

Full wwPDB X-ray Structure Validation Report (i)

May 28, 2020 – 07:57 pm BST

PDB ID : 1LMH

Title : Crystal Structure of S. aureus peptide deformylase

Authors : Baldwin, E.T.; Harris, M.S.

Deposited on : 2002-05-01

Resolution : 1.90 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 (i) symbol.

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) : NOT EXECUTED EDS : NOT EXECUTED

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)

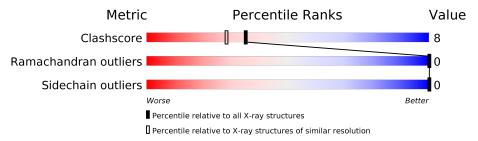
Validation Pipeline (wwPDB-VP) : 2.11

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 1.90 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	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 <=5%

Note EDS was not executed.

$oldsymbol{\Lambda}$	/Iol	Chain	Length	Quality of chain	
	1	Δ	187	85%	15%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1879 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 PROTEIN (S.aureus peptide deformylase).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	184	Total 1451	C 914	N 255	O 275	S 1	Se 6	0	0	0

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	427	Total O 427 427	0	0

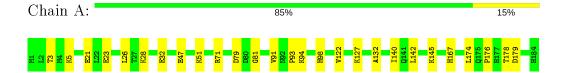


3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: PROTEIN (S.aureus peptide deformylase)





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	C 2 2 21	Depositor	
Cell constants	94.13Å 121.87Å 47.58Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	9.99 - 1.90	Depositor	
% Data completeness	95.5 (9.99-1.90)	Depositor	
(in resolution range)	30.0 (3.33 1.30)	Depositor	
R_{merge}	(Not available)	Depositor	
R_{sym}	0.04	Depositor	
Refinement program	CNX 2000.1	Depositor	
R, R_{free}	0.180 , 0.212	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1879	wwPDB-VP	
Average B, all atoms (Å ²)	18.0	wwPDB-VP	



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: ZN

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	0.26	0/1473	0.58	0/1983

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	1451	0	1459	24	1
2	A	1	0	0	0	0
3	A	427	0	0	9	2
All	All	1879	0	1459	24	3

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 8.

All (24) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1			Clash overlap (Å)	
1:A:127:LYS:HE2	1:A:145:LYS:HD3	1.56	0.88	

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A 4 1	A 4 0	Interatomic	Clash	
Atom-1	Atom-2	${f distance}({f \AA})$	$overlap(\AA)$	
1:A:174:LEU:HD23	3:A:578:HOH:O	1.99	0.62	
1:A:23:GLU:HG2	3:A:494:HOH:O	1.98	0.62	
1:A:28:LYS:O	1:A:32:GLU:HG3	2.00	0.62	
1:A:140:ILE:HD11	3:A:278:HOH:O	2.00	0.61	
1:A:51:LYS:HG2	3:A:335:HOH:O	2.03	0.58	
1:A:178:THR:O	1:A:179:ASP:HB2	2.08	0.52	
1:A:174:LEU:HD22	3:A:484:HOH:O	2.12	0.49	
1:A:145:LYS:NZ	1:A:145:LYS:HB3	2.27	0.49	
1:A:142:LEU:N	1:A:142:LEU:HD12	2.29	0.48	
1:A:21:GLU:OE2	1:A:71:ARG:HD3	2.16	0.45	
1:A:28:LYS:HD2	3:A:536:HOH:O	2.15	0.45	
1:A:145:LYS:NZ	1:A:145:LYS:CB	2.79	0.44	
1:A:21:GLU:HG2	3:A:276:HOH:O	2.16	0.44	
1:A:91:VAL:HG23	3:A:537:HOH:O	2.16	0.44	
1:A:98:HIS:HE1	3:A:292:HOH:O	2.01	0.44	
1:A:94:LYS:HB3	1:A:94:LYS:NZ	2.34	0.43	
1:A:3:THR:OG1	1:A:5:LYS:HG2	2.19	0.42	
1:A:93:PRO:HA	1:A:132:ALA:HB2	2.01	0.42	
1:A:79:ASP:OD1	1:A:81:GLY:N	2.53	0.41	
1:A:174:LEU:O	1:A:176:PRO:HD3	2.21	0.41	
1:A:26:LEU:HD11	1:A:91:VAL:HG21	2.01	0.41	
1:A:47:GLU:O	1:A:51:LYS:HG2	2.20	0.41	
1:A:122:VAL:HG13	1:A:167:HIS:HB2	2.04	0.40	

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$egin{array}{c} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
3:A:608:HOH:O	3:A:608:HOH:O[3_656]	1.01	1.19
3:A:369:HOH:O	3:A:369:HOH:O[3_656]	1.99	0.21
1:A:140:ILE:CD1	1:A:140:ILE:CD1[3_656]	2.08	0.12

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	Percentile	\mathbf{s}
1	A	182/184 (99%)	181 (100%)	1 (0%)	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	160/154 (104%)	160 (100%)	0	100 100

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

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	HIS
1	A	141	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 carbohydrates in this entry.



5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

