Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 06:59 AM EDT

PDB ID	:	6MJH
Title	:	The S31N mutant of the influenza A M2 proton channel in two distinct conformational states
Authors	:	Thomaston, J.L.; DeGrado, W.F.
Deposited on	:	2018-09-20
Resolution	:	2.06 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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
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-RAY DIFFRACTION

The reported resolution of this entry is 2.06 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1666 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 Matrix protein 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	B	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	C	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	D	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	E	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	F	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	G	27	Total	C	N	O	0	0	1
			198	132	33	33			
1	H	27	Total	C	N	O	0	0	1
			198	132	33	33			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ACE	-	acetylation	UNP A0A0R5TVW3
A	47	NH2	-	amidation	UNP A0A0R5TVW3
B	21	ACE	-	acetylation	UNP A0A0R5TVW3
B	47	NH2	-	amidation	UNP A0A0R5TVW3
C	21	ACE	-	acetylation	UNP A0A0R5TVW3
C	47	NH2	-	amidation	UNP A0A0R5TVW3
D	21	ACE	-	acetylation	UNP A0A0R5TVW3
D	47	NH2	-	amidation	UNP A0A0R5TVW3
E	21	ACE	-	acetylation	UNP A0A0R5TVW3
E	47	NH2	-	amidation	UNP A0A0R5TVW3
F	21	ACE	-	acetylation	UNP A0A0R5TVW3
F	47	NH2	-	amidation	UNP A0A0R5TVW3
G	21	ACE	-	acetylation	UNP A0A0R5TVW3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	47	NH2	-	amidation	UNP A0A0R5TVW3
H	21	ACE	-	acetylation	UNP A0A0R5TVW3
H	47	NH2	-	amidation	UNP A0A0R5TVW3

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Cl 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O 7 7	0	0
4	B	10	Total O 10 10	0	0
4	C	8	Total O 8 8	0	0
4	D	10	Total O 10 10	0	0
4	E	9	Total O 9 9	0	0
4	F	11	Total O 11 11	0	0
4	G	12	Total O 12 12	0	0
4	H	10	Total O 10 10	0	0

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

3 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	36.29Å 36.15Å 76.45Å 90.00° 103.60° 90.00°	Depositor
Resolution (Å)	35.24 – 2.06	Depositor
% Data completeness (in resolution range)	90.3 (35.24-2.06)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.02 (at 2.06Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.217 , 0.248	Depositor
Wilson B-factor (Å^2)	24.9	Xtriage
Anisotropy	0.358	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	0.467 for h,-k,-h-l	Xtriage
Total number of atoms	1666	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.02 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.2161e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

4 Model quality

4.1 Standard geometry

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

4.2 Too-close contacts

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

4.3 Torsion angles

4.3.1 Protein backbone

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

4.3.2 Protein sidechains

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

4.3.3 RNA

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

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

Of 5 ligands modelled in this entry, 5 are 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.

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

5.1 Protein, DNA and RNA chains

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

5.2 Non-standard residues in protein, DNA, RNA chains

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

5.3 Carbohydrates

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

5.4 Ligands

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

5.5 Other polymers

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