1	A	173	LYS	2.8
1	A	175	ALA	2.7
1	A	60	ASP	2.7
1	A	256	VAL	2.6
1	A	321	ARG	2.5
1	A	291	LEU	2.5
1	A	118	VAL	2.5
1	A	130	GLN	2.4
1	A	110	SER	2.4
1	A	174	LEU	2.3
1	A	94	ILE	2.3
1	A	308	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	47	MET	2.2
1	A	220	LYS	2.2
1	A	229	VAL	2.2
1	A	266	LEU	2.2
1	A	306	ARG	2.2
1	A	179	VAL	2.1
1	A	96	GLY	2.1
1	A	62	GLY	2.0
1	A	147	ARG	2.0
1	A	93	GLU	2.0
1	A	136	ILE	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($\text{\AA}^2$)	Q<0.9
3	NA	A	363	1/1	0.78	0.41	63,63,63,63	0
2	ZN	A	362	1/1	0.99	0.02	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.