



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:32 PM UTC

PDB ID : 1BN5 / pdb_00001bn5
Title : HUMAN METHIONINE AMINOPEPTIDASE 2
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Deposited on : 1998-07-31
Resolution : 1.80 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

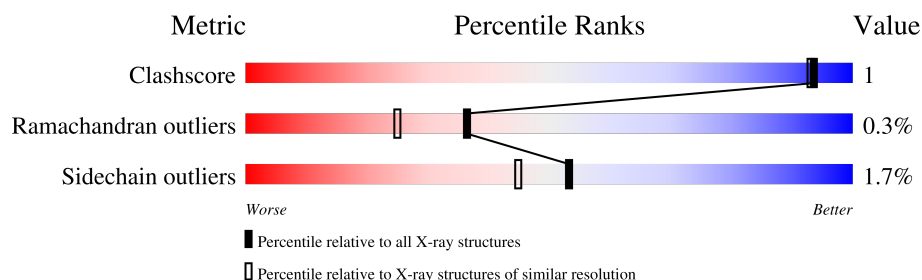
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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	478	 67% 6% • 26%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3031 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 METHIONINE AMINOPEPTIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	S	0	3	0
			2780	1750	475	529	26			

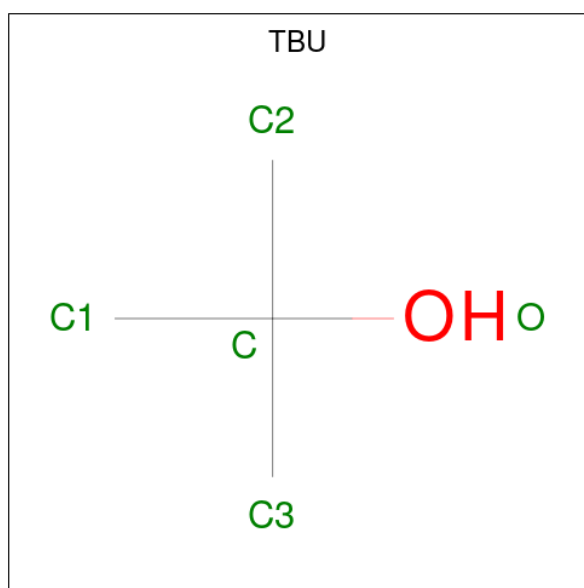
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	347	ILE	VAL	conflict	UNP P50579

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Co	0	0
			2	2		

- Molecule 3 is TERTIARY-BUTYL ALCOHOL (CCD ID: TBU) (formula: C₄H₁₀O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			5	4	1		
3	A	1	Total	C	O	0	0
			5	4	1		

- Molecule 4 is water.

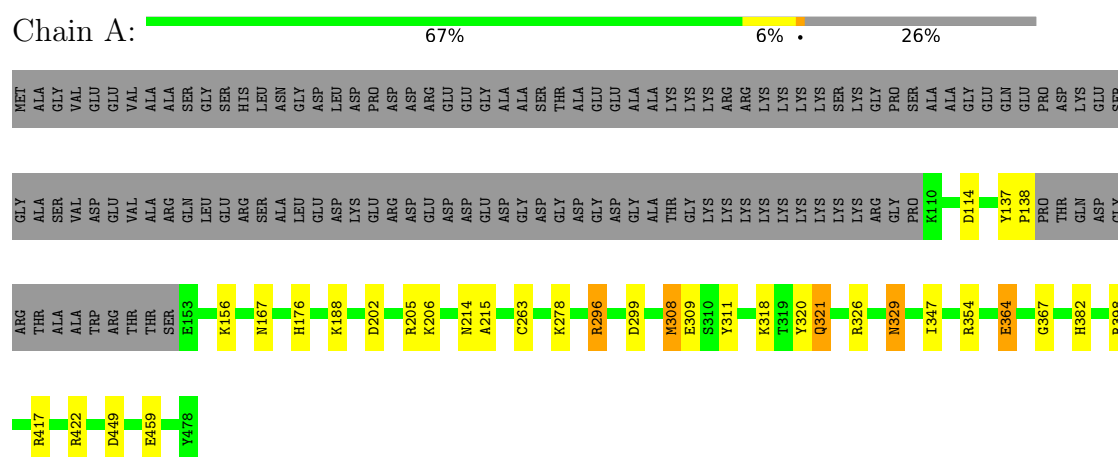
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	239	Total	O	0	0
			239	239		

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: METHIONINE AMINOPEPTIDASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	90.49Å 99.38Å 101.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.80	Depositor
% Data completeness (in resolution range)	98.4 (25.00-1.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.228	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3031	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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: TBU, CO

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	0.78	1/2850 (0.0%)	1.42	23/3855 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	138	PRO	N-CD	5.45	1.55	1.47

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	329	ASN	CA-CB-CG	12.91	125.52	112.60
1	A	417	ARG	NE-CZ-NH2	-9.97	110.23	119.20
1	A	422	ARG	NE-CZ-NH2	-9.65	110.51	119.20
1	A	296	ARG	CD-NE-CZ	8.92	136.89	124.40
1	A	188	LYS	O-C-N	-8.37	115.99	121.85
1	A	321	GLN	OE1-CD-NE2	-8.06	114.54	122.60
1	A	205	ARG	NE-CZ-NH1	-7.08	114.42	121.50
1	A	188	LYS	CA-C-O	6.84	126.89	119.91
1	A	137	TYR	CA-C-O	6.40	126.83	120.17
1	A	354	ARG	CD-NE-CZ	6.20	133.08	124.40
1	A	167	ASN	OD1-CG-ND2	6.09	128.69	122.60
1	A	321	GLN	CB-CG-CD	6.01	122.82	112.60
1	A	367	GLY	CA-C-O	-5.90	115.80	121.11
1	A	417	ARG	NH1-CZ-NH2	5.74	126.76	119.30
1	A	382	HIS	CA-CB-CG	5.58	119.38	113.80
1	A	214	ASN	OD1-CG-ND2	-5.52	117.08	122.60
1	A	449	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	422	ARG	CD-NE-CZ	5.25	131.75	124.40
1	A	398	ARG	CD-NE-CZ	5.23	131.72	124.40
1	A	308	MET	CG-SD-CE	5.08	112.08	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	ALA	CA-C-N	-5.02	114.04	120.72
1	A	215	ALA	C-N-CA	-5.02	114.04	120.72
1	A	364	GLU	CA-CB-CG	5.02	124.15	114.10

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	2780	0	2722	8	0
2	A	2	0	0	0	0
3	A	10	0	20	0	0
4	A	239	0	0	1	0
All	All	3031	0	2742	8	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 1.

All (8) 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:326:ARG:HB2	1:A:347:ILE:HD13	1.74	0.70
1:A:296:ARG:HD3	1:A:299:ASP:OD2	2.13	0.49
1:A:318:LYS:HE2	1:A:320:TYR:CE2	2.48	0.48
1:A:364:GLU:HB3	1:A:459:GLU:HG3	1.98	0.45
1:A:309:GLU:O	1:A:321:GLN:NE2	2.52	0.43
1:A:176:HIS:CE1	1:A:263:CYS:HB3	2.54	0.42
1:A:347:ILE:HD12	4:A:599:HOH:O	2.20	0.40
1:A:278:LYS:NZ	1:A:311:TYR:OH	2.55	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	354/478 (74%)	346 (98%)	7 (2%)	1 (0%)	36	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	ASP

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	306/399 (77%)	301 (98%)	5 (2%)	55	47

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	156	LYS
1	A	202	ASP
1	A	206	LYS
1	A	308	MET
1	A	329	ASN

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

Mol	Chain	Res	Type
1	A	160	GLN
1	A	214	ASN
1	A	329	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](#)

Of 4 ligands modelled in this entry, 2 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	$\# Z > 2$
3	TBU	A	689	-	4,4,4	0.82	0	6,6,6	1.77	2 (33%)
3	TBU	A	690	-	4,4,4	0.87	0	6,6,6	1.80	1 (16%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	690	TBU	O-C-C2	3.64	118.12	108.00
3	A	689	TBU	O-C-C2	3.33	117.26	108.00
3	A	689	TBU	O-C-C1	-2.21	101.87	108.00

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

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.