



Full wwPDB EM Validation Report ⓘ

May 31, 2026 – 12:10 AM JST

PDB ID : 9X58 / pdb_00009x58
EMDB ID : EMD-66577
Title : The GluA4-ATD in Complex with the 1D8-Fab
Authors : Li, X.; Li, R.; Wei, Y.; Zhao, Y.
Deposited on : 2025-10-12
Resolution : 3.20 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 ⓘ 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

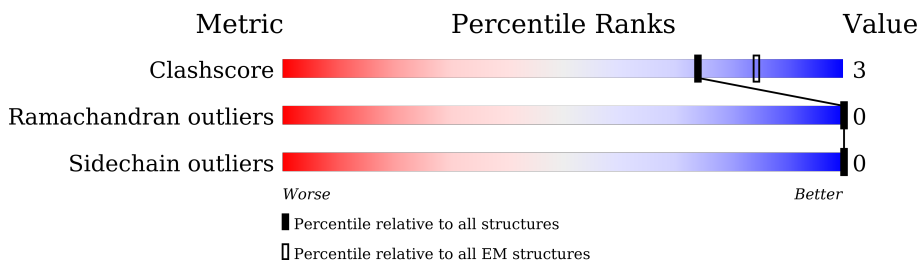
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

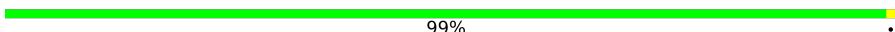
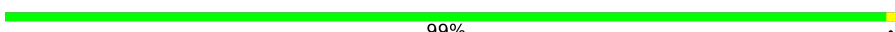
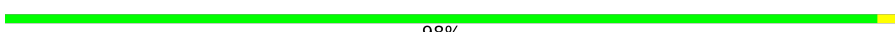
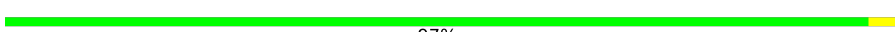
The reported resolution of this entry is 3.20 Å.

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	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	381	 88% 11% .
1	B	381	 88% 10% .
2	D	216	 99% .
2	L	216	 99% .
3	C	217	 98% .
3	H	217	 97% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10386 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 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	377	Total	C	N	O	S	0	0
			3028	1931	528	556	13		
1	B	377	Total	C	N	O	S	0	0
			3028	1931	528	556	13		

- Molecule 2 is a protein called Light Chain of 1D8 Fab.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	L	216	Total	C	N	O	0	0
			1080	648	216	216		
2	D	216	Total	C	N	O	0	0
			1080	648	216	216		

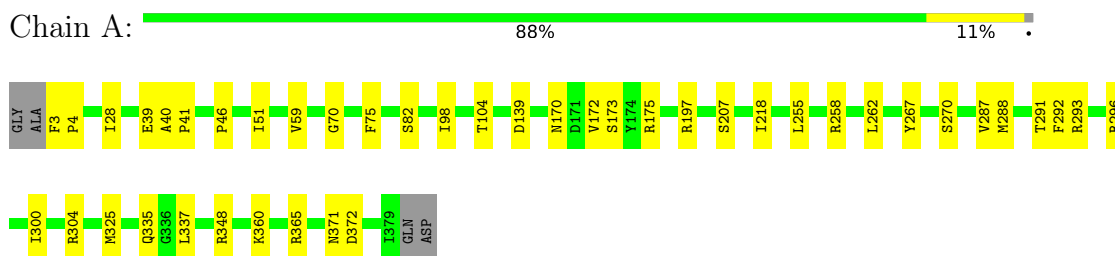
- Molecule 3 is a protein called Heavy Chain of 1D8 Fab.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	217	Total	C	N	O	0	0
			1085	651	217	217		
3	H	217	Total	C	N	O	0	0
			1085	651	217	217		

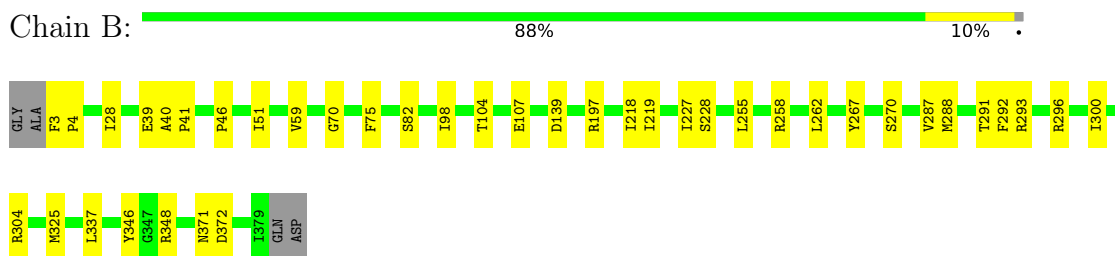
3 Residue-property plots [i](#)

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. 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.

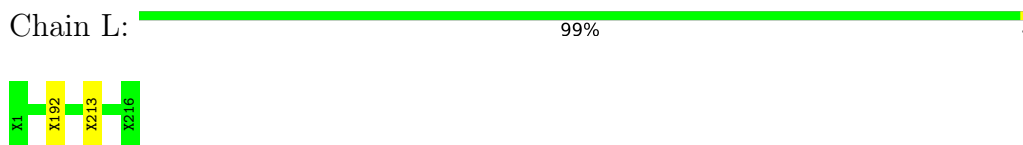
- Molecule 1: Glutamate receptor 4



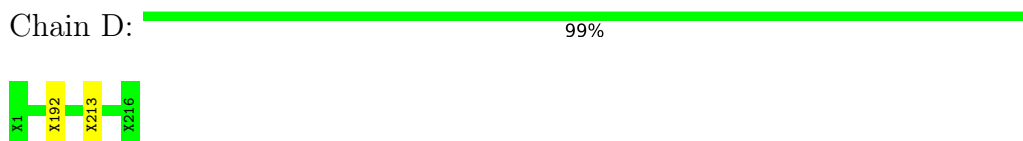
- Molecule 1: Glutamate receptor 4



- Molecule 2: Light Chain of 1D8 Fab

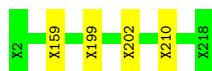


- Molecule 2: Light Chain of 1D8 Fab



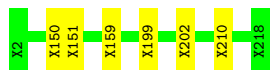
- Molecule 3: Heavy Chain of 1D8 Fab





- Molecule 3: Heavy Chain of 1D8 Fab

Chain H:  97% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	182287	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 BIOQUANTUM (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	0.21	0/3099	0.38	0/4197
1	B	0.20	0/3099	0.39	0/4197
All	All	0.21	0/6198	0.39	0/8394

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	3028	0	2974	25	0
1	B	3028	0	2974	23	0
2	D	1080	0	231	1	0
2	L	1080	0	232	1	0
3	C	1085	0	240	2	0
3	H	1085	0	241	3	0
All	All	10386	0	6892	55	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 3.

All (55) 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:B:139:ASP:OD2	1:B:197:ARG:NH1	2.22	0.73
1:A:139:ASP:OD2	1:A:197:ARG:NH1	2.21	0.73
3:H:202:UNK:O	3:H:210:UNK:HA	1.99	0.63
3:C:202:UNK:O	3:C:210:UNK:HA	2.00	0.62
1:B:75:PHE:HB2	1:B:288:MET:HE1	1.87	0.57
1:A:360:LYS:HD2	1:A:365:ARG:HD3	1.85	0.56
1:B:39:GLU:OE1	1:B:293:ARG:NE	2.41	0.54
1:A:300:ILE:O	1:A:300:ILE:HG22	2.08	0.53
1:A:39:GLU:OE1	1:A:293:ARG:NE	2.41	0.53
1:B:300:ILE:HG22	1:B:300:ILE:O	2.08	0.53
1:A:75:PHE:HB2	1:A:288:MET:HE1	1.89	0.53
1:A:70:GLY:HA2	1:A:304:ARG:NH1	2.24	0.53
1:A:267:TYR:O	1:A:270:SER:OG	2.26	0.52
1:B:28:ILE:HD13	1:B:46:PRO:HG3	1.92	0.52
1:B:267:TYR:O	1:B:270:SER:OG	2.25	0.52
1:B:107:GLU:HG3	1:B:346:TYR:HE2	1.75	0.51
1:A:28:ILE:HD13	1:A:46:PRO:HG3	1.92	0.51
1:B:70:GLY:HA2	1:B:304:ARG:NH1	2.26	0.50
1:A:287:VAL:O	1:A:291:THR:HG22	2.11	0.50
1:B:292:PHE:CE1	1:B:325:MET:HE1	2.47	0.50
1:A:292:PHE:CE1	1:A:325:MET:HE1	2.47	0.49
1:A:255:LEU:HD22	1:A:337:LEU:HD11	1.94	0.49
1:B:287:VAL:O	1:B:291:THR:HG22	2.12	0.49
1:A:40:ALA:N	1:A:41:PRO:HD2	2.28	0.49
1:B:40:ALA:N	1:B:41:PRO:HD2	2.27	0.49
1:A:3:PHE:N	1:A:296:ARG:HH11	2.12	0.48
1:B:3:PHE:N	1:B:296:ARG:HH11	2.12	0.48
1:B:255:LEU:HD22	1:B:337:LEU:HD11	1.94	0.48
1:B:371:ASN:OD1	1:B:372:ASP:N	2.46	0.47
1:A:104:THR:O	1:A:348:ARG:NH1	2.50	0.45
1:B:98:ILE:HD13	1:B:288:MET:HE2	1.98	0.45
1:A:98:ILE:HD13	1:A:288:MET:HE2	1.99	0.44
1:B:4:PRO:HD2	1:B:296:ARG:NH1	2.33	0.44
1:A:4:PRO:HD2	1:A:296:ARG:NH1	2.33	0.44
1:A:371:ASN:OD1	1:A:372:ASP:N	2.49	0.44
3:C:159:UNK:N	3:C:199:UNK:O	2.51	0.44
1:A:170:ASN:H	1:A:173:SER:HB2	1.82	0.44
1:B:104:THR:O	1:B:348:ARG:NH1	2.51	0.43
2:D:192:UNK:O	2:D:213:UNK:N	2.52	0.43
3:H:159:UNK:N	3:H:199:UNK:O	2.51	0.43
3:H:150:UNK:HA	3:H:151:UNK:HA	1.63	0.43
2:L:192:UNK:O	2:L:213:UNK:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:VAL:HG21	1:A:82:SER:OG	2.20	0.42
1:B:218:ILE:O	1:B:218:ILE:HG22	2.19	0.42
1:A:218:ILE:HG22	1:A:218:ILE:O	2.19	0.42
1:A:258:ARG:O	1:A:262:LEU:HD23	2.20	0.42
1:A:51:ILE:HD12	1:A:51:ILE:HA	1.90	0.42
1:A:175:ARG:NH2	1:A:207:SER:OG	2.53	0.41
1:B:59:VAL:HG21	1:B:82:SER:OG	2.20	0.41
1:A:170:ASN:HB3	1:A:172:VAL:H	1.85	0.41
1:A:335:GLN:HE21	1:A:335:GLN:HB3	1.76	0.41
1:B:51:ILE:HD12	1:B:51:ILE:HA	1.86	0.40
1:B:219:ILE:O	1:B:219:ILE:HG13	2.20	0.40
1:B:227:ILE:HG22	1:B:228:SER:N	2.37	0.40
1:B:258:ARG:O	1:B:262:LEU:HD23	2.22	0.40

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	375/381 (98%)	336 (90%)	39 (10%)	0	100	100
1	B	375/381 (98%)	339 (90%)	36 (10%)	0	100	100
All	All	750/762 (98%)	675 (90%)	75 (10%)	0	100	100

There are no Ramachandran outliers to report.

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	329/332 (99%)	329 (100%)	0	100	100
1	B	329/332 (99%)	329 (100%)	0	100	100
All	All	658/664 (99%)	658 (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 (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
1	A	128	HIS
1	A	157	ASN
1	A	176	GLN
1	B	128	HIS
1	B	148	GLN
1	B	160	HIS
1	B	176	GLN
1	B	340	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.