

wwPDB X-ray Structure Validation Summary Report (i)

Oct 4, 2023 – 06:53 PM EDT

siella pneumoniae LpxH-lipid X complex

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
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7(2018)
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)	:	2.35.1

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 1.92 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.



Motria	Whole archive	Similar resolution
wietric	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)



6PH9

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 2256 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 UDP-2,3-diacylglucosamine hydrolase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	244	Total 1962	C 1250	N 356	0 346	S 10	0	7	1

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	VAL	-	insertion	UNP A0A1S0WIC1
А	241	LEU	-	expression tag	UNP A0A1S0WIC1
А	242	GLU	-	expression tag	UNP A0A1S0WIC1
А	243	GLU	-	expression tag	UNP A0A1S0WIC1
А	244	ASN	-	expression tag	UNP A0A1S0WIC1
А	245	LEU	-	expression tag	UNP A0A1S0WIC1
А	246	TYR	-	expression tag	UNP A0A1S0WIC1
А	247	PHE	-	expression tag	UNP A0A1S0WIC1
А	248	GLN	-	expression tag	UNP A0A1S0WIC1
А	249	SER	-	expression tag	UNP A0A1S0WIC1
А	250	HIS	-	expression tag	UNP A0A1S0WIC1
А	251	HIS	-	expression tag	UNP A0A1S0WIC1
А	252	HIS	-	expression tag	UNP A0A1S0WIC1
А	253	HIS	-	expression tag	UNP A0A1S0WIC1
А	254	HIS	-	expression tag	UNP A0A1S0WIC1
А	255	HIS	-	expression tag	UNP A0A1S0WIC1
А	256	HIS	-	expression tag	UNP A0A1S0WIC1
A	257	HIS	-	expression tag	UNP A0A1S0WIC1
A	258	HIS	-	expression tag	UNP A0A1S0WIC1
A	259	HIS	-	expression tag	UNP A0A1S0WIC1

There are 20 discrepancies between the modelled and reference sequences:

• Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	4	$\begin{array}{cc} \text{Total} & \text{Mn} \\ 4 & 4 \end{array}$	0	0



• Molecule 3 is (R)-((2R,3S,4R,5R,6R)-3-HYDROXY-2-(HYDROXYMETHYL)-5-((R) -3-HYDROXYTETRADECANAMIDO)-6-(PHOSPHONOOXY)TETRAHYDRO-2H-PYRAN-4-YL) 3-HYDROXYTETRADECANOATE (three-letter code: LP5) (formula: $C_{34}H_{66}NO_{12}P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	Λ	1	Total	С	Ν	Ο	Р	0	0
3	3 A	1	48	34	1	12	1	0	0

• Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total C O 13 8 5	0	0
4	А	1	Total C O 13 8 5	0	0

• Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total Ca 1 1	0	0

• Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Ato	\mathbf{ms}		ZeroOcc	AltConf
6	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	O 2	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	205	Total O 211 211	0	6

SEQUENCE-PLOTS INFOmissingINFO



3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	105.99Å 105.99 Å 52.57 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.90 - 1.92	Depositor
% Data completeness	100.0 (45.90-1.92)	Depositor
(in resolution range)	100.0 (19.50 1.52)	Depositor
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.03 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.178 , 0.199	Depositor
Wilson B-factor ($Å^2$)	35.2	Xtriage
Anisotropy	0.418	Xtriage
L-test for twinning ²	$< L >=0.50, < L^2>=0.34$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
Total number of atoms	2256	wwPDB-VP
Average B, all atoms $(Å^2)$	37.0	wwPDB-VP

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.27% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, LP5, PG4, MN, CA

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	А	0.25	0/2012	0.43	0/2738

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 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	А	1962	0	1895	2	0
2	А	4	0	0	0	0
3	А	48	0	64	0	0
4	А	26	0	36	0	0
5	А	1	0	0	0	0
6	А	4	0	6	0	0
7	А	211	0	0	1	0
All	All	2256	0	2001	2	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 0.

All (2) 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:A:120:THR:HA	1:A:126:LEU:HD11	1.97	0.46
1:A:12:GLN:NE2	7:A:401:HOH:O	2.27	0.43

There are no symmetry-related clashes.

4.3 Torsion angles (i)

4.3.1 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	А	249/260~(96%)	244 (98%)	5(2%)	0	100 100

There are no Ramachandran outliers to report.

4.3.2 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	А	197/217~(91%)	196 (100%)	1 (0%)	88 89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	204	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.



4.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and sufficient the outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

