

Full wwPDB X-ray Structure Validation Report (i)

Dec 25, 2023 – 12:02 AM EST

PDB ID : 1XOV

Title: The crystal structure of the listeria monocytogenes bacteriophage PSA en-

dolysin PlyPSA

Authors : Korndoerfer, I.P.; Skerra, A.

Deposited on : 2004-10-07

Resolution : 1.80 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 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:

Mol Probity : 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)

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

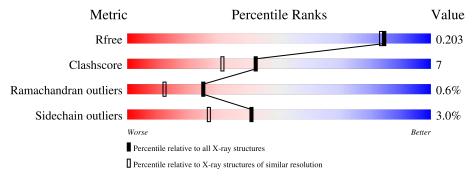
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.80 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
Wiedlie	(# Entries)	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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%

Mol	Chain	Length	Quality of chain				
1	A	326	83%	12%	.		

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:

\mathbf{Mol}	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	TRS	A	1008	-	-	X	-



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 2828 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 Ply protein.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	315	Total	С	N	О	S	0	0	0
1	Α	310	2488	1583	436	458	11	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

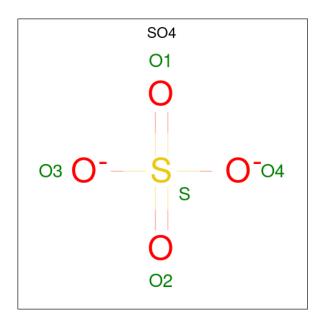
Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	ALA	-	expression tag	UNP Q8W5Y8
A	-10	SER	-	expression tag	UNP Q8W5Y8
A	-9	TRP	-	expression tag	UNP Q8W5Y8
A	-8	SER	-	expression tag	UNP Q8W5Y8
A	-7	HIS	-	expression tag	UNP Q8W5Y8
A	-6	PRO	-	expression tag	UNP Q8W5Y8
A	-5	GLN	-	expression tag	UNP Q8W5Y8
A	-4	PHE	-	expression tag	UNP Q8W5Y8
A	-3	GLU	-	expression tag	UNP Q8W5Y8
A	-2	LYS	-	expression tag	UNP Q8W5Y8
A	-1	GLY	-	expression tag	UNP Q8W5Y8
A	0	ALA	-	expression tag	UNP Q8W5Y8

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

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

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



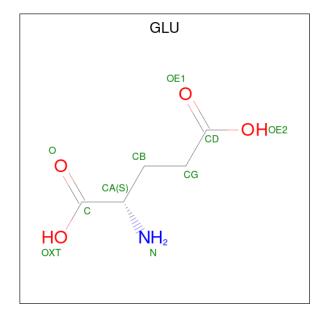


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	A	1	Total 5	O 4	S 1	0	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0

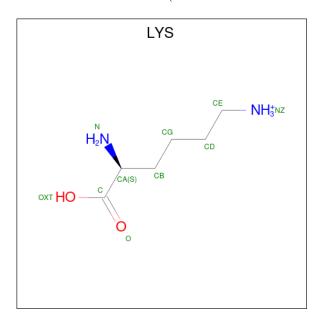
• Molecule 5 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).





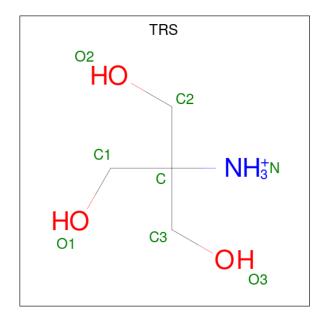
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
E	Λ	1	Total	С	N	О	0	0
)	A	1	9	5	1	3	U	0

• Molecule 6 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O 9 6 2 1	0	0

• Molecule 7 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N O 8 4 1 3	0	0

• Molecule 8 is water.

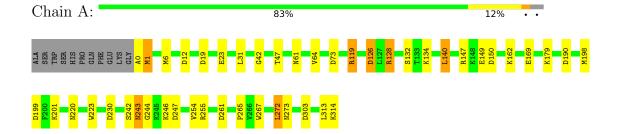
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	307	Total O 307 307	0	0



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.

• Molecule 1: Ply protein





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants	90.59Å 90.59Å 213.67Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 - 1.80	Depositor
Resolution (A)	78.45 - 1.50	EDS
% Data completeness	99.9 (25.00-1.80)	Depositor
(in resolution range)	99.9 (78.45-1.50)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	0.00 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.170 , 0.198	Depositor
R, R_{free}	0.178 , 0.203	DCC
R_{free} test set	2442 reflections (2.91%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 45.3	EDS
L-test for twinning ²	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2828	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.54% 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: CL, SO4, TRS, 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	Boı	Bond lengths		Bond angles	
Moi Cha	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.64	$1/2542 \ (0.0\%)$	0.89	$12/3422 \ (0.4\%)$	

All (1) bond length outliers are listed below:

]	Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$Ideal(\AA)$
	1	A	140	LEU	CG-CD1	-5.31	1.32	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
1	A	73	ASP	CB-CG-OD2	8.33	125.80	118.30
1	A	126	ASP	CB-CG-OD2	6.68	124.31	118.30
1	A	199	ASP	CB-CG-OD2	6.57	124.21	118.30
1	A	255	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	A	119	ARG	NE-CZ-NH1	-6.22	117.19	120.30
1	A	261	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	190	ASP	CB-CG-OD2	5.85	123.56	118.30
1	A	247	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	140	LEU	CB-CG-CD1	5.62	120.56	111.00
1	A	12	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	303	ASP	CB-CG-OD2	5.26	123.04	118.30
1	A	230	ASP	CB-CG-OD2	5.10	122.89	118.30

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	2488	0	2512	32	1
2	A	1	0	0	0	0
3	A	5	0	0	0	0
4	A	1	0	0	0	0
5	A	9	0	5	1	0
6	A	9	0	13	2	0
7	A	8	0	11	6	1
8	A	307	0	0	4	1
All	All	2828	0	2541	35	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 7.

All (35) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
1:A:119:ARG:HH12	7:A:1008:TRS:H22	1.19	1.08
1:A:147:ARG:HD2	1:A:149:GLU:OE1	1.61	1.01
1:A:119:ARG:HH22	7:A:1008:TRS:H31	1.26	0.98
7:A:1008:TRS:O2	8:A:2249:HOH:O	1.85	0.94
1:A:0:ALA:O	1:A:1:MET:HB3	1.72	0.89
6:A:2002:LYS:C	8:A:2307:HOH:O	2.12	0.87
1:A:243:ASN:C	1:A:243:ASN:HD22	1.84	0.79
1:A:198:MET:HE2	1:A:223:TRP:CD1	2.20	0.77
1:A:119:ARG:HH22	7:A:1008:TRS:C3	2.02	0.72
1:A:201:LYS:HG2	1:A:272:LEU:HD22	1.73	0.71
1:A:198:MET:CE	1:A:220:ASN:HD21	2.04	0.69
1:A:198:MET:CE	1:A:223:TRP:CD1	2.80	0.65
6:A:2002:LYS:HB2	8:A:2082:HOH:O	1.95	0.64
1:A:198:MET:HE1	1:A:220:ASN:HD21	1.64	0.62
1:A:0:ALA:O	1:A:1:MET:CB	2.47	0.62
1:A:6:MET:HE2	1:A:31:LEU:HD22	1.82	0.61
1:A:147:ARG:CD	1:A:149:GLU:OE1	2.45	0.59
1:A:162:LYS:HE3	8:A:2141:HOH:O	2.03	0.58
1:A:119:ARG:NH1	7:A:1008:TRS:H22	2.03	0.57

Continued on next page...



Continued from previous page...

Atom-1	Atom-2	Interatomic	Clash
Atom-1 Atom-2		${f distance}({ m \AA})$	overlap (Å)
1:A:313:LEU:O	1:A:314:LYS:HD3	2.06	0.55
1:A:119:ARG:NH2	7:A:1008:TRS:H31	2.09	0.54
1:A:0:ALA:HB2	1:A:42:GLY:HA3	1.90	0.54
1:A:198:MET:HE3	1:A:220:ASN:HD21	1.73	0.51
1:A:242:SER:HB2	1:A:254:VAL:HG12	1.94	0.50
1:A:64:VAL:HG11	1:A:132:SER:HB3	1.96	0.48
1:A:243:ASN:HD22	1:A:244:GLY:N	2.11	0.48
1:A:265:PRO:HG2	1:A:267:TRP:CH2	2.50	0.47
1:A:23:GLU:OE1	5:A:2001:GLU:HG2	2.14	0.46
1:A:0:ALA:HA	1:A:42:GLY:C	2.37	0.45
1:A:243:ASN:C	1:A:243:ASN:ND2	2.61	0.44
1:A:61:ASN:OD1	1:A:128:ARG:NH1	2.47	0.43
1:A:243:ASN:O	1:A:246:LYS:NZ	2.52	0.42
1:A:6:MET:O	1:A:47:THR:HA	2.20	0.41
1:A:169:GLU:OE2	1:A:179:LYS:HE3	2.20	0.41
1:A:198:MET:HE3	1:A:220:ASN:ND2	2.36	0.41

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
8:A:2070:HOH:O	8:A:2146:HOH:O[8_565]	2.04	0.16
1:A:126:ASP:OD1	1:A:126:ASP:OD1[12_545]	2.05	0.15
7:A:1008:TRS:O3	7:A:1008:TRS:O3[8_555]	2.05	0.15

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	313/326 (96%)	304 (97%)	7 (2%)	2 (1%)	25 12

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	1	MET
1	A	19	ASP

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	263/272 (97%)	256 (97%)	7 (3%)	44 31

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	ARG
1	A	134	LYS
1	A	140	LEU
1	A	150	ASP
1	A	243	ASN
1	A	272	LEU
1	A	273	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	220	ASN
1	A	243	ASN
1	A	273	ASN
1	A	310	ASN

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)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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 T	Tuno	Chain	Res	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	1002	-	4,4,4	0.32	0	6,6,6	0.91	0
6	LYS	A	2002	5	7,8,9	0.49	0	3,8,10	0.26	0
5	GLU	A	2001	6,2	7,8,9	0.97	0	4,9,11	1.00	0
7	TRS	A	1008	-	7,7,7	1.43	1 (14%)	9,9,9	1.43	2 (22%)

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
6	LYS	A	2002	5	-	2/6/7/9	-
5	GLU	A	2001	6,2	-	1/6/7/9	-
7	TRS	A	1008	-	-	6/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\textup{\AA})$	$Ideal(\AA)$
7	A	1008	TRS	O2-C2	-2.96	1.32	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
7	A	1008	TRS	O3-C3-C	-2.79	102.15	111.00
7	A	1008	TRS	O2-C2-C	2.07	117.56	111.00



There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2002	LYS	C-CA-CB-CG
7	A	1008	TRS	N-C-C1-O1
7	A	1008	TRS	C2-C-C1-O1
5	A	2001	GLU	CA-CB-CG-CD
7	A	1008	TRS	C1-C-C3-O3
7	A	1008	TRS	C3-C-C2-O2
7	A	1008	TRS	C2-C-C3-O3
7	A	1008	TRS	N-C-C3-O3
6	A	2002	LYS	CE-CD-CG-CB

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	2002	LYS	2	0
5	A	2001	GLU	1	0
7	A	1008	TRS	6	1

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

