



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:40 AM UTC

PDB ID : 1LM4 / pdb_00001lm4
Title : Structure of Peptide Deformylase from Staphylococcus aureus at 1.45 Å
Authors : Kreusch, A.; Spraggon, G.; Lee, C.C.; Klock, H.; McMullan, D.; Ng, K.; Shin, T.; Vincent, J.; Warner, I.; Ericson, C.; Lesley, S.A.
Deposited on : 2002-04-30
Resolution : 1.45 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

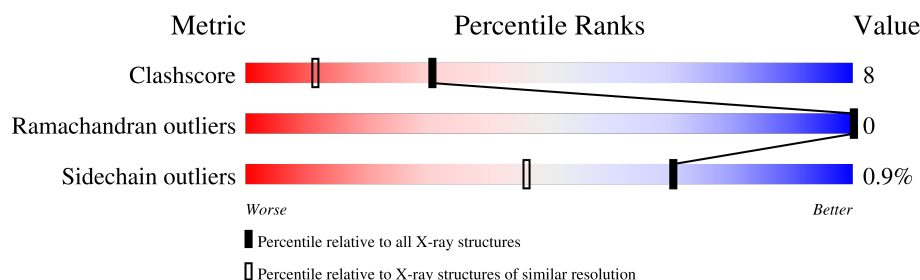
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)

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	194	
1	B	194	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	601	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3495 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 peptide deformylase PDF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1501	941	267	286	7			
1	B	184	Total	C	N	O	S	0	0	0
			1456	914	258	277	7			

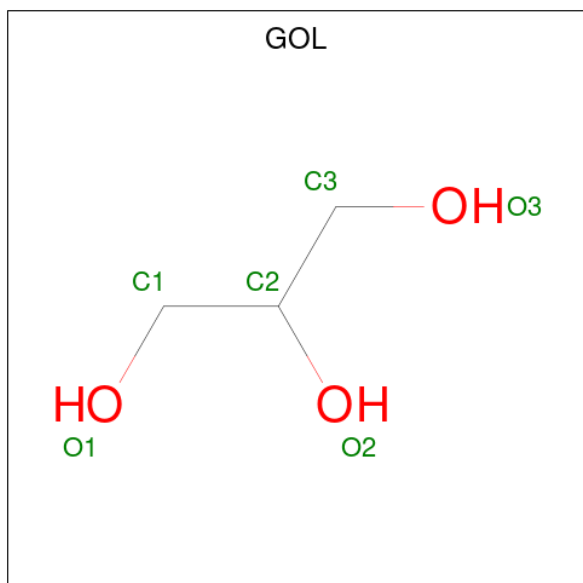
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	SEE REMARK 999	UNP P68826
A	-9	SER	-	SEE REMARK 999	UNP P68826
A	-8	ASP	-	SEE REMARK 999	UNP P68826
A	-7	LYS	-	SEE REMARK 999	UNP P68826
A	-6	ILE	-	SEE REMARK 999	UNP P68826
A	-5	HIS	-	SEE REMARK 999	UNP P68826
A	-4	HIS	-	SEE REMARK 999	UNP P68826
A	-3	HIS	-	SEE REMARK 999	UNP P68826
A	-2	HIS	-	SEE REMARK 999	UNP P68826
A	-1	HIS	-	SEE REMARK 999	UNP P68826
A	0	HIS	-	SEE REMARK 999	UNP P68826
A	111	OCS	CYS	modified residue	UNP P68826
B	-10	GLY	-	SEE REMARK 999	UNP P68826
B	-9	SER	-	SEE REMARK 999	UNP P68826
B	-8	ASP	-	SEE REMARK 999	UNP P68826
B	-7	LYS	-	SEE REMARK 999	UNP P68826
B	-6	ILE	-	SEE REMARK 999	UNP P68826
B	-5	HIS	-	SEE REMARK 999	UNP P68826
B	-4	HIS	-	SEE REMARK 999	UNP P68826
B	-3	HIS	-	SEE REMARK 999	UNP P68826
B	-2	HIS	-	SEE REMARK 999	UNP P68826
B	-1	HIS	-	SEE REMARK 999	UNP P68826
B	0	HIS	-	SEE REMARK 999	UNP P68826
B	111	OCS	CYS	modified residue	UNP P68826

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



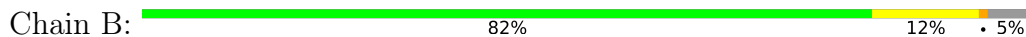
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	265	Total	O	0	0
			265	265		
4	B	265	Total	O	0	0
			265	265		

Note EDS was not executed.

- Chain A: 85% 12% ..



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	38.22Å 76.70Å 112.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.26 – 1.45	Depositor
% Data completeness (in resolution range)	99.1 (45.26-1.45)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.170 , 0.200	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3495	wwPDB-VP
Average B, all atoms (Å ²)	22.0	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: GOL, OCS, FE

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	0.87	2/1519 (0.1%)	1.06	3/2048 (0.1%)
1	B	0.87	0/1474	1.04	3/1990 (0.2%)
All	All	0.87	2/2993 (0.1%)	1.05	6/4038 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	99	SER	CA-CB	6.43	1.64	1.53
1	A	99	SER	CB-OG	5.63	1.53	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ALA	N-CA-C	8.51	122.57	110.23
1	A	99	SER	CA-CB-OG	7.38	125.86	111.10
1	A	105	LEU	N-CA-C	-5.30	102.97	109.65
1	B	105	LEU	N-CA-C	-5.22	103.07	109.65
1	B	98	HIS	CA-C-N	5.12	131.32	121.54
1	B	98	HIS	C-N-CA	5.12	131.32	121.54

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	1501	0	1505	21	0
1	B	1456	0	1460	28	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	B	6	0	5	0	0
4	A	265	0	0	3	0
4	B	265	0	0	7	0
All	All	3495	0	2970	49	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 8.

All (49) 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:B:99:SER:HB3	1:B:127:ARG:HB2	1.11	1.07
1:B:12:HIS:HD2	1:B:14:THR:H	1.17	0.92
1:A:99:SER:HB2	1:A:127:ARG:HB2	1.56	0.87
1:A:71:ARG:HH22	1:A:160:ASN:HD21	1.26	0.83
1:A:71:ARG:HH22	1:A:160:ASN:ND2	1.80	0.79
1:B:99:SER:HB2	4:B:612:HOH:O	1.82	0.79
1:B:5:LYS:N	1:B:5:LYS:HD2	2.03	0.74
1:A:99:SER:HB3	1:A:127:ARG:O	1.88	0.74
1:B:51:LYS:HE2	4:B:762:HOH:O	1.88	0.73
1:B:12:HIS:CD2	1:B:14:THR:H	2.08	0.68
1:B:18:LYS:NZ	1:B:18:LYS:HB3	2.11	0.65
1:B:99:SER:HB3	1:B:127:ARG:CB	2.07	0.64
1:A:123:HIS:CE1	1:A:177:HIS:H	2.16	0.63
1:B:102:GLU:HG2	4:B:787:HOH:O	1.99	0.62
1:B:1:MET:HE1	1:B:53:TYR:CD2	2.36	0.60
1:B:99:SER:CB	1:B:127:ARG:HB2	2.07	0.60
1:A:99:SER:HB3	1:A:127:ARG:H	1.66	0.59
1:B:98:HIS:HE1	4:B:717:HOH:O	1.85	0.59
1:A:99:SER:O	1:A:125:HIS:HD2	1.86	0.59
1:A:99:SER:CB	1:A:127:ARG:HB2	2.29	0.59
1:A:123:HIS:HE1	1:A:177:HIS:H	1.50	0.59
1:B:5:LYS:N	1:B:5:LYS:CD	2.66	0.59
1:B:5:LYS:CD	1:B:5:LYS:H	2.17	0.57
1:B:125:HIS:HD2	4:B:734:HOH:O	1.87	0.57
1:B:157:ASP:OD2	1:B:167:HIS:HE1	1.87	0.57
1:A:71:ARG:NH2	1:A:160:ASN:HD21	1.98	0.56
1:B:5:LYS:HD3	4:B:776:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ASP:OD2	1:A:167:HIS:HE1	1.91	0.54
1:A:150:ILE:HD12	1:A:183:VAL:HG21	1.90	0.53
1:A:99:SER:CB	1:A:127:ARG:H	2.25	0.49
1:A:-10:GLY:HA2	1:A:60:GLY:O	2.12	0.49
1:A:150:ILE:CD1	1:A:183:VAL:HG21	2.43	0.49
1:A:147:TYR:HB3	1:A:148:PRO:HD3	1.97	0.47
1:B:139:ASP:O	1:B:140:ILE:HD13	2.14	0.47
1:B:98:HIS:HD2	1:B:99:SER:O	1.98	0.46
1:A:16:ARG:NH2	4:A:712:HOH:O	2.47	0.46
1:B:147:TYR:HB3	1:B:148:PRO:HD3	1.99	0.45
1:B:18:LYS:HB3	1:B:18:LYS:HZ3	1.82	0.45
1:A:22:LEU:CD2	4:A:836:HOH:O	2.66	0.44
1:B:95:ILE:HD11	1:B:153:GLN:HG2	2.00	0.43
1:B:40:PHE:CD1	1:B:40:PHE:C	2.96	0.43
1:B:1:MET:HE1	1:B:53:TYR:CG	2.54	0.43
1:B:5:LYS:CD	4:B:776:HOH:O	2.64	0.42
1:B:103:ALA:HB1	1:B:183:VAL:HG23	2.01	0.42
1:A:94:LYS:HD2	4:A:825:HOH:O	2.21	0.41
1:B:5:LYS:HD2	1:B:5:LYS:H	1.74	0.41
1:A:71:ARG:HA	1:A:159:LEU:HD22	2.02	0.41
1:A:-8:ASP:OD2	1:A:110:GLY:HA3	2.20	0.41
1:B:18:LYS:HB3	1:B:18:LYS:HZ2	1.85	0.41

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	185/194 (95%)	185 (100%)	0	0	100	100
1	B	181/194 (93%)	178 (98%)	3 (2%)	0	100	100
All	All	366/388 (94%)	363 (99%)	3 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	164/168 (98%)	161 (98%)	3 (2%)	51	19
1	B	159/168 (95%)	159 (100%)	0	100	100
All	All	323/336 (96%)	320 (99%)	3 (1%)	70	46

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-8	ASP
1	A	67	ASN
1	A	99	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-5	HIS
1	A	17	GLN
1	A	67	ASN
1	A	123	HIS
1	A	125	HIS
1	A	126	ASN
1	A	141	GLN
1	A	160	ASN
1	A	167	HIS
1	B	12	HIS
1	B	17	GLN
1	B	43	ASN
1	B	98	HIS
1	B	125	HIS
1	B	126	ASN
1	B	167	HIS
1	B	171	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OCS	A	111	2,1	2,7,9	0.72	0	2,8,13	4.87	2 (100%)
1	OCS	B	111	2,1	2,7,9	0.69	0	2,8,13	4.81	2 (100%)

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
1	OCS	A	111	2,1	-	1/3/6/9	-
1	OCS	B	111	2,1	-	0/3/6/9	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	OCS	OD1-SG-CB	5.48	113.24	105.35
1	B	111	OCS	OD3-SG-CB	5.21	112.85	105.35
1	B	111	OCS	OD1-SG-CB	4.37	111.64	105.35
1	A	111	OCS	OD3-SG-CB	4.17	111.35	105.35

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	111	OCS	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	GOL	B	601	-	5,5,5	1.97	2 (40%)	5,5,5	2.46	5 (100%)

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
3	GOL	B	601	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	GOL	C3-C2	-3.22	1.39	1.51
3	B	601	GOL	O2-C2	-2.35	1.36	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	601	GOL	O3-C3-C2	2.66	122.36	110.38
3	B	601	GOL	O2-C2-C3	2.63	120.08	109.18
3	B	601	GOL	C3-C2-C1	2.45	120.79	111.80
3	B	601	GOL	O2-C2-C1	2.40	119.13	109.18
3	B	601	GOL	O1-C1-C2	2.12	119.94	110.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	601	GOL	C1-C2-C3-O3
3	B	601	GOL	O1-C1-C2-O2

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

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.