



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 10:03 AM BST

PDB ID : 1YJ3
Title : Crystal structure analysis of product bound methionine aminopeptidase Type 1c from Mycobacterium Tuberculosis
Authors : Addlagatta, A.; Quillin, M.L.; Omotoso, O.; Liu, J.O.; Matthews, B.W.
Deposited on : 2005-01-13
Resolution : 1.60 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

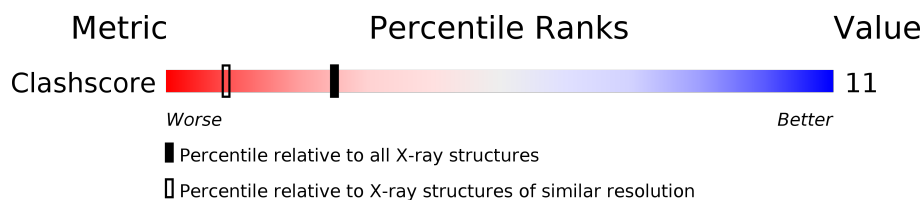
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	141614	3665 (1.60-1.60)

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 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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	291	 77% 20% •

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2490 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	282	Total	C	N	O	S	0	0	0
			2153	1359	371	414	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP P0A5J2
A	-4	HIS	-	EXPRESSION TAG	UNP P0A5J2
A	-3	HIS	-	EXPRESSION TAG	UNP P0A5J2
A	-2	HIS	-	EXPRESSION TAG	UNP P0A5J2
A	-1	HIS	-	EXPRESSION TAG	UNP P0A5J2
A	0	HIS	-	EXPRESSION TAG	UNP P0A5J2

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

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

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 4 is METHIONINE (three-letter code: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

- Molecule 5 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	321	Total 321	O 321	0	0

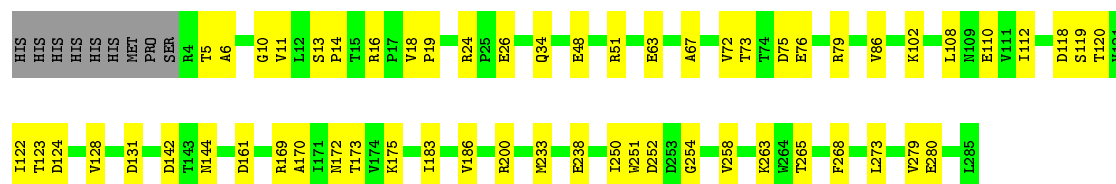
3 Residue-property plots [i](#)

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. 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 failed to run properly.

- Molecule 1: Methionine aminopeptidase

Chain A: 



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.36Å 48.16Å 56.54Å 90.00° 95.05° 90.00°	Depositor
Resolution (Å)	50.00 – 1.60	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 1.50Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.203 , 0.247	Depositor
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	1.177	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2490	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.60% 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: K, CO, BME

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	0.85	1/2203 (0.0%)	0.95	3/3011 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	233	MET	SD-CE	-7.94	1.33	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	LEU	CA-CB-CG	5.76	128.55	115.30
1	A	161	ASP	CB-CG-OD2	-5.62	113.25	118.30
1	A	142	ASP	CB-CG-OD1	-5.06	113.74	118.30

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	2153	0	2111	46	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	9	0	8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	4	0	0
6	A	321	0	0	7	0
All	All	2490	0	2123	46	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 11.

All (46) 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:48:GLU:OE2	1:A:51:ARG:HD2	1.88	0.73
1:A:16:ARG:NH2	1:A:79:ARG:HG3	2.05	0.71
1:A:11:VAL:N	1:A:119:SER:OG	2.24	0.71
1:A:110:GLU:HG2	1:A:258:VAL:HG13	1.74	0.69
1:A:63:GLU:HG2	6:A:579:HOH:O	1.95	0.65
1:A:263:LYS:HE2	6:A:808:HOH:O	1.98	0.63
1:A:79:ARG:CZ	1:A:79:ARG:HB3	2.30	0.61
1:A:173:THR:HG21	1:A:186:VAL:HG21	1.82	0.60
1:A:5:THR:HG22	1:A:6:ALA:O	2.03	0.59
1:A:108:LEU:HD21	1:A:122:ILE:HG12	1.85	0.59
1:A:108:LEU:HD23	1:A:128:VAL:HB	1.87	0.57
1:A:252:ASP:C	1:A:254:GLY:H	2.08	0.56
1:A:279:VAL:HG22	1:A:280:GLU:N	2.23	0.54
1:A:123:THR:HG22	1:A:124:ASP:H	1.75	0.52
1:A:252:ASP:C	1:A:254:GLY:N	2.63	0.52
1:A:19:PRO:HG2	1:A:86:VAL:HG13	1.92	0.52
1:A:72:VAL:HG12	1:A:73:THR:N	2.26	0.50
1:A:123:THR:HG22	1:A:124:ASP:N	2.27	0.49
1:A:13:SER:HB2	1:A:14:PRO:HD2	1.95	0.49
1:A:110:GLU:CG	1:A:258:VAL:HG13	2.42	0.48
1:A:238:GLU:HA	1:A:268:PHE:O	2.13	0.48
1:A:16:ARG:CZ	1:A:79:ARG:HG3	2.42	0.48
1:A:76:GLU:OE1	1:A:79:ARG:NH2	2.47	0.48
1:A:76:GLU:OE2	1:A:79:ARG:NH2	2.47	0.48
1:A:169:ARG:O	1:A:173:THR:HG23	2.14	0.47
1:A:48:GLU:OE2	1:A:51:ARG:NH1	2.45	0.46
1:A:175:LYS:HB2	1:A:175:LYS:HE2	1.72	0.46
1:A:252:ASP:O	1:A:254:GLY:N	2.49	0.45
1:A:76:GLU:CD	1:A:79:ARG:NH2	2.70	0.45
1:A:102:LYS:HE3	6:A:819:HOH:O	2.17	0.45
1:A:112:ILE:HA	1:A:265:THR:HG21	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:THR:HA	1:A:120:THR:O	2.16	0.45
1:A:263:LYS:NZ	6:A:809:HOH:O	2.49	0.44
1:A:26:GLU:OE2	1:A:34:GLN:OE1	2.36	0.44
1:A:67:ALA:O	1:A:72:VAL:HG21	2.17	0.44
1:A:170:ALA:HB1	1:A:183:ILE:HG23	2.00	0.44
1:A:75:ASP:OD1	6:A:819:HOH:O	2.21	0.43
1:A:18:VAL:HG22	1:A:24:ARG:NH2	2.34	0.43
1:A:250:ILE:HG22	1:A:251:TRP:O	2.19	0.43
1:A:10:GLY:N	1:A:118:ASP:OD2	2.48	0.42
1:A:200:ARG:NE	6:A:569:HOH:O	2.45	0.42
1:A:172:ASN:HA	1:A:172:ASN:HD22	1.67	0.41
1:A:131:ASP:HA	1:A:144:ASN:CB	2.50	0.41
1:A:279:VAL:CG2	1:A:280:GLU:N	2.84	0.41
1:A:72:VAL:HG21	6:A:591:HOH:O	2.21	0.41
1:A:18:VAL:HG22	1:A:24:ARG:CZ	2.51	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 3 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	$\# Z > 2$
5	BME	A	425	1	3,3,3	2.04	1 (33%)	1,2,2	2.12	1 (100%)
4	MET	A	500	2	4,8,8	0.88	0	2,9,9	0.55	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BME	A	425	1	-	0/1/1/1	-
4	MET	A	500	2	-	0/4/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	425	BME	O1-C1	-3.53	1.23	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	425	BME	O1-C1-C2	2.12	119.19	110.83

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 failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section is therefore empty.