

Dec 2, 2023 - 08:24 am GMT

PDB ID	:	80LO
EMDB ID	:	EMD-16960
Title	:	Murine type III Abeta fibril from ARTE10 mouse
Authors	:	Zielinski, M.; Peralta Reyes, F.S.; Gremer, L.; Schemmert, S.; Frieg, B.;
		Willuweit, A.; Donner, L.; Elvers, M.; Nilsson, L.N.G.; Syvanen, S.; Sehlin,
		D.; Ingelsson, M.; Willbold, D.; Schroeder, G.F.
Deposited on	:	2023-03-30
Resolution	:	3.50 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp 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:

EMDB validation analysis	:	0.0.1. dev 70
MolProbity	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
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: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 3.50 Å.

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

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



2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2330 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

Mol	Chain	Residues	Atoms				AltConf	Trace			
1	1 Λ	91	Total	С	Ν	Ο	S	0	0		
1 A	31	233	152	39	41	1	0	0			
1 D	D	31	Total	С	Ν	Ο	S	0	0		
	D		233	152	39	41	1	0	0		
1	В	31	Total	С	Ν	Ο	\mathbf{S}	0	0		
1		51	233	152	39	41	1	0	0		
1	1 C	31	Total	С	Ν	Ο	\mathbf{S}	0	0		
1		51	233	152	39	41	1	0	0		
1	Е	31	Total	С	Ν	Ο	\mathbf{S}	0	0		
	1 12		233	152	39	41	1				
1	F	F	F	31	Total	С	Ν	Ο	\mathbf{S}	0	0
	1	01	233	152	39	41	1	0	0		
1	G	31	Total	С	Ν	Ο	\mathbf{S}	0	0		
			233	152	39	41	1	Ŭ	0		
1	Н	31	Total	С	Ν	Ο	\mathbf{S}	0	0		
		01	233	152	39	41	1		0		
1	Ι	T	31	Total	С	Ν	Ο	\mathbf{S}	0	0	
	-		233	152	39	41	1	Ŭ			
1	J	31	Total	С	Ν	Ο	\mathbf{S}	0	0		
		01	233	152	39	41	1		Ŭ		

• Molecule 1 is a protein called Amyloid-beta protein 42.

SEQUENCE-PLOTS INFOmissingINFO



3 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-1.91°, rise=4.74 Å, axial	Depositor
	sym=C2	
Number of segments used	10369	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor



4 Model quality (i)

4.1 Standard geometry (i)

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

4.2 Too-close contacts (i)

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

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

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

4.3.2 Protein sidechains (i)

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

4.3.3 RNA (i)

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

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)

There are no ligands in this entry.

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 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-16960. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections (i)

This section was not generated.

5.2 Central slices (i)

This section was not generated.

5.3 Largest variance slices (i)

This section was not generated.

5.4 Orthogonal standard-deviation projections (False-color) (i)

This section was not generated.

5.5 Orthogonal surface views (i)

This section was not generated.

5.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.



6 Map analysis (i)

This section contains the results of statistical analysis of the map.

6.1 Map-value distribution (i)

This section was not generated.

6.2 Volume estimate versus contour level (i)

This section was not generated.

6.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum had issues being displayed.



7 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.



8 Map-model fit (i)

This section was not generated.

