



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2023 – 02:07 PM JST

PDB ID : 8I99
Title : N-carbamoyl-D-amino-acid hydrolase mutant - M4Th3
Authors : Hu, J.M.; Ni, Y.; Xu, G.C.
Deposited on : 2023-02-06
Resolution : 3.17 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.32.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.1

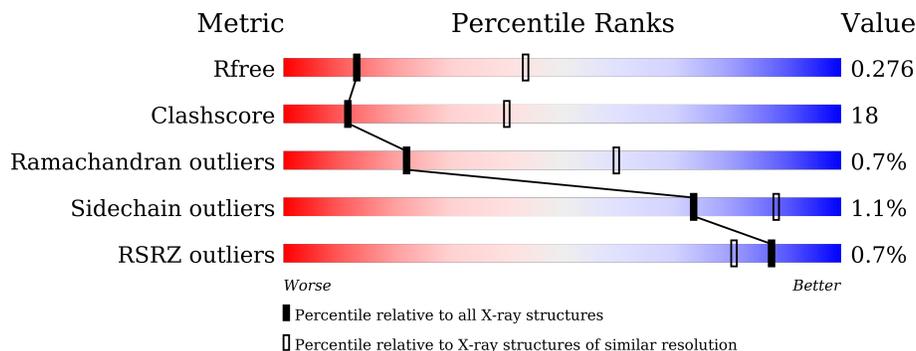
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.17 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}	130704	1467 (3.20-3.16)
Clashscore	141614	1599 (3.20-3.16)
Ramachandran outliers	138981	1574 (3.20-3.16)
Sidechain outliers	138945	1573 (3.20-3.16)
RSRZ outliers	127900	1423 (3.20-3.16)

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	307	 65% 34% ..
1	B	307	 61% 38% .
1	C	307	 % 61% 36% ..
1	D	307	 % 64% 35% .

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 9680 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 N-carbamoyl-D-amino-acid hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	304	2410	1517	434	445	14	0	0	0
1	B	307	2430	1529	437	450	14	0	0	0
1	C	304	2410	1517	434	445	14	0	0	0
1	D	307	2430	1529	437	450	14	0	0	0

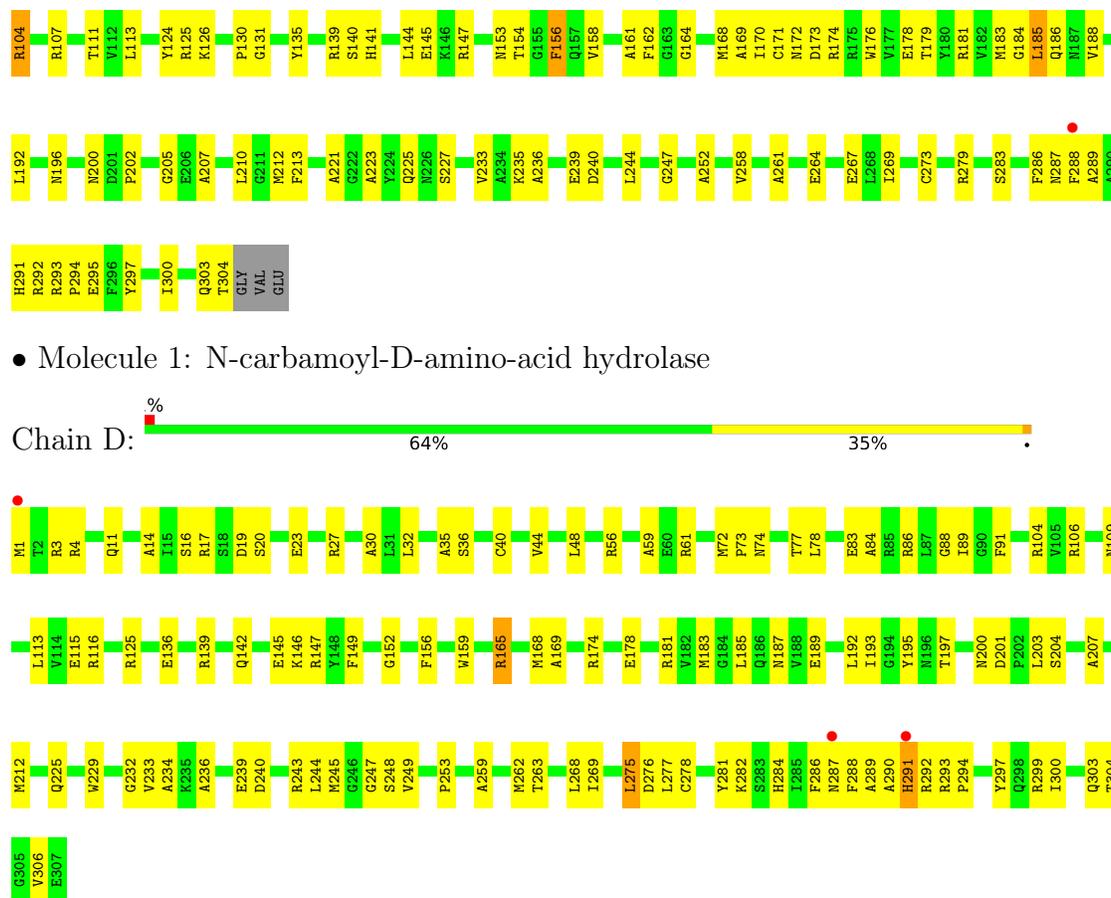
There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	ASN	ASP	conflict	UNP K2NMS4
A	200	ASN	ALA	conflict	UNP K2NMS4
A	202	PRO	SER	engineered mutation	UNP K2NMS4
A	207	ALA	SER	conflict	UNP K2NMS4
A	208	ASP	GLU	engineered mutation	UNP K2NMS4
A	211	GLY	ARG	conflict	UNP K2NMS4
A	277	LEU	ARG	engineered mutation	UNP K2NMS4
B	187	ASN	ASP	conflict	UNP K2NMS4
B	200	ASN	ALA	conflict	UNP K2NMS4
B	202	PRO	SER	engineered mutation	UNP K2NMS4
B	207	ALA	SER	conflict	UNP K2NMS4
B	208	ASP	GLU	engineered mutation	UNP K2NMS4
B	211	GLY	ARG	conflict	UNP K2NMS4
B	277	LEU	ARG	engineered mutation	UNP K2NMS4
C	187	ASN	ASP	conflict	UNP K2NMS4
C	200	ASN	ALA	conflict	UNP K2NMS4
C	202	PRO	SER	engineered mutation	UNP K2NMS4
C	207	ALA	SER	conflict	UNP K2NMS4
C	208	ASP	GLU	engineered mutation	UNP K2NMS4
C	211	GLY	ARG	conflict	UNP K2NMS4
C	277	LEU	ARG	engineered mutation	UNP K2NMS4

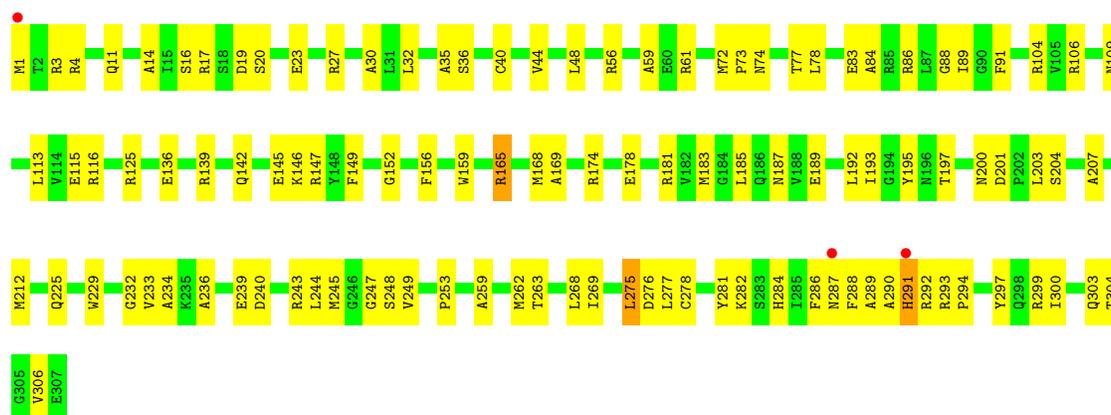
Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	187	ASN	ASP	conflict	UNP K2NMS4
D	200	ASN	ALA	conflict	UNP K2NMS4
D	202	PRO	SER	engineered mutation	UNP K2NMS4
D	207	ALA	SER	conflict	UNP K2NMS4
D	208	ASP	GLU	engineered mutation	UNP K2NMS4
D	211	GLY	ARG	conflict	UNP K2NMS4
D	277	LEU	ARG	engineered mutation	UNP K2NMS4



- Molecule 1: N-carbamoyl-D-amino-acid hydrolase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.14Å 73.55Å 77.71Å 84.08° 88.20° 89.73°	Depositor
Resolution (Å)	23.98 – 3.17 23.98 – 3.17	Depositor EDS
% Data completeness (in resolution range)	98.9 (23.98-3.17) 98.9 (23.98-3.17)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 3.17Å)	Xtrriage
Refinement program	PHENIX v1.20	Depositor
R, R_{free}	0.201 , 0.278 0.202 , 0.276	Depositor DCC
R_{free} test set	1334 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtrriage
Anisotropy	0.533	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 8.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.209 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	9680	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.52	0/2462	0.76	0/3325
1	B	0.51	0/2482	0.76	0/3352
1	C	0.52	0/2462	0.75	0/3325
1	D	0.52	0/2482	0.77	0/3352
All	All	0.52	0/9888	0.76	0/13354

There are no bond length outliers.

There are no bond angle outliers.

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	2410	0	2350	91	0
1	B	2430	0	2368	98	0
1	C	2410	0	2350	99	0
1	D	2430	0	2368	100	0
All	All	9680	0	9436	337	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 18.

The worst 5 of 337 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:D:115:GLU:HG3	1:D:116:ARG:H	1.28	0.97
1:D:20:SER:HB3	1:D:23:GLU:HG3	1.51	0.92
1:B:20:SER:HB2	1:B:23:GLU:HG3	1.49	0.92
1:A:304:THR:HG21	1:B:292:ARG:HH11	1.40	0.86
1:D:115:GLU:HG3	1:D:116:ARG:N	1.88	0.86

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	302/307 (98%)	285 (94%)	16 (5%)	1 (0%)	41	73
1	B	305/307 (99%)	279 (92%)	24 (8%)	2 (1%)	22	60
1	C	302/307 (98%)	280 (93%)	20 (7%)	2 (1%)	22	60
1	D	305/307 (99%)	275 (90%)	27 (9%)	3 (1%)	15	52
All	All	1214/1228 (99%)	1119 (92%)	87 (7%)	8 (1%)	22	60

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	3	ARG
1	A	285	ILE
1	D	275	LEU
1	D	291	HIS
1	B	287	ASN

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	249/251 (99%)	245 (98%)	4 (2%)	62	83
1	B	251/251 (100%)	248 (99%)	3 (1%)	71	87
1	C	249/251 (99%)	247 (99%)	2 (1%)	81	92
1	D	251/251 (100%)	249 (99%)	2 (1%)	81	92
All	All	1000/1004 (100%)	989 (99%)	11 (1%)	73	88

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	104	ARG
1	C	156	PHE
1	D	243	ARG
1	D	165	ARG
1	B	115	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	141	HIS
1	B	215	ASN
1	C	172	ASN
1	C	100	GLN
1	A	298	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [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	304/307 (99%)	-0.63	1 (0%) 94 92	5, 15, 45, 70	0
1	B	307/307 (100%)	-0.60	1 (0%) 94 92	6, 16, 47, 75	0
1	C	304/307 (99%)	-0.63	3 (0%) 82 72	6, 16, 48, 76	0
1	D	307/307 (100%)	-0.59	3 (0%) 82 72	6, 16, 46, 82	0
All	All	1222/1228 (99%)	-0.61	8 (0%) 87 81	5, 16, 47, 82	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	287	ASN	3.5
1	C	1	MET	2.7
1	A	1	MET	2.6
1	D	291	HIS	2.5
1	D	1	MET	2.5

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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.