



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 12:01 pm GMT

PDB ID : 4YKK  
Title : Mnemiopsis leidyi ML032222a iGluR LBD D-serine complex  
Authors : Alberstein, R.G.; Mayer, M.L.  
Deposited on : 2015-03-04  
Resolution : 1.38 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

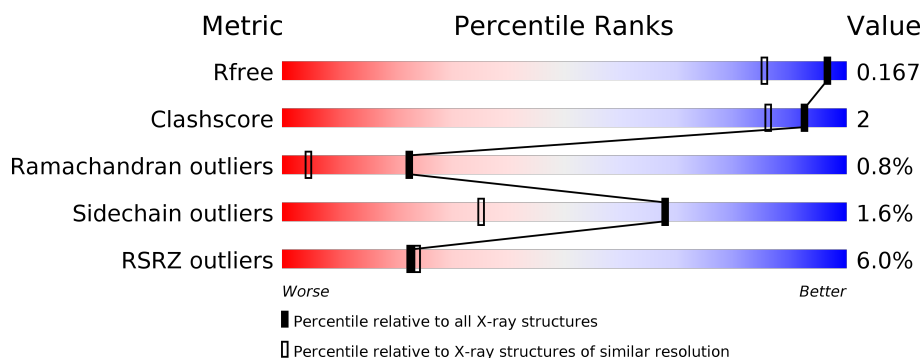
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.38 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))
$R_{free}$	100719	2133 (1.40-1.36)
Clashscore	112137	2266 (1.40-1.36)
Ramachandran outliers	110173	2215 (1.40-1.36)
Sidechain outliers	110143	2214 (1.40-1.36)
RSRZ outliers	101464	2141 (1.40-1.36)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	256	<div> <div>7%</div> <div>91%</div> <div>5%</div> <div>.</div> </div>
1	B	256	<div> <div>5%</div> <div>93%</div> <div>7%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DSN	B	301[A]	-	-	-	X
4	GLY	B	302[B]	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9055 atoms, of which 4070 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.

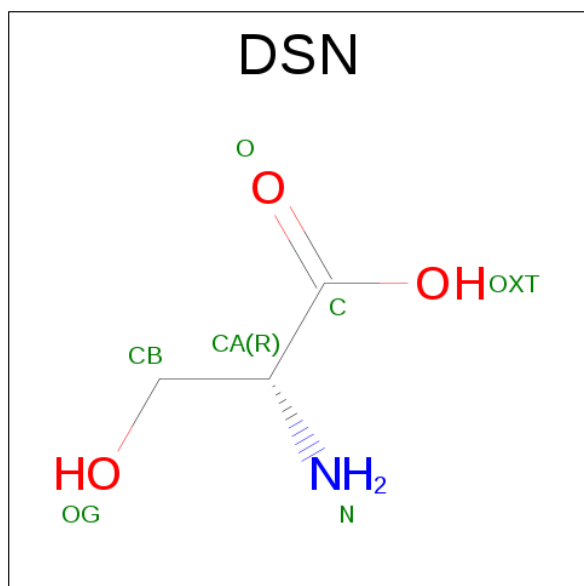
- Molecule 1 is a protein called ML032222a iGluR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	247	Total	C	H	N	O	S	0	19	0
			4031	1297	1983	339	403	9			
1	B	255	Total	C	H	N	O	S	0	27	0
			4209	1347	2075	355	422	10			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is D-SERINE (three-letter code: DSN) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>3</sub>).



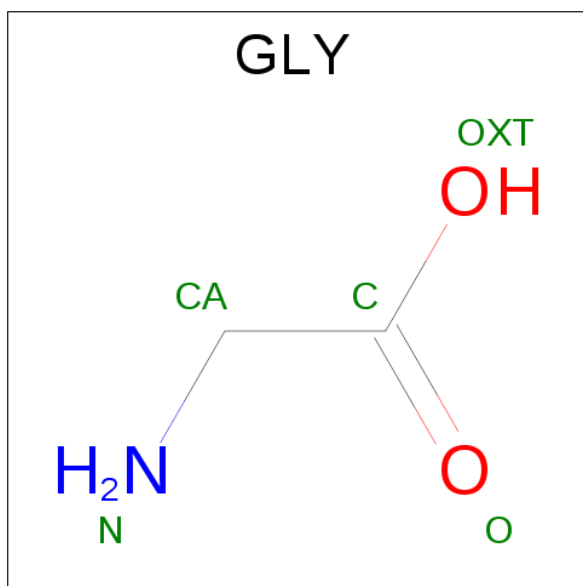
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	1
			13	3	6	1	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	0	1
			13	3	6	1	3		

- Molecule 4 is GLYCINE (three-letter code: GLY) (formula:  $C_2H_5NO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	1
			5	2	1	2		
4	B	1	Total	C	N	O	0	1
			5	2	1	2		

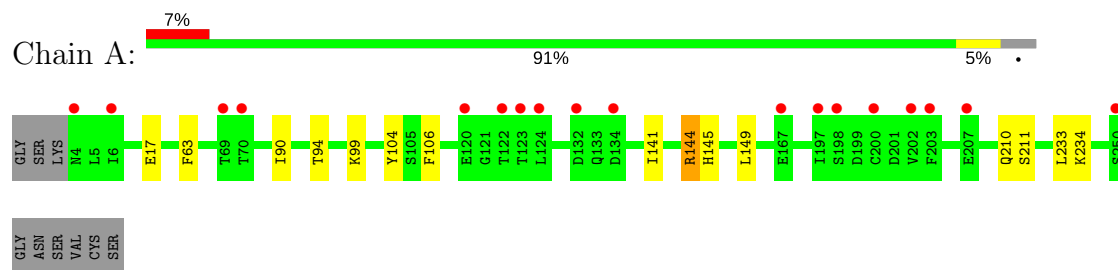
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	339	Total	O	0	5
			339	339		
5	B	439	Total	O	0	3
			439	439		

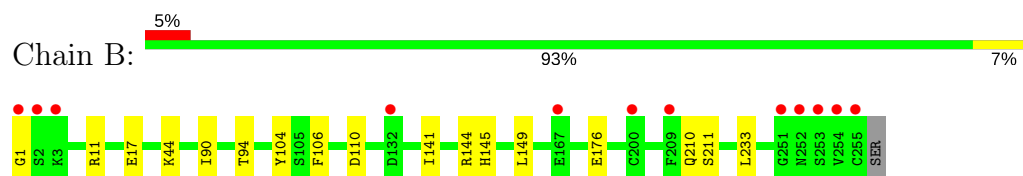
### 3 Residue-property plots [i](#)

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 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: ML032222a iGluR



#### • Molecule 1: ML032222a iGluR



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.95Å 123.75Å 54.51Å 90.00° 111.78° 90.00°	Depositor
Resolution (Å)	35.13 – 1.38 35.13 – 1.38	Depositor EDS
% Data completeness (in resolution range)	99.4 (35.13-1.38) 99.4 (35.13-1.38)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 1.38Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.144 , 0.167 0.144 , 0.167	Depositor DCC
$R_{free}$ test set	5806 reflections (5.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	11.6	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 50.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9055	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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](#)

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

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	0.40	0/2165	0.61	0/2921
1	B	0.47	0/2281	0.65	0/3073
All	All	0.44	0/4446	0.63	0/5994

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	2048	1983	1904	6	0
1	B	2134	2075	1967	8	0
2	A	1	0	0	0	0
3	A	7	6	6	1	0
3	B	7	6	6	1	0
4	A	5	0	2	0	0
4	B	5	0	2	0	0
5	A	339	0	0	1	0
5	B	439	0	0	4	1
All	All	4985	4070	3887	15	1

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 2.

All (15) 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:44[B]:LYS:NZ	5:B:401:HOH:O	2.28	0.64
1:A:141:ILE:HB	1:A:144:ARG:HD3	1.86	0.58
1:B:1:GLY:N	5:B:748:HOH:O	2.39	0.52
1:B:141:ILE:HB	1:B:144:ARG:HD3	1.96	0.48
1:A:145:HIS:CE1	1:A:149:LEU:HG	2.49	0.48
1:A:234[A]:LYS:NZ	5:A:732:HOH:O	2.48	0.46
1:A:63:PHE:CE2	3:A:302[A]:DSN:HA	2.50	0.46
1:A:94:THR:HA	1:A:104:TYR:CZ	2.51	0.45
1:B:94:THR:HA	1:B:104:TYR:CZ	2.51	0.45
1:B:145:HIS:CE1	1:B:149:LEU:HG	2.54	0.43
1:B:110[A]:ASP:OD1	5:B:597:HOH:O	2.21	0.43
1:B:106:PHE:CZ	1:B:233:LEU:HD13	2.54	0.42
1:A:106:PHE:CZ	1:A:233:LEU:HD13	2.53	0.42
1:B:176[A]:GLU:HG2	5:B:640:HOH:O	2.20	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:464:HOH:O	5:B:483:HOH:O[1_556]	2.19	0.01

## 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 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	264/256 (103%)	259 (98%)	3 (1%)	2 (1%)	22	5
1	B	280/256 (109%)	272 (97%)	6 (2%)	2 (1%)	25	6
All	All	544/512 (106%)	531 (98%)	9 (2%)	4 (1%)	22	6

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	GLN
1	B	210	GLN
1	A	90	ILE
1	B	90	ILE

### 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 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	233/224 (104%)	228 (98%)	5 (2%)	59	23
1	B	246/224 (110%)	243 (99%)	3 (1%)	75	48
All	All	479/448 (107%)	471 (98%)	8 (2%)	68	32

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	GLU
1	A	99[A]	LYS
1	A	99[B]	LYS
1	A	144	ARG
1	A	211	SER
1	B	11	ARG
1	B	17	GLU
1	B	211	SER

Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	DSN	A	302[A]	-	2,6,6	0.25	0	1,7,7	0.03	0
4	GLY	A	303[B]	-	1,4,4	0.44	0	0,4,4	0.00	-
3	DSN	B	301[A]	-	2,6,6	0.21	0	1,7,7	0.06	0
4	GLY	B	302[B]	-	1,4,4	0.47	0	0,4,4	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DSN	A	302[A]	-	-	0/2/6/6	0/0/0/0
4	GLY	A	303[B]	-	-	0/0/2/2	0/0/0/0
3	DSN	B	301[A]	-	-	0/2/6/6	0/0/0/0
4	GLY	B	302[B]	-	-	0/0/2/2	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302[A]	DSN	1	0
3	B	301[A]	DSN	1	0

## 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	247/256 (96%)	0.15	18 (7%) 16 17	8, 16, 38, 52	0
1	B	255/256 (99%)	0.02	12 (4%) 32 34	6, 13, 30, 95	0
All	All	502/512 (98%)	0.08	30 (5%) 23 24	6, 14, 36, 95	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	254	VAL	11.5
1	B	252	ASN	10.0
1	B	1	GLY	8.5
1	B	2	SER	8.3
1	B	255	CYS	5.9
1	B	253	SER	5.8
1	A	197	ILE	5.3
1	B	251[A]	GLY	5.1
1	A	69	THR	4.5
1	A	124	LEU	4.3
1	A	250	SER	4.3
1	A	122	THR	4.2
1	A	123	THR	3.9
1	A	198	SER	3.7
1	A	4	ASN	3.3
1	B	3	LYS	3.2
1	A	70	THR	3.1
1	A	207	GLU	3.1
1	B	209	PHE	3.0
1	A	202	VAL	2.9
1	A	203	PHE	2.8
1	A	120	GLU	2.7
1	B	167	GLU	2.5
1	B	132	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	132	ASP	2.4
1	B	200	CYS	2.4
1	A	134	ASP	2.3
1	A	200	CYS	2.2
1	A	6	ILE	2.2
1	A	167	GLU	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	DSN	B	301[A]	7/7	0.99	0.10	2.23	7,9,12,14	13
4	GLY	B	302[B]	5/5	0.99	0.10	2.01	7,8,9,11	5
3	DSN	A	302[A]	7/7	0.99	0.09	0.32	8,11,18,18	13
4	GLY	A	303[B]	5/5	0.99	0.09	0.23	8,9,11,11	5
2	MG	A	301	1/1	0.92	0.10	-0.76	24,24,24,24	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.