Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 07:17 PM EST

PDB ID	:	3NSW
Title	:	Crystal Structure of Ancylostoma ceylanicum Excretory-Secretory Protein 2
Authors	:	Kucera, K.; Modis, Y.
Deposited on	:	2010-07-02
Resolution	:	1.75 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)	:	2.36

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 1.75 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.

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
2	MPD	A	103	X	-	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6946 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 Excretory-secretory protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	106	Total	C	N	O	S	0	6	0
			877	553	145	173	6			
1	B	106	Total	C	N	O	S	0	3	0
			863	538	144	174	7			
1	C	106	Total	C	N	O	S	0	5	0
			878	554	144	173	7			
1	D	106	Total	C	N	O	S	0	5	0
			872	547	143	176	6			
1	E	106	Total	C	N	O	S	0	4	0
			870	544	146	172	8			
1	F	106	Total	C	N	O	S	0	7	0
			890	564	146	173	7			
1	G	94	Total	C	N	O	S	0	0	0
			745	469	124	147	5			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q6R7N7
A	-2	SER	-	expression tag	UNP Q6R7N7
A	-1	HIS	-	expression tag	UNP Q6R7N7
A	0	MET	-	expression tag	UNP Q6R7N7
B	-3	GLY	-	expression tag	UNP Q6R7N7
B	-2	SER	-	expression tag	UNP Q6R7N7
B	-1	HIS	-	expression tag	UNP Q6R7N7
B	0	MET	-	expression tag	UNP Q6R7N7
C	-3	GLY	-	expression tag	UNP Q6R7N7
C	-2	SER	-	expression tag	UNP Q6R7N7
C	-1	HIS	-	expression tag	UNP Q6R7N7
C	0	MET	-	expression tag	UNP Q6R7N7
D	-3	GLY	-	expression tag	UNP Q6R7N7
D	-2	SER	-	expression tag	UNP Q6R7N7
D	-1	HIS	-	expression tag	UNP Q6R7N7

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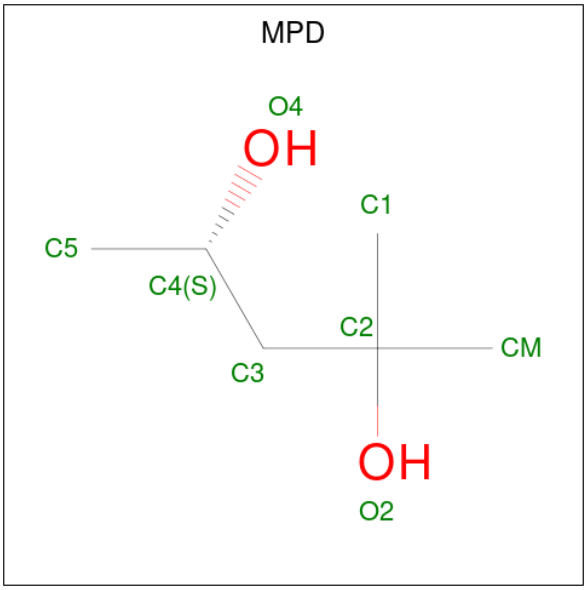
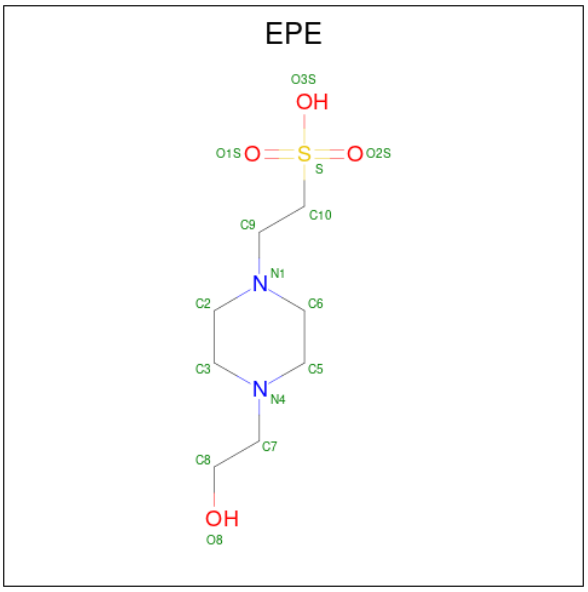
Chain	Residue	Modelled	Actual	Comment	Reference
D	0	MET	-	expression tag	UNP Q6R7N7
E	-3	GLY	-	expression tag	UNP Q6R7N7
E	-2	SER	-	expression tag	UNP Q6R7N7
E	-1	HIS	-	expression tag	UNP Q6R7N7
E	0	MET	-	expression tag	UNP Q6R7N7
F	-3	GLY	-	expression tag	UNP Q6R7N7
F	-2	SER	-	expression tag	UNP Q6R7N7
F	-1	HIS	-	expression tag	UNP Q6R7N7
F	0	MET	-	expression tag	UNP Q6R7N7
G	-3	GLY	-	expression tag	UNP Q6R7N7
G	-2	SER	-	expression tag	UNP Q6R7N7
G	-1	HIS	-	expression tag	UNP Q6R7N7
G	0	MET	-	expression tag	UNP Q6R7N7

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 8 6 2	0	0

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	148	Total	O	0	0
			148	148		
4	B	151	Total	O	0	0
			151	151		
4	C	143	Total	O	0	0
			143	143		
4	D	138	Total	O	0	0
			138	138		
4	E	109	Total	O	0	0
			109	109		
4	F	173	Total	O	0	0
			173	173		
4	G	66	Total	O	0	0
			66	66		

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 43	Depositor
Cell constants a, b, c, α, β, γ	52.21Å 52.21Å 345.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.91 – 1.75	Depositor
% Data completeness (in resolution range)	90.4 (36.91-1.75)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.80 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.146 , 0.175	Depositor
Wilson B-factor (Å^2)	26.1	Xtriage
Anisotropy	0.225	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	0.235 for h,-k,-l	Xtriage
Reported twinning fraction	0.768 for H, K, L 0.232 for -H, K, -L	Depositor
Outliers	0 of 83543 reflections	Xtriage
Total number of atoms	6946	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 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

2 ligands 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	$\#\|Z\| > 2$
3	EPE	B	103	-	15,15,15	0.81	1 (6%)	18,20,20	2.33	6 (33%)
2	MPD	A	103	-	7,7,7	0.22	0	9,10,10	0.51	0

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	EPE	B	103	-	-	8/9/19/19	0/1/1/1
2	MPD	A	103	-	1/1/2/2	1/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	103	EPE	C10-S	2.68	1.81	1.77

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	103	EPE	C5-N4-C3	6.18	122.73	108.83
3	B	103	EPE	O1S-S-C10	3.81	111.50	106.92
3	B	103	EPE	C7-N4-C5	3.15	119.30	111.23
3	B	103	EPE	C6-C5-N4	2.72	116.22	110.64
3	B	103	EPE	C7-N4-C3	2.62	117.92	111.23
3	B	103	EPE	O2S-S-C10	2.31	109.70	106.92

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	103	MPD	C4

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	103	EPE	N4-C7-C8-O8
3	B	103	EPE	C10-C9-N1-C2

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Mol	Chain	Res	Type	Atoms
3	B	103	EPE	C10-C9-N1-C6
2	A	103	MPD	C2-C3-C4-C5
3	B	103	EPE	C9-C10-S-O1S
3	B	103	EPE	S-C10-C9-N1
3	B	103	EPE	C8-C7-N4-C3
3	B	103	EPE	C8-C7-N4-C5
3	B	103	EPE	C9-C10-S-O3S

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.