



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 05:08 PM EDT

PDB ID : 6GJE  
Title : Structure of the Amnionless(20-357)-Cubilin(36-135) complex  
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Deposited on : 2018-05-16  
Resolution : 2.30 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](mailto: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>.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

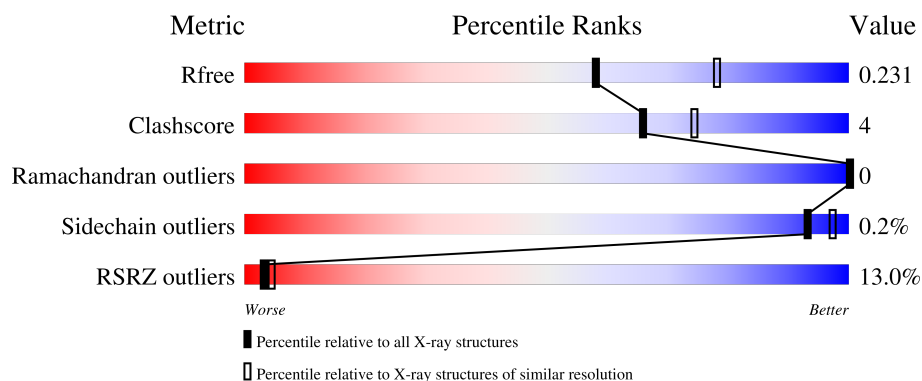
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	338	<div> <div>8%</div> <div>93%</div> <div>7%</div> </div>
2	B	110	<div> <div>16%</div> <div>62%</div> <div>12%</div> <div>•</div> <div>25%</div> </div>
2	C	110	<div> <div>14%</div> <div>67%</div> <div>8%</div> <div>25%</div> </div>
2	D	110	<div> <div>15%</div> <div>66%</div> <div>8%</div> <div>25%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4551 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 Protein amnionless.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	1	0
			2521	1573	461	472	15			

- Molecule 2 is a protein called Cubilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	82	Total	C	N	O	S	0	0	0
			642	398	113	129	2			
2	C	83	Total	C	N	O	S	0	0	0
			649	403	115	129	2			
2	D	82	Total	C	N	O	S	0	0	0
			641	397	114	128	2			

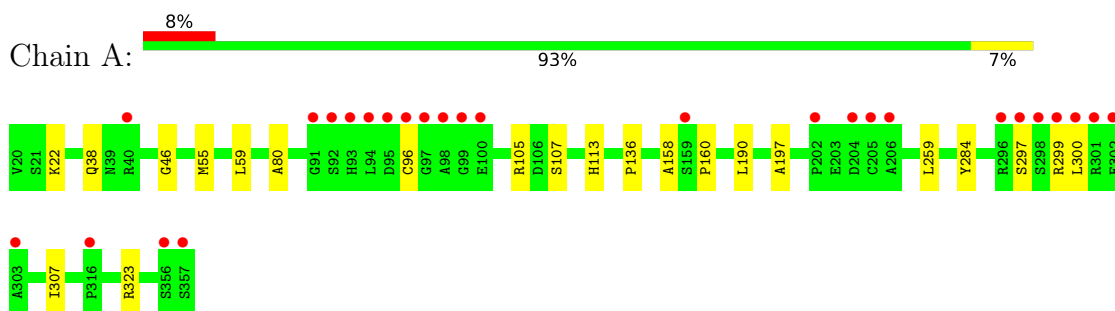
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total	O	0	0
			57	57		
3	B	17	Total	O	0	0
			17	17		
3	C	16	Total	O	0	0
			16	16		
3	D	8	Total	O	0	0
			8	8		

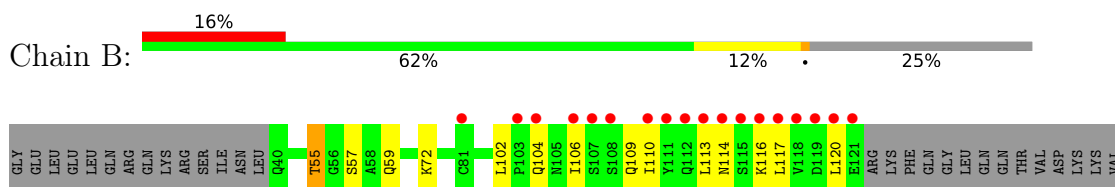
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

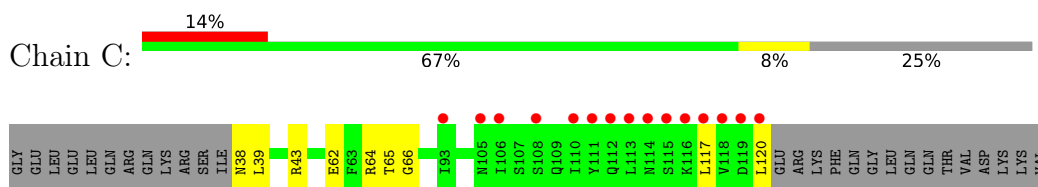
- Molecule 1: Protein amnionless



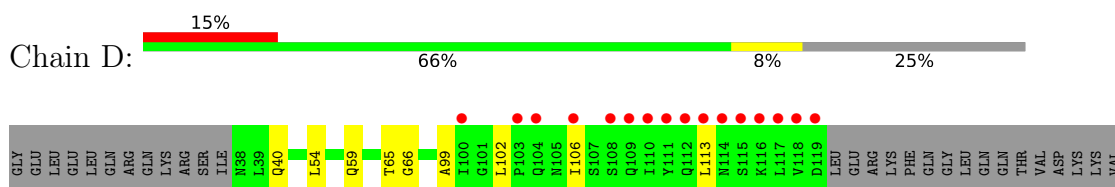
- Molecule 2: Cubilin



- Molecule 2: Cubilin



- Molecule 2: Cubilin



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.28Å 158.84Å 237.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.51 – 2.30 47.51 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.51-2.30) 99.7 (47.51-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 2.29Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.211 , 0.230 0.211 , 0.231	Depositor DCC
$R_{free}$ test set	2562 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.6	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 58.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4551	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.29	0/2585	0.52	0/3519
2	B	0.25	0/647	0.47	0/868
2	C	0.28	0/654	0.47	0/878
2	D	0.26	0/646	0.48	0/867
All	All	0.28	0/4532	0.50	0/6132

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 [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	A	2521	0	2427	12	0
2	B	642	0	652	14	0
2	C	649	0	663	10	0
2	D	641	0	652	9	0
3	A	57	0	0	1	0
3	B	17	0	0	0	0
3	C	16	0	0	2	0
3	D	8	0	0	1	0
All	All	4551	0	4394	35	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 4.

All (35) 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:107:SER:OG	3:A:501:HOH:O	1.97	0.82
2:B:113:LEU:HD13	2:D:113:LEU:HD11	1.72	0.70
2:B:114:ASN:HA	2:B:117:LEU:HG	1.74	0.68
1:A:297:SER:HB3	1:A:299:ARG:HG3	1.75	0.66
2:B:102:LEU:HD13	2:D:99:ALA:HB3	1.78	0.65
2:B:116:LYS:HD2	2:C:117:LEU:HD13	1.84	0.60
2:B:120:LEU:HD21	2:C:120:LEU:HD13	1.85	0.58
2:B:104:GLN:OE1	2:B:109:GLN:NE2	2.37	0.57
2:B:55:THR:HG22	2:D:65:THR:HA	1.85	0.57
1:A:160:PRO:HB3	1:A:197:ALA:HB3	1.87	0.56
1:A:259:LEU:HB2	1:A:307:ILE:HB	1.87	0.56
2:C:38:ASN:O	3:C:3701:HOH:O	2.18	0.55
2:C:117:LEU:HD23	2:C:120:LEU:HD12	1.88	0.54
2:C:65:THR:OG1	2:D:59:GLN:O	2.25	0.54
2:C:38:ASN:ND2	3:C:3703:HOH:O	2.39	0.53
2:D:102:LEU:HD12	2:D:106:ILE:HD11	1.91	0.53
2:C:39:LEU:O	2:C:43:ARG:NH1	2.44	0.51
2:B:72:LYS:HB2	2:C:62:GLU:HG2	1.94	0.50
2:C:64:ARG:HB2	2:D:54:LEU:HD23	1.94	0.49
2:B:106:ILE:O	2:B:110:ILE:HG13	2.13	0.47
2:B:106:ILE:HD12	2:B:109:GLN:HB2	1.97	0.47
2:D:40:GLN:NE2	3:D:3701:HOH:O	2.25	0.47
1:A:284:TYR:HE1	1:A:323:ARG:HG2	1.80	0.46
2:C:65:THR:HG23	2:C:66:GLY:O	2.16	0.46
2:B:57:SER:HA	2:D:66:GLY:HA3	1.97	0.45
1:A:113:HIS:NE2	1:A:158:ALA:HB1	2.32	0.45
1:A:59:LEU:HD11	1:A:80:ALA:HB2	1.99	0.45
1:A:38:GLN:HA	1:A:105[B]:ARG:HH22	1.82	0.45
2:B:55:THR:HG23	2:B:59:GLN:HB2	2.00	0.44
2:B:113:LEU:HD22	2:D:113:LEU:HD13	2.00	0.44
1:A:46:GLY:HA3	1:A:96:CYS:SG	2.59	0.43
2:B:110:ILE:HA	2:B:113:LEU:CD1	2.50	0.41
1:A:22:LYS:HG3	1:A:136:PRO:HA	2.03	0.41
1:A:55:MET:HG2	1:A:190:LEU:HD23	2.02	0.40
1:A:300:LEU:O	1:A:300:LEU:HD13	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	A	337/338 (100%)	321 (95%)	16 (5%)	0	100	100
2	B	80/110 (73%)	77 (96%)	3 (4%)	0	100	100
2	C	81/110 (74%)	80 (99%)	1 (1%)	0	100	100
2	D	80/110 (73%)	79 (99%)	1 (1%)	0	100	100
All	All	578/668 (86%)	557 (96%)	21 (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 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	A	262/261 (100%)	262 (100%)	0	100	100
2	B	73/99 (74%)	72 (99%)	1 (1%)	67	81
2	C	74/99 (75%)	74 (100%)	0	100	100
2	D	73/99 (74%)	73 (100%)	0	100	100
All	All	482/558 (86%)	481 (100%)	1 (0%)	93	97

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

Mol	Chain	Res	Type
2	B	55	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are



no such sidechains identified.

### 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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	338/338 (100%)	0.57	27 (7%)	12 16	47, 69, 153, 243	0
2	B	82/110 (74%)	1.85	18 (21%)	0 1	48, 66, 182, 223	0
2	C	83/110 (75%)	1.53	15 (18%)	1 1	49, 64, 195, 263	0
2	D	82/110 (74%)	1.41	16 (19%)	1 1	47, 71, 185, 214	0
All	All	585/668 (87%)	1.00	76 (12%)	3 4	47, 68, 177, 263	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	118	VAL	14.7
2	B	120	LEU	13.8
2	C	117	LEU	13.4
2	B	121	GLU	11.6
2	B	111	TYR	11.5
2	C	113	LEU	10.5
2	D	115	SER	10.4
2	D	119	ASP	10.3
1	A	300	LEU	10.3
2	B	117	LEU	9.7
2	C	120	LEU	9.3
2	C	118	VAL	9.1
2	C	119	ASP	8.8
1	A	302	GLU	8.5
2	B	118	VAL	8.4
2	D	110	ILE	8.3
2	B	113	LEU	8.0
2	B	119	ASP	8.0
2	C	111	TYR	7.8
2	D	117	LEU	7.2
1	A	357	SER	7.2

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Mol	Chain	Res	Type	RSRZ
2	B	115	SER	7.0
2	B	112	GLN	7.0
1	A	96	CYS	6.9
2	D	114	ASN	6.5
1	A	92	SER	6.4
1	A	301	ARG	6.4
1	A	94	LEU	6.2
2	D	103	PRO	6.2
1	A	98	ALA	6.1
2	C	116	LYS	5.9
1	A	299	ARG	5.9
1	A	297	SER	5.6
2	B	108	SER	5.5
2	C	115	SER	5.3
2	D	104	GLN	5.1
2	B	114	ASN	5.0
2	D	111	TYR	5.0
2	D	106	ILE	4.9
1	A	93	HIS	4.9
1	A	99	GLY	4.7
2	B	104	GLN	4.7
2	D	116	LYS	4.6
2	D	112	GLN	4.5
2	D	113	LEU	4.5
1	A	303	ALA	4.5
2	D	109	GLN	4.5
1	A	316	PRO	4.4
2	C	110	ILE	4.3
1	A	298	SER	4.1
1	A	356	SER	4.1
1	A	97	GLY	3.8
2	C	114	ASN	3.8
2	C	105	ASN	3.7
2	C	106	ILE	3.7
2	B	107	SER	3.6
1	A	91	GLY	3.6
2	C	112	GLN	3.5
2	B	110	ILE	3.5
2	D	108	SER	3.1
2	B	106	ILE	3.0
1	A	159	SER	2.9
1	A	204	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	95	ASP	2.8
1	A	202	PRO	2.7
2	B	116	LYS	2.6
2	C	108	SER	2.5
1	A	296	ARG	2.5
1	A	100	GLU	2.4
2	B	103	PRO	2.3
2	D	100	ILE	2.3
1	A	40	ARG	2.3
2	C	93	ILE	2.3
2	B	81	CYS	2.1
1	A	205	CYS	2.1
1	A	206	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.