



wwPDB EM Validation Summary Report ⓘ

May 31, 2026 – 12:20 AM JST

PDB ID : 9J95 / pdb_00009j95
EMDB ID : EMD-61253
Title : Native GluA1/GluA4-CNIH3 complex in desensitized state
Authors : Li, X.; Li, R.; Wei, Y.; Zhao, Y.
Deposited on : 2024-08-22
Resolution : 4.26 Å(reported)

This is a wwPDB EM Validation Summary 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 ⓘ 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:

EMDB validation analysis	: FAILED
MolProbity	: 4-5-2 with Phenix2.0
Percentile statistics	: 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	: NOT EXECUTED
MapQ	: FAILED
Ideal geometry (proteins)	: Engh & Huber (2001)
Ideal geometry (DNA, RNA)	: Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: 2.49

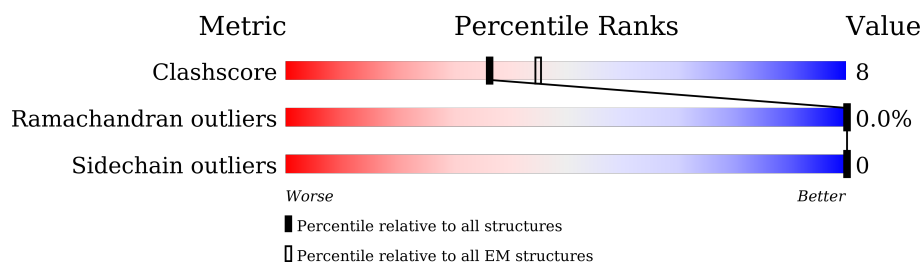
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.26 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 of 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	906	36% 7% 57%
1	C	906	36% 8% 57%
2	B	884	37% 8% 55%
2	D	884	36% 9% 55%
3	E	159	67% 10% 23%
3	F	159	58% 19% 23%
3	G	159	68% 9% 23%
3	H	159	51% 26% 23%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16528 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 Glutamate receptor.

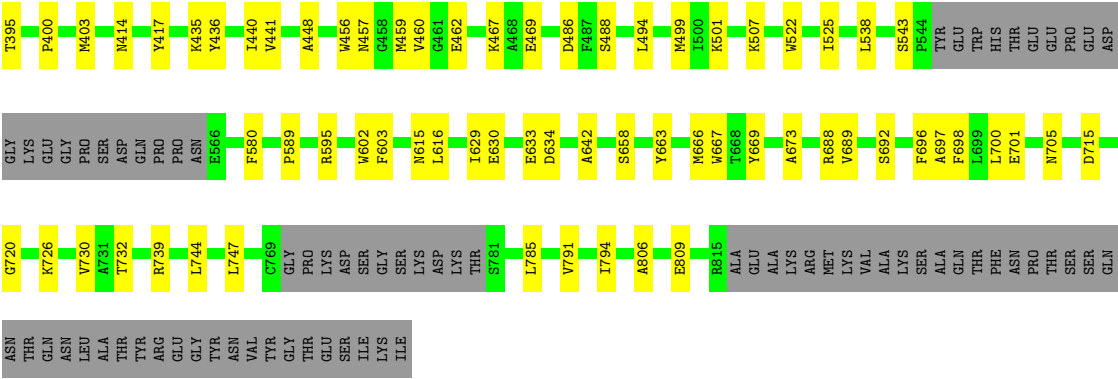
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	394	Total	C	N	O	S	0	0
			3097	2014	500	564	19		
1	C	394	Total	C	N	O	S	2	0
			3107	2019	502	566	20		

- Molecule 2 is a protein called Glutamate receptor.

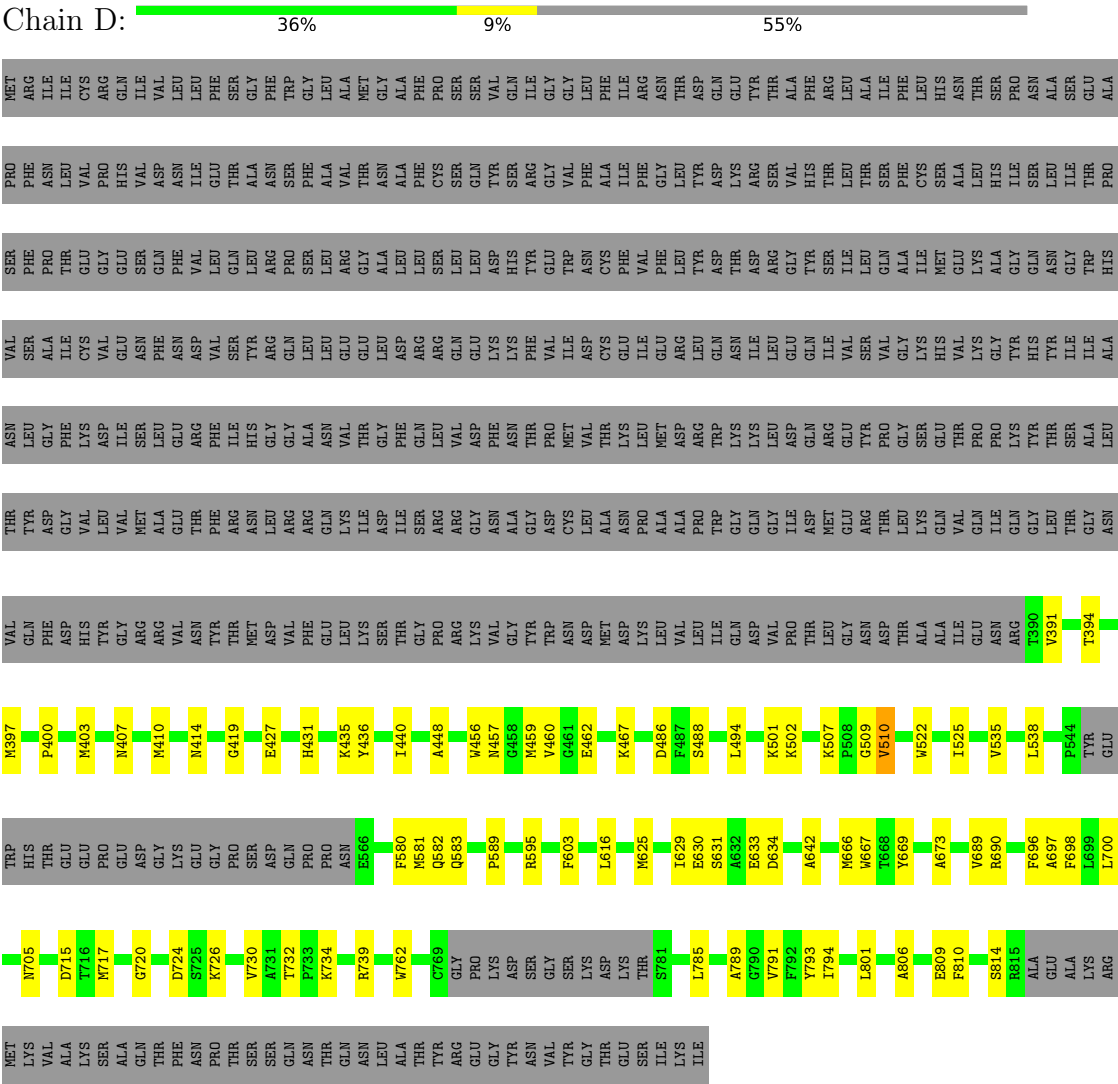
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3086	2010	497	559	20		
2	D	394	Total	C	N	O	S	0	0
			3086	2010	497	559	20		

- Molecule 3 is a protein called Cornichon family AMPA receptor auxiliary protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	122	Total	C	N	O	S	0	0
			1038	714	153	159	12		
3	F	122	Total	C	N	O	S	0	0
			1038	714	153	159	12		
3	G	122	Total	C	N	O	S	0	0
			1038	714	153	159	12		
3	H	122	Total	C	N	O	S	0	0
			1038	714	153	159	12		

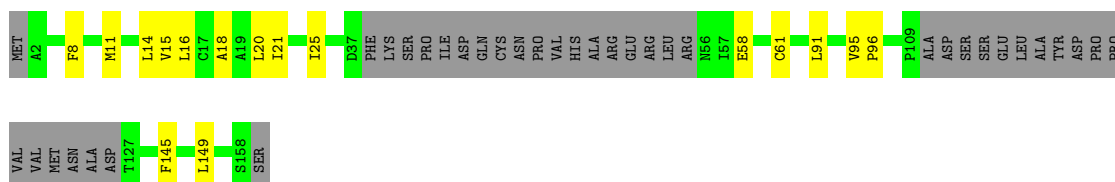


● Molecule 2: Glutamate receptor



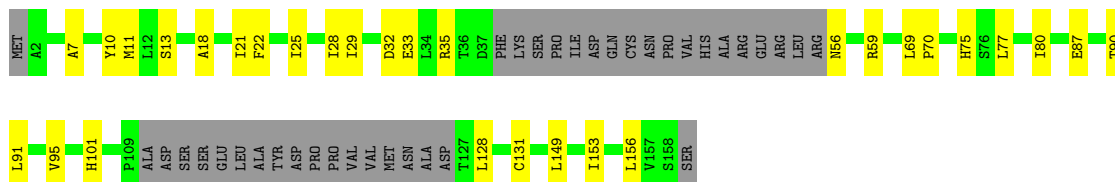
● Molecule 3: Cornichon family AMPA receptor auxiliary protein 3





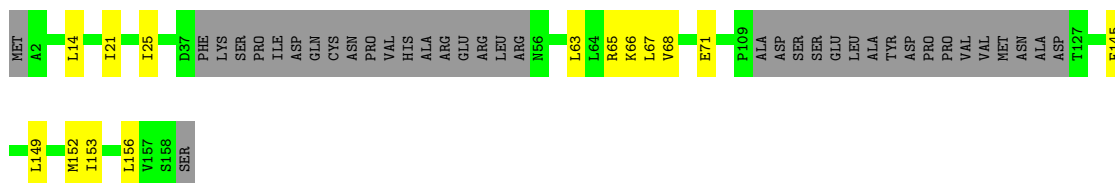
• Molecule 3: Cornichon family AMPA receptor auxiliary protein 3

Chain F: 58% 19% 23%



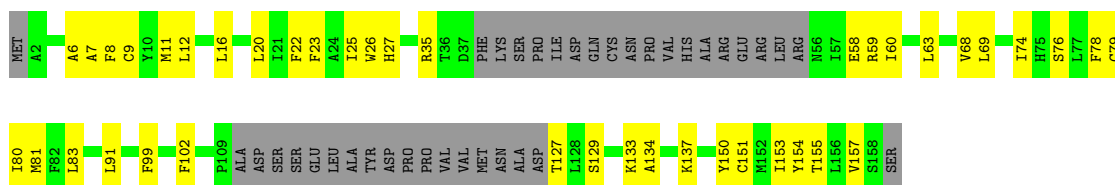
• Molecule 3: Cornichon family AMPA receptor auxiliary protein 3

Chain G: 68% 9% 23%



• Molecule 3: Cornichon family AMPA receptor auxiliary protein 3

Chain H: 51% 26% 23%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20638	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor

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	0.13	0/3166	0.28	0/4275
1	C	0.14	0/3176	0.29	0/4288
2	B	0.15	0/3155	0.31	0/4259
2	D	0.18	0/3155	0.34	0/4259
3	E	0.16	0/1075	0.31	0/1460
3	F	0.15	0/1075	0.32	0/1460
3	G	0.12	0/1075	0.28	0/1460
3	H	0.26	0/1075	0.49	0/1460
All	All	0.16	0/16952	0.32	0/22921

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	3097	0	3131	52	0
1	C	3107	0	3138	44	0
2	B	3086	0	3137	46	0
2	D	3086	0	3137	56	0
3	E	1038	0	1029	12	0
3	F	1038	0	1029	18	0
3	G	1038	0	1029	11	0
3	H	1038	0	1029	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	16528	0	16659	254	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 8.

The worst 5 of 254 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)
3:F:32:ASP:OD1	3:F:33:GLU:N	2.15	0.79
1:A:409:ASN:OD1	1:A:410:GLN:N	2.15	0.78
2:B:494:LEU:CD1	2:B:701:GLU:OE1	2.35	0.75
2:B:494:LEU:HD13	2:B:701:GLU:OE1	1.86	0.74
1:C:409:ASN:OD1	1:C:410:GLN:N	2.23	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	388/906 (43%)	374 (96%)	14 (4%)	0	100	100
1	C	390/906 (43%)	378 (97%)	12 (3%)	0	100	100
2	B	388/884 (44%)	373 (96%)	15 (4%)	0	100	100
2	D	388/884 (44%)	367 (95%)	20 (5%)	1 (0%)	36	71
3	E	116/159 (73%)	114 (98%)	2 (2%)	0	100	100
3	F	116/159 (73%)	114 (98%)	2 (2%)	0	100	100
3	G	116/159 (73%)	114 (98%)	2 (2%)	0	100	100
3	H	116/159 (73%)	113 (97%)	3 (3%)	0	100	100
All	All	2018/4216 (48%)	1947 (96%)	70 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	510	VAL

5.3.2 Protein sidechains [i](#)

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	332/769 (43%)	332 (100%)	0	100	100
1	C	333/769 (43%)	333 (100%)	0	100	100
2	B	333/757 (44%)	333 (100%)	0	100	100
2	D	333/757 (44%)	333 (100%)	0	100	100
3	E	111/144 (77%)	111 (100%)	0	100	100
3	F	111/144 (77%)	111 (100%)	0	100	100
3	G	111/144 (77%)	111 (100%)	0	100	100
3	H	111/144 (77%)	111 (100%)	0	100	100
All	All	1775/3628 (49%)	1775 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	F	132	GLN
3	H	101	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 oligosaccharides 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.