

wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 05:35 AM EST

PDB ID : 4Q4I

Title: Crystal structure of E.coli aminopeptidase N in complex with amastatin

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Deposited on : 2014-04-14

Resolution : 2.31 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 (i) 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 (1)) 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 : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

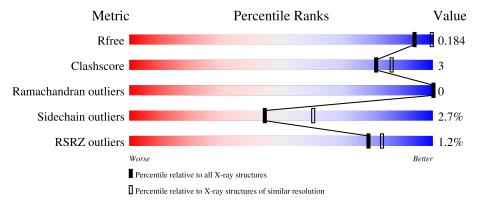
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.31 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 <=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	891	.% 89%		7% • •		
2	С	4	50%	25%	25%		



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7647 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 Aminopeptidase N.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	ı	
1	A	866	Total 7069	C 4466	N 1232	O 1343	S 28	0	14	0	Ì

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP P04825
A	-19	GLY	-	expression tag	UNP P04825
A	-18	SER	-	expression tag	UNP P04825
A	-17	SER	-	expression tag	UNP P04825
A	-16	HIS	-	expression tag	UNP P04825
A	-15	HIS	-	expression tag	UNP P04825
A	-14	HIS	-	expression tag	UNP P04825
A	-13	HIS	-	expression tag	UNP P04825
A	-12	HIS	-	expression tag	UNP P04825
A	-11	HIS	-	expression tag	UNP P04825
A	-10	SER	-	expression tag	UNP P04825
A	-9	SER	-	expression tag	UNP P04825
A	-8	GLY	-	expression tag	UNP P04825
A	-7	GLU	-	expression tag	UNP P04825
A	-6	ASN	-	expression tag	UNP P04825
A	-5	LEU	-	expression tag	UNP P04825
A	-4	TYR	-	expression tag	UNP P04825
A	-3	PHE	-	expression tag	UNP P04825
A	-2	GLN	-	expression tag	UNP P04825
A	-1	GLY		expression tag	UNP P04825
A	0	HIS	-	expression tag	UNP P04825

• Molecule 2 is a protein called Amastatin.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	С	4	Total 33	C 21	N 4	O 8	0	0	0

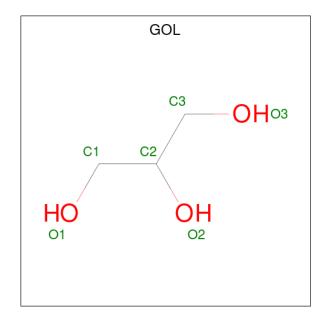
• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

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

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0

• Molecule 6 is water.

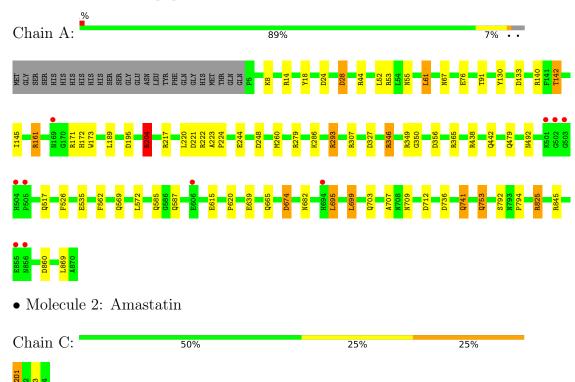
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	510	Total O 510 510	0	0
6	С	1	Total O 1 1	0	0



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: Aminopeptidase N





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	119.39Å 119.39Å 170.13Å	Domositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.72 - 2.31	Depositor
Resolution (A)	49.72 - 2.31	EDS
% Data completeness	99.7 (49.72-2.31)	Depositor
(in resolution range)	99.7 (49.72-2.31)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.32 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
D.D.	0.140 , 0.179	Depositor
R, R_{free}	0.149 , 0.184	DCC
R_{free} test set	3152 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.42 , 54.0	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7647	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, L2O, 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	Bo	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.93	3/7224 (0.0%)	0.98	$27/9805 \ (0.3\%)$	
2	С	0.83	0/22	1.97	0/28	
All	All	0.93	3/7246 (0.0%)	0.99	$27/9833 \ (0.3\%)$	

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	С	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	161	ARG	CD-NE	6.43	1.57	1.46
1	A	161	ARG	NE-CZ	6.37	1.41	1.33
1	A	161	ARG	CG-CD	5.96	1.66	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	A	161	ARG	NE-CZ-NH1	14.54	127.57	120.30
1	A	14	ARG	NE-CZ-NH1	9.61	125.10	120.30
1	A	349	ARG	NE-CZ-NH2	-9.35	115.62	120.30
1	A	222	ARG	NE-CZ-NH1	8.93	124.77	120.30
1	A	222	ARG	NE-CZ-NH2	-8.20	116.20	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
2	С	1	L2O	Peptide, Mainchain

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	7069	0	6884	36	0
2	С	33	0	29	1	0
3	A	1	0	0	0	0
4	A	3	0	0	0	0
5	A	30	0	40	1	0
6	A	510	0	0	6	0
6	С	1	0	0	0	0
All	All	7647	0	6953	36	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.

The worst 5 of 36 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	${f distance}({ m \AA})$	${ m overlap}({ m \AA})$	
1:A:442:GLN:HE22	1:A:479:GLN:H	1.24	0.81	
1:A:279:ARG:HD2	6:A:1459:HOH:O	1.84	0.77	
1:A:695:LEU:HD22	1:A:699:LEU:HD22	1.65	0.77	
1:A:350:GLY:C	6:A:1106:HOH:O	2.27	0.73	
1:A:140[B]:ARG:HG2	6:A:1183:HOH:O	1.90	0.71	

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	Perce	ntiles	
1	A	878/891 (98%)	862 (98%)	16 (2%)	0	100	100
2	С	2/4~(50%)	2 (100%)	0	0	100	100
All	All	880/895 (98%)	864 (98%)	16 (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	755/763~(99%)	733 (97%)	22 (3%)	42 57		
2	С	3/3 (100%)	3 (100%)	0	100 100		
All	All	758/766 (99%)	736 (97%)	22 (3%)	44 57		

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	572	LEU
1	A	695	LEU
1	A	674	ASP
1	A	699	LEU
1	A	142	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	587	GLN
1	A	661	ASN
1	A	753	GLN
1	A	709	ASN
1	A	741	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	Mol Type Chain Res Link				Bond lengths			Bond angles		
WIOI	$oxed{Type} oxed{Chain} oxed{Res} oxed{L}$	Link	Counts RMSZ $\# Z > 2$			Counts	RMSZ	# Z > 2		
2	L2O	С	1	2,3	7,9,10	0.63	0	6,11,13	1.44	1 (16%)

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
2	L2O	С	1	2,3	-	5/9/10/12	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	1	L2O	O1-C6-CA	2.43	111.17	107.31

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	С	1	L2O	O1-C6-CA-N
2	С	1	L2O	C-C6-CA-N
2	С	1	L2O	O1-C6-CA-C2
2	С	1	L2O	C-C6-CA-C2
2	С	1	L2O	C3-C2-CA-C6



There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	Trmo	Chain	Dog	Link	Bond lengths			Bond angles		
MIOI	Type		Res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	A	909	-	5,5,5	0.53	0	5,5,5	0.66	0
5	GOL	A	908	-	5,5,5	0.58	0	5,5,5	0.70	0
5	GOL	A	907	-	5,5,5	1.09	0	5,5,5	0.91	0
5	GOL	A	906	-	5,5,5	0.94	0	5,5,5	1.00	0
5	GOL	A	905	-	5,5,5	0.84	0	5,5,5	0.32	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	GOL	A	909	-	-	0/4/4/4	-
5	GOL	A	908	-	-	0/4/4/4	-
5	GOL	A	907	-	-	3/4/4/4	-
5	GOL	A	906	-	-	2/4/4/4	-
5	GOL	A	905	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	906	GOL	C1-C2-C3-O3
5	A	907	GOL	C1-C2-C3-O3
5	A	907	GOL	O2-C2-C3-O3
5	A	907	GOL	O1-C1-C2-O2
5	A	906	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	908	GOL	1	0

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, 95^{th} 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	866/891 (97%)	-0.45	10 (1%) 79 83	14, 24, 41, 83	0
2	C	3/4 (75%)	1.02	0 100 100	23, 23, 39, 58	0
All	All	869/895 (97%)	-0.44	10 (1%) 79 83	14, 24, 41, 83	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	504	HIS	5.4
1	A	503	GLY	4.0
1	A	501	LYS	2.6
1	A	855	GLU	2.6
1	A	169	ASN	2.4

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	L2O	С	1	10/11	0.99	0.20	16,19,21,25	0

6.3 Carbohydrates (i)

There are no monosaccharides 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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
5	GOL	A	909	6/6	0.89	0.14	41,48,53,54	0
5	GOL	A	907	6/6	0.91	0.12	33,45,47,49	0
4	NA	A	903	1/1	0.92	0.06	32,32,32,32	0
5	GOL	A	908	6/6	0.94	0.21	44,50,52,52	0
4	NA	A	902	1/1	0.96	0.08	31,31,31,31	0
5	GOL	A	905	6/6	0.96	0.11	23,28,29,29	0
5	GOL	A	906	6/6	0.96	0.13	31,34,37,38	0
4	NA	A	904	1/1	0.99	0.06	26,26,26,26	0
3	ZN	A	901	1/1	1.00	0.09	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.

