



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:29 PM UTC

PDB ID : 1RTQ / pdb_00001rtq
Title : The 0.95 Angstrom Resolution Crystal Structure of the Aminopeptidase from *Aeromonas proteolytica*
Authors : Desmarais, W.; Bienvenue, D.L.; Krzysztof, B.P.; Holz, R.C.; Petsko, G.A.; Ringe, D.
Deposited on : 2003-12-10
Resolution : 0.95 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

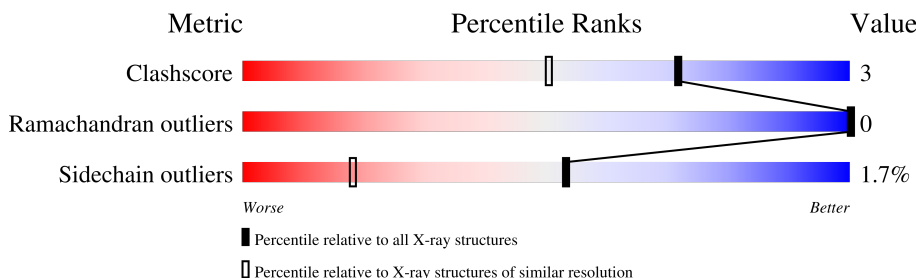
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 0.95 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))
Clashscore	190562	1090 (1.00-0.92)
Ramachandran outliers	187476	1032 (1.00-0.92)
Sidechain outliers	187428	1033 (1.00-0.92)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	299	 85% 9% . .

2 Entry composition [i](#)

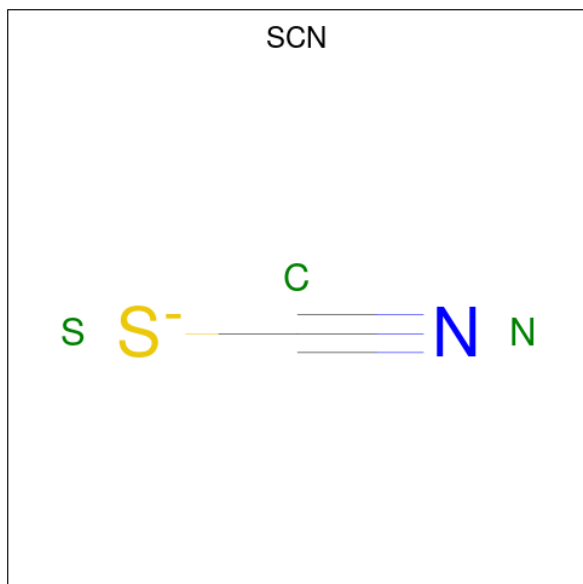
There are 5 unique types of molecules in this entry. The entry contains 4635 atoms, of which 2085 are hydrogens and 0 are deuteriums.

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 Bacterial leucyl aminopeptidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	291	Total	C	H	N	O	S	0	2	0
			4300	1381	2085	366	458	10			

- Molecule 2 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	S	0	0
			3	1	1	1		
2	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	324	Total 324	O 324	0	0

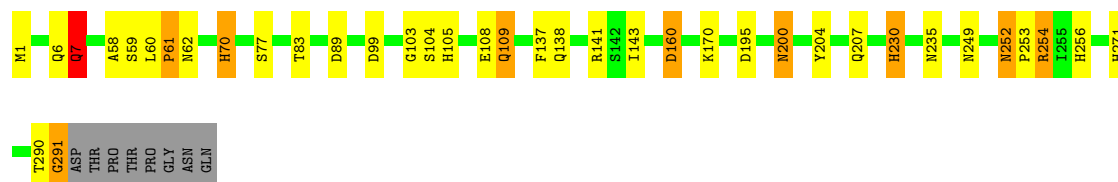
3 Residue-property plots

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.

Note EDS was not executed.

- Molecule 1: Bacterial leucyl aminopeptidase

Chain A:  85% 9%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	109.94Å 109.94Å 91.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 0.95	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-0.95)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS, SHELXL-97	Depositor
R, R_{free}	0.135 , 0.151	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4635	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.16	4/2275 (0.2%)	1.65	52/3103 (1.7%)

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	1	0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	70	HIS	ND1-CE1	5.88	1.38	1.32
1	A	6	GLN	C-N	-5.85	1.26	1.33
1	A	254	ARG	CZ-NH1	5.75	1.40	1.32
1	A	271	HIS	CG-ND1	-5.33	1.32	1.38

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	254	ARG	CD-NE-CZ	24.22	158.30	124.40
1	A	254	ARG	NE-CZ-NH1	-15.38	106.12	121.50
1	A	105	HIS	CA-CB-CG	14.85	128.65	113.80
1	A	109	GLN	CB-CG-CD	14.76	137.70	112.60
1	A	254	ARG	NH1-CZ-NH2	14.01	137.51	119.30
1	A	104	SER	O-C-N	-11.38	107.54	122.33
1	A	7	GLN	OE1-CD-NE2	-10.46	112.14	122.60
1	A	104	SER	CA-C-N	-9.98	106.66	122.73
1	A	104	SER	C-N-CA	-9.98	106.66	122.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	HIS	N-CA-CB	9.68	125.13	110.70
1	A	104	SER	CA-CB-OG	-8.60	93.89	111.10
1	A	207	GLN	OE1-CD-NE2	8.40	131.00	122.60
1	A	291	GLY	CA-C-O	8.40	138.44	120.80
1	A	290	THR	CA-C-N	8.36	136.75	121.70
1	A	290	THR	C-N-CA	8.36	136.75	121.70
1	A	138	GLN	CG-CD-NE2	8.02	128.43	116.40
1	A	230	HIS	CB-CG-CD2	-7.94	120.88	131.20
1	A	138	GLN	CB-CG-CD	7.87	125.98	112.60
1	A	70	HIS	CB-CG-CD2	-7.56	121.38	131.20
1	A	195	ASP	CA-CB-CG	7.42	120.02	112.60
1	A	105	HIS	N-CA-C	7.39	121.15	112.72
1	A	58	ALA	O-C-N	7.16	130.59	122.22
1	A	89	ASP	CB-CG-OD1	6.60	133.59	118.40
1	A	70	HIS	CB-CG-ND1	6.57	132.55	122.70
1	A	83	THR	CA-C-N	6.41	126.07	119.92
1	A	83	THR	C-N-CA	6.41	126.07	119.92
1	A	138	GLN	N-CA-CB	6.39	120.60	111.21
1	A	235	ASN	CA-CB-CG	6.16	118.76	112.60
1	A	58	ALA	CA-C-O	-6.09	113.22	120.10
1	A	109	GLN	OE1-CD-NE2	-6.04	116.56	122.60
1	A	256	HIS	CG-CD2-NE2	5.78	112.98	107.20
1	A	6	GLN	CA-C-N	5.78	128.02	120.28
1	A	6	GLN	C-N-CA	5.78	128.02	120.28
1	A	99	ASP	CA-CB-CG	5.76	118.36	112.60
1	A	160	ASP	CA-CB-CG	5.76	118.36	112.60
1	A	170	LYS	CG-CD-CE	5.56	124.08	111.30
1	A	105	HIS	CB-CG-ND1	5.54	131.00	122.70
1	A	59	SER	CA-C-O	-5.50	112.92	119.35
1	A	104	SER	N-CA-C	5.49	119.48	112.34
1	A	104	SER	CA-C-O	5.46	126.05	119.61
1	A	7	GLN	CG-CD-NE2	5.26	124.29	116.40
1	A	108	GLU	CG-CD-OE2	5.25	130.48	118.40
1	A	207	GLN	CB-CG-CD	5.25	121.52	112.60
1	A	138	GLN	CG-CD-OE1	-5.23	110.33	120.80
1	A	200	ASN	CA-CB-CG	5.22	117.82	112.60
1	A	103	GLY	CA-C-N	-5.20	112.27	120.63
1	A	103	GLY	C-N-CA	-5.20	112.27	120.63
1	A	230	HIS	CB-CG-ND1	5.15	130.43	122.70
1	A	61	PRO	CA-C-O	5.11	127.13	121.36
1	A	137	PHE	CA-CB-CG	5.08	118.89	113.80
1	A	104	SER	N-CA-CB	-5.05	101.10	110.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	LEU	O-C-N	5.03	125.59	121.31

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	105	HIS	CA

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	2215	2085	2079	14	0
2	A	6	0	0	0	0
3	A	2	0	0	0	0
4	A	3	0	0	0	0
5	A	324	0	0	4	0
All	All	2550	2085	2079	14	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 3.

All (14) 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:7:GLN:HE21	1:A:7:GLN:H	1.50	0.60
1:A:70:HIS:HE1	1:A:77:SER:OG	1.88	0.56
1:A:252:ASN:C	1:A:252:ASN:HD22	2.19	0.50
1:A:249:ASN:ND2	5:A:1151:HOH:O	2.37	0.47
1:A:7:GLN:NE2	5:A:1162:HOH:O	2.47	0.47
1:A:230:HIS:HE1	5:A:1030:HOH:O	1.96	0.47
1:A:70:HIS:HD2	1:A:160:ASP:OD2	1.97	0.47
1:A:253:PRO:HA	5:A:1275:HOH:O	2.17	0.45
1:A:61:PRO:O	1:A:62:ASN:HB2	2.16	0.44
1:A:252:ASN:HD22	1:A:254:ARG:H	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:HE1	1:A:200:ASN:HB3	2.00	0.44
1:A:1:MET:HG2	1:A:204:TYR:CG	2.53	0.43
1:A:230:HIS:H	1:A:230:HIS:CD2	2.36	0.43
1:A:141:ARG:HH21	1:A:291:GLY:C	2.28	0.42

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	291/299 (97%)	285 (98%)	6 (2%)	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	241/246 (98%)	237 (98%)	4 (2%)	53	18

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

Mol	Chain	Res	Type
1	A	7	GLN
1	A	109	GLN

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Mol	Chain	Res	Type
1	A	143	ILE
1	A	252	ASN

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	7	GLN
1	A	62	ASN
1	A	70	HIS
1	A	75	GLN
1	A	159	GLN
1	A	171	ASN
1	A	200	ASN
1	A	207	GLN
1	A	230	HIS
1	A	252	ASN
1	A	277	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 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SCN	A	1974	-	1,2,2	0.66	0	0,1,1	-	-
2	SCN	A	1973	-	1,2,2	2.66	1 (100%)	0,1,1	-	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1973	SCN	C-N	2.66	1.24	1.15

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.