



wwPDB EM Model Validation Summary Report ⓘ

Feb 26, 2020 – 01:44 PM EST

PDB ID : 6Y1A
EMDB ID : EMD-10669
Title : Amyloid fibril structure of islet amyloid polypeptide
Authors : Roeder, C.; Kupreichyk, T.; Gremer, L.; Schaefer, L.U.; Pothula, K.R.; Ravelli, R.B.G.; Willbold, D.; Hoyer, W.; Schroder, G.F.
Deposited on : 2020-02-11
Resolution : 4.20 Å(reported)

This is a wwPDB EM Model Validation Summary Report for a publicly released PDB/EMDB 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.8

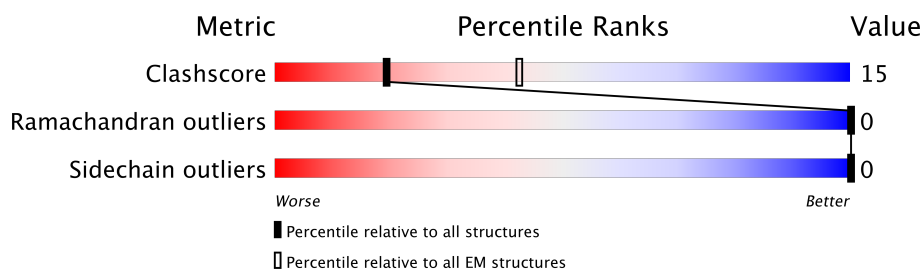
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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 (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments on the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	37	57% 11% 32%
1	B	37	59% 8% 32%
1	C	37	54% 14% 32%
1	D	37	57% 11% 32%
1	E	37	54% 14% 32%
1	F	37	54% 14% 32%
1	G	37	54% 14% 32%
1	H	37	54% 14% 32%
1	I	37	54% 14% 32%

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Mol	Chain	Length	Quality of chain
1	J	37	
1	K	37	
1	L	37	
1	M	37	
1	N	37	
1	O	37	
1	P	37	

2 Entry composition

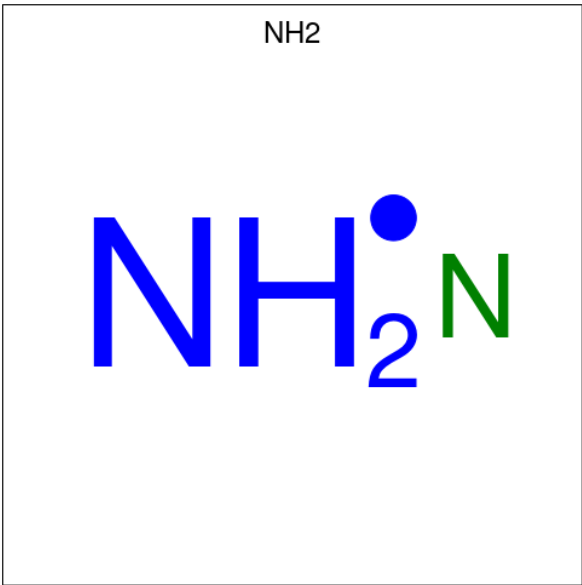
There are 2 unique types of molecules in this entry. The entry contains 2960 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

- Molecule 1 is a protein called Islet amyloid polypeptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	25	Total	C	N	O	0	0
			184	114	32	38		
1	B	25	Total	C	N	O	0	0
			184	114	32	38		
1	C	25	Total	C	N	O	0	0
			184	114	32	38		
1	D	25	Total	C	N	O	0	0
			184	114	32	38		
1	E	25	Total	C	N	O	0	0
			184	114	32	38		
1	F	25	Total	C	N	O	0	0
			184	114	32	38		
1	G	25	Total	C	N	O	0	0
			184	114	32	38		
1	H	25	Total	C	N	O	0	0
			184	114	32	38		
1	I	25	Total	C	N	O	0	0
			184	114	32	38		
1	J	25	Total	C	N	O	0	0
			184	114	32	38		
1	K	25	Total	C	N	O	0	0
			184	114	32	38		
1	L	25	Total	C	N	O	0	0
			184	114	32	38		
1	M	25	Total	C	N	O	0	0
			184	114	32	38		
1	N	25	Total	C	N	O	0	0
			184	114	32	38		
1	O	25	Total	C	N	O	0	0
			184	114	32	38		
1	P	25	Total	C	N	O	0	0
			184	114	32	38		

- Molecule 2 is AMINO GROUP (three-letter code: NH2) (formula: H₂N).



Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	N	0
			1	1	
2	B	1	Total	N	0
			1	1	
2	C	1	Total	N	0
			1	1	
2	D	1	Total	N	0
			1	1	
2	E	1	Total	N	0
			1	1	
2	F	1	Total	N	0
			1	1	
2	G	1	Total	N	0
			1	1	
2	H	1	Total	N	0
			1	1	
2	I	1	Total	N	0
			1	1	
2	J	1	Total	N	0
			1	1	
2	K	1	Total	N	0
			1	1	
2	L	1	Total	N	0
			1	1	
2	M	1	Total	N	0
			1	1	
2	N	1	Total	N	0
			1	1	

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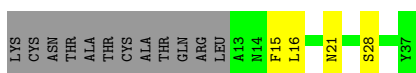
Mol	Chain	Residues	Atoms		AltConf
2	O	1	Total	N	0
			1	1	
2	P	1	Total	N	0
			1	1	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

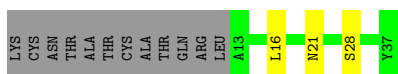
- Molecule 1: Islet amyloid polypeptide

Chain A:  57% 11% 32%



- Molecule 1: Islet amyloid polypeptide

Chain B:  59% 8% 32%



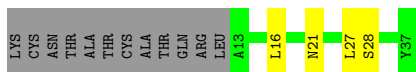
- Molecule 1: Islet amyloid polypeptide

Chain C:  54% 14% 32%



- Molecule 1: Islet amyloid polypeptide

Chain D:  57% 11% 32%



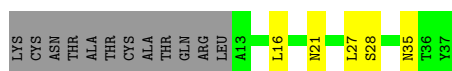
- Molecule 1: Islet amyloid polypeptide

Chain E:  54% 14% 32%



- Molecule 1: Islet amyloid polypeptide

Chain F:  54% 14% 32%



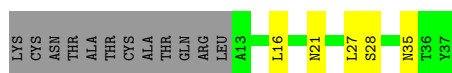
- Molecule 1: Islet amyloid polypeptide



- Molecule 1: Islet amyloid polypeptide



- Molecule 1: Islet amyloid polypeptide



- Molecule 1: Islet amyloid polypeptide



- Molecule 1: Islet amyloid polypeptide



- Molecule 1: Islet amyloid polypeptide

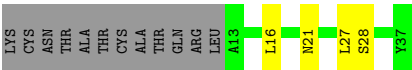


- Molecule 1: Islet amyloid polypeptide

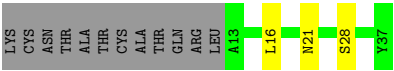




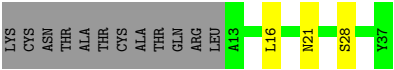
● Molecule 1: Islet amyloid polypeptide



● Molecule 1: Islet amyloid polypeptide



● Molecule 1: Islet amyloid polypeptide



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=178.23°, rise=2.351 Å, axial sym=C1	Depositor
Number of segments used	37120	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.4	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NH2

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	A	0.31	0/187	0.42	0/254
1	B	0.30	0/187	0.42	0/254
1	C	0.30	0/187	0.42	0/254
1	D	0.30	0/187	0.41	0/254
1	E	0.30	0/187	0.41	0/254
1	F	0.29	0/187	0.42	0/254
1	G	0.29	0/187	0.41	0/254
1	H	0.30	0/187	0.41	0/254
1	I	0.29	0/187	0.42	0/254
1	J	0.30	0/187	0.42	0/254
1	K	0.30	0/187	0.41	0/254
1	L	0.30	0/187	0.41	0/254
1	M	0.30	0/187	0.42	0/254
1	N	0.30	0/187	0.42	0/254
1	O	0.30	0/187	0.42	0/254
1	P	0.30	0/187	0.41	0/254
All	All	0.30	0/2992	0.42	0/4064

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	184	0	169	5	0
1	B	184	0	169	4	0
1	C	184	0	169	12	0
1	D	184	0	169	11	0
1	E	184	0	169	13	0
1	F	184	0	169	13	0
1	G	184	0	169	12	0
1	H	184	0	169	13	0
1	I	184	0	169	11	0
1	J	184	0	169	12	0
1	K	184	0	169	10	0
1	L	184	0	169	12	0
1	M	184	0	169	9	0
1	N	184	0	169	11	0
1	O	184	0	169	4	0
1	P	184	0	169	4	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
All	All	2960	0	2704	86	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 15.

The worst 5 of 86 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:L:27:LEU:HD23	1:N:27:LEU:HB3	1.67	0.77
1:D:27:LEU:HD23	1:F:27:LEU:HB3	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:27:LEU:HD23	1:J:27:LEU:HB3	1.70	0.73
1:L:27:LEU:HD22	1:N:27:LEU:HD23	1.71	0.73
1:K:27:LEU:HD23	1:M:27:LEU:HB3	1.71	0.72

There are no symmetry-related clashes.

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 PDB entries followed by that with respect to all EM entries.

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	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	B	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	C	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	D	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	E	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	F	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	G	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	H	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	I	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	J	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	K	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	L	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	M	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	N	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	O	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
1	P	23/37 (62%)	22 (96%)	1 (4%)	0	100	100
All	All	368/592 (62%)	352 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	21/31 (68%)	21 (100%)	0	100	100
1	B	21/31 (68%)	21 (100%)	0	100	100
1	C	21/31 (68%)	21 (100%)	0	100	100
1	D	21/31 (68%)	21 (100%)	0	100	100
1	E	21/31 (68%)	21 (100%)	0	100	100
1	F	21/31 (68%)	21 (100%)	0	100	100
1	G	21/31 (68%)	21 (100%)	0	100	100
1	H	21/31 (68%)	21 (100%)	0	100	100
1	I	21/31 (68%)	21 (100%)	0	100	100
1	J	21/31 (68%)	21 (100%)	0	100	100
1	K	21/31 (68%)	21 (100%)	0	100	100
1	L	21/31 (68%)	21 (100%)	0	100	100
1	M	21/31 (68%)	21 (100%)	0	100	100
1	N	21/31 (68%)	21 (100%)	0	100	100
1	O	21/31 (68%)	21 (100%)	0	100	100
1	P	21/31 (68%)	21 (100%)	0	100	100
All	All	336/496 (68%)	336 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	18	HIS
1	I	18	HIS
1	N	18	HIS

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Mol	Chain	Res	Type
1	G	18	HIS
1	M	18	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 16 are modelled with single atom - 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.

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.